

501

```

201 TATCCGTCAG GGTTCGAGG AAGGCGGCAA AACGTCCGAA CAGGGCGGTT
251 TGGTTCACGT CGGCATACCA CGCGCTGACC CCCTGCCACA TCGGATTGCC
301 GCCTTCGGGC AGCATCCAGC CCAATATCAT GCGTTCTACC GCCTGCTTCC
351 AGGTGAACAG CTGATCCGTG CCGCCGCGCA TTTCTCCGTC CAAACCCAG
401 CGGACGTTCA AATCGGCAAC CATGTCGTGC AAAAGCGGCA AATCGTCTC
451 AGTCAGTCCG AAATGGCGCA ACACGGGCGC GGTTCCTAAA AGCACAAGCA
501 CTTTATCGAC TTCAAATCGG CTTTCCAACA AGTCGAACAG GCATGACAAA
551 GCATGAAACA GCGGTTGTCG GCGGCTGATT TTCACATCCG AAACGGAATA
601 CGGCAATGCC TCGCGCCCGG GCTGCGCCTG TCCGAACACG GCTTCGATAA
651 AAGGCGTATA GGATTGCATA TTCGGGGTTA A

```

This corresponds to the amino acid sequence <SEQ ID 768; ORF 217.a>:

```

a217.pep
  1 VADDGVQRQL SGKLRQFGFR LPFDPFVFEEA LDCLLVIAFD LEQCFKQIPA
 51 TRHFPVNRRL LPPYPYNIRQ GFEEGGKTSE QGGLVHVIGIP RADPLPHRIA
101 AFGQHPAQYH AFYRLLPGEQ LIRAAAHFSV QTPADVQIGN HVVQKRQIVL
151 SQSEMAQHGR GF*KHKHFID FKSAFQQVEQ A*QSMKQRLS AADFHIRNGI
201 RQCLRAGLRL SEHGFDKRR I GFDIRG*

```

m217/a217 90.3% identity in 226 aa overlap

	10	20	30	40	50	60
m217.pep	MADDGVRRLSGKLRQFGFR	LPFDPFVFEEA	LDCLLVIAFD	LEQCFKQIPA	TRHFPVNRRL	ADPDRCG
a217	VADDGVQRQLSGKLRQFGFR	LPFDPFVFEEA	LDCLLVIAFD	LEQCFKQIPA	TRHFPVNRRL	ADPDRCG
	70	80	90	100	110	120
m217.pep	LPPYPYNIRQGFEEGGKTSE	HGGLVHVIGIP	RADPLPHRIA	AFGQHPAQYH	AFYRLLPGEQ	
a217	LPPYPYNIRQGFEEGGKTSE	HGGLVHVIGIP	RADPLPHRIA	AFGQHPAQYH	AFYRLLPGEQ	
	130	140	150	160	170	180
m217.pep	LIRAAAHFSVQTPVDVQIGN	HVVQKRQIVLSQSE	TAQHGRGFXKHKHFID	FKSAFQQVEQ		
a217	LIRAAAHFSVQTPADVQIGN	HVVQKRQIVLSQSE	MAQHGRGFXKHKHFID	FKSAFQQVEQ		
	190	200	210	220		
m217.pep	AXQSMKQRLAAADFHVXHGIR	QCLRTGLRLSEHGFDKRRIG	FDIRGX			
a217	AXQSMKQRLSAAADFHIRNGIR	QCLRAGLRLSEHGFDKRRIG	FDIRGX			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 769>:

```

g218.seq
  1 atggttgccg tggatcctta tacggcaaaa gtggtaaca ccatgccgcg
 51 caatcagggg tggatcacca ctatggatga aatccacggc gatatgatgc
101 tcggtgcggc aggcgattat cttttggaaa cggcagcttc actgaccatt
151 attatgggtg tcagcggcgt gtacctttgg tgggcgaaac agcgcggcat
201 taaagcgatg ctgctgccgc caaaaagcag ggcgcgttct tgggtggcgga
251 atctgcacgg cgcgtttgga acttgggtgt cgttgatttt actgttggtc
301 tgcctgtcgg gtattgcttg ggcaggtatt tggggcgga aattcgtgca
351 ggcttggaat cagttcccgg ccggcaaatg ggggtgcgaa ccgaaccccg
401 tttcaatcgt gccgaccac gccgaggtat tgaatgacgg caagggttaag
451 gaagtgccgt ggattttgga gcttatgcct atgcctgtct cagggacgac
501 tgtgggtgaa aacggcatta accccaccga gcccataaac attggaaacc
551 gtcgaccgtt tcgcgcggga aatcggtttc aaagggcggt atcagttgaa
601 tttgcccataa ggcgaggacg ggggtatggac tttgtcgag gattctatga
651 gttatga

```

This corresponds to the amino acid sequence <SEQ ID 770; ORF 218.ng>:

```

g218.pep
  1 MVAVDPYTAK VVNTMPRNQG WYHTMDEIHG DMMLGAAGDY LLETAASLTI

```

51 IMVVSGLYLW WAKQRGIKAM LLPPKSRARS WWRNLHGAFG TWVSLILLLF
 101 CLSGIAWAGI WGGKFVQAWN QFPAGKWGVE PNPVSIVPTH GEVLNDGKVK
 151 EVPWILELMP MPVSGTTVGE NGINPTEPNN IGNNRPFRAG NRFQRLSVE
 201 FAQRRGRGMD FVAGFYEL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 771>:

m218.seq

1 ATGGTCGCGG TCGATCCTTA TACGGCAAAA GTGGTCAGTA CCATGCCGCG
 51 CAATCAGGGT TGGTATTACA CGATGGATGA AATCCACAGC GATATGATGC
 101 TCGGTGCGGC AGGCGATTAT CTTTGGAAA CGGCAGCTTC ACTGACCATT
 151 ATTATGGTTG TCAGCGGCTT GTACCTTTGG TGGGTGAAAC GGCGCGGCAT
 201 CAAGCGATG CTGCTGCCGT CAAAAGGCAr GGCGCGTTCT TGGTGGCGGA
 251 ATCTGCACGG CACGTTTGA ACTTGGGTGT CGTTGATTTT GCTGTTGTTC
 301 TGCTGTGCGG GTATTGCTTG GGCGGGTATT TGGGGCGGCA AGTTCGTACA
 351 GGCTTGGAGT CAGTTCCTTG CCGGTAAATG GGGTGTGCGA CCGAACCCCG
 401 TTTCAGTCGT GCCGACCCAC GGCGAGGTAT TGAATGACGG CAAGGTTAAG
 451 GAAGTGCCGT GGGTTTGA GCTTACGCCT ATGCCTGTTT CAGGGACGaC
 501 yGtgGGCAA GACGGCATT ACCCTGACGA GCCGATGACA TTGGAAACCG
 551 TCGACCGCTT TGC GCGnGA AATCGGTTT AAAGGGCGTT ATCAGTTGAA
 601 TTTGCCCCAA GGCGAGGACG GCGTATGGAC TTTGTCGCAG GATTCTATGA
 651 GTTA

This corresponds to the amino acid sequence <SEQ ID 772; ORF 218>:

m218.pep

1 MVAVDPYTAK VVSTMPRNQG WYYTMDEIHS DMMLGAAGDY LLETAASLTI
 51 IMVVSGLYLW WVKRRGIKAM LLPSKGXARS WWRNLHGTFG TWVSLILLLF
 101 CLSGIAWAGI WGGKFVQAWS QFPAGKWGVE PNPVSIVPTH GEVLNDGKVK
 151 EVPWVLELTP MPVSGTTVGK DGINPDEPMT LETVDRFARX NRFQRLSVE
 201 FAQRRGRMD FVAGFYEL

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 218 shows 87.2% identity over a 218 aa overlap with a predicted ORF (ORF 218.ng) from *N. gonorrhoeae*:

m218/g218

	10	20	30	40	50	60
m218.pep	MVAVDPYTAKVVSTMPRNQGWYYTMDEIHS DMMLGAAGDY LLETAASLTI IMVVSGLYLW					
	: : : :					
g218	MVAVDPYTAKVVNTMPRNQGWYHTMDEIHG DMMLGAAGDY LLETAASLTI IMVVSGLYLW					
	10	20	30	40	50	60
70	80	90	100	110	120	
m218.pep	WVKRRGIKAMLLPSKGXARSWWRNLHGTFGTWVSLILLLFCLSGIAWAGIWGGKFVQAWS					
	: : : : : :					
g218	WAKQRGIKAMLLPPKSRARSWWRNLHGAFGTWVSLILLLFCLSGIAWAGIWGGKFVQAWN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m218.pep	QFPAGKWGVEPNPVSIVPTHGEVLNDGKVKVPWPVLELTPMPVSGTTVGKDGINPDEPMT					
	: : : :					
g218	QFPAGKWGVEPNPVSIVPTHGEVLNDGKVKVPWILELMPMPVSGTTVGENGINPTEPNN					
	130	140	150	160	170	180
	190	200	210			
m218.pep	LETVDRFARXNRFQRLSVEFAQRRGRMD FVAGFYEL					
	: :					
g218	IGNRRPFRAGNRFQRLSVEFAQRRGRMD FVAGFYEL					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 773>:

a218.seq

```

1 ATGGTCGCGG TCGATCCTTA TACGGCAAAA GTGGTCAGTA CCATGCCGCG
51 CAATCAGGGT TGGTATTACG CGATGGATGA AATCCACAGC GATATGATGC
101 TCGGTTTCGAC AGGTGATTAT CTTTGGAAA CGGCTGCATC GCTGACGATT
151 ATCATGATAA TCAGCGGTTT GTACCTTTGG TGGGTGAAAC GGCGCGGCAT
201 CAAGGCGATG CTGCTGCCGC CAAAAGGCAG GGCGCGTTCT TGGTGGCGGA
251 ATCTGCACGG CGCGTTTGGA ACTTGGGTGT CGTTGATTTT ACTGTTGTTC
301 TGCCTGTCGG GTATTGCTTG GGCAGGTATT TGGGGCGGCA AGTTCGTGCA
351 GGCTTGGAGT CAGTTCCTCG CAGGCAAATG GGGTGTGCGA CCGAACCCTG
401 TTTCACTCGT GCCGACCCAC GGCGAGGTAT TGAATGACGG CAAGGTTAAG
451 GAAGTGCCGT GGGTTTTGGA GCTTACGCCT ATGCCTGTTT CAGGGACGAC
501 TGTGGGCAAA GACGGTATTA ACCCTGACGA GCCGATGACA TTGGAACCG
551 TCGACCGTTT TGCGCGG.GA AATCGGTTTC AAAGGGCGTT ATCAGCTGAA
601 TTTGCCCAAA GGCGAGGACG GCGTATGGAC TTTGTGCGAG GATTCTATGA
651 GTTA

```

This corresponds to the amino acid sequence <SEQ ID 774; ORF 218.a>:

a218.pep

```

1 MVAVDPYTAK VVSTMPRNQG WYYAMDEIHS DMMLGSTGDY LLETAASLTI
51 IMIISGLYLW WVKRRGIKAM LLPPKGRARS WWRNLHGAFG TWVSLILLLF
101 CLSGIAWAGI WGGKFVQAWS QFPAGKWGVE PNPVSVVPTH GEVLNDGKVK
151 EVPWVLELTP MPVSGTTVGK DGINPDEPMT LETVDRFARX NRFQRALSAE
201 FAQRRGRMD FVAGFYEL

```

m218/a218 95.9% identity in 218 aa overlap

m218.pep	10	20	30	40	50	60
	MVAVDPYTAKVVSTMPRNQGWYYTMDDEIHS DMMLGAAGDYLLETAASLTIIMVVSGLYLW					
a218	: : : : :					
	10	20	30	40	50	60
	MVAVDPYTAKVVSTMPRNQGWYYAMDEIHS DMMLGSTGDYLLETAASLTIIMIISGLYLW					
	70	80	90	100	110	120
m218.pep	WVKRRGIKAMLLPSKGXARSWWRNLHGTFGTWVSLILLLFCLSGIAWAGIWGGKFVQAWS					
a218	: : : : :					
	70	80	90	100	110	120
	WVKRRGIKAMLLPPKGRARSWWRNLHGAFGTWVSLILLLFCLSGIAWAGIWGGKFVQAWS					
	130	140	150	160	170	180
m218.pep	QFPAGKWGVEPNPVSVVPTHGEVLNDGKVKVPEVPWVLELTPMPVSGTTVGKDGINPDEPMT					
a218	: : : : :					
	130	140	150	160	170	180
	QFPAGKWGVEPNPVSVVPTHGEVLNDGKVKVPEVPWVLELTPMPVSGTTVGKDGINPDEPMT					
	190	200	210			
m218.pep	LETVDRFARXNRFQALSAEFAQRRGRMD FVAGFYEL					
a218	: : : : :					
	LETVDRFARXNRFQALSAEFAQRRGRMD FVAGFYEL					
	190	200	210			

This corresponds to the amino acid sequence <SEQ ID 776; ORF 219.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 777>:

This corresponds to the amino acid sequence <SEQ ID 778; ORF 219>:

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 219 shows 86.9% identity over a 213 aa overlap with a predicted ORF (ORF 219.ng) from *N. gonorrhoeae*:

[illegible]

505

	70	80	90	100	110	120
	130	140	150	160	170	180
m219.pep	LGWWSVL	ANVLFCL	AVIFIGIS	GCVMWVK	RRTGAVG	IVPPAQK
g219	LGWWSVL	ANVVFCL	AVIFIGIS	GCVMWVK	RPSGAVG	IVPPAQK
	130	140	150	160	170	180
	190	200	210			
m219.pep	ALLFPTS	LLAIAVI	WLLDTLL	LSRIPVL	RRLRWFK	X
g219	ALLFPTA	LLAIAVI	WLLDTLL	LSRIPVL	RRLRWFK	X
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 779>:

```

a219.seq
1  ATGACGGCAA GGTAAAGGAA GTGCCGTGGG TTTTGGAGCT TACGCCTATG
51  CCTGTTTCAG GGACGACTGT GGGCAAAGAC GGTATTAACC CTGACGAGCC
101 GATGACATTG GAAACCGTCG ACCGTTTTCG GCGG.GAAAT CGGTTTCAAA
151 GGGCGTTATC AGCTGAATTT GCCCAAAGGC GAGGACGGCG TATGGACTTT
201 GTCGCAGGAT TCTATGAGTT ACGACATGAT CAGCCCGTTT GCTGACCGCA
251 CGGTGCATAT CGACCAGTAC AGCGGCAAGA TTCTTGCCGA CATCCGTTTT
301 GACGATTACA ACCCGTTCGG CAAATTTATG GCGGCAAGCA TTGCGCTGCA
351 TATGGGGACT TTGGGCTGGT GGAGCGTGTG GCGGAACGTT TTGTTCTGCC
401 TTGCCGTGAT TTTTATCGGC ATCAGCGGCT GCGTGATGTG GTGGAAACGC
451 CGTCCGTCCG GCGCGGTGGG CATGGTTCCG CCGGCGCAAA AAATCAAGCT
501 GCCCGTCTGG TGGGCAATGG CGGTGCCGCT GCTGCTGATT GCATTGCTTT
551 TCCCGACCGC GTTGCTTGCC ATTGCCGTGA TTTGGCTGTT GGATACGCTG
601 CTGTTGTCGC GGATTCTCTG TTTGAGGAGA TGGTTTAAAT GA
  
```

This corresponds to the amino acid sequence <SEQ ID 780; ORF 219.a>:

```

a219.pep
1  MTARLRKCRG FWSLRCLCFQ GRLWAKTVLT LTSR*HWKPS TVLRXEIGFK
51  GRYQLNLPKG EDGVWTLSDQ SMSYDMISPF ADRTVHIDQY SGKILADIRF
101 DDYNPFGKFM AASIALHMGT LGWWSVLANV LFCLAVIFIG ISGCVMWWRK
151 RPSGAVGMVP PAQKIKLPVW WAMAVPLLLI ALLFPTALLA IAVIWLLDTL
201 LLSRIPVLRR WFK*
  
```

m219/a219 94.8% identity in 213 aa overlap

	10	20	30	40	50	60
m219.pep	MTARLRKCRG	FWSLRCLCFQ	GRXWAKTAL	TLTSRXHWK	PSTALRGEI	GFKGRYQLN
a219	MTARLRKCRG	FWSLRCLCFQ	GRXWAKTAL	TLTSRXHWK	PSTVLRXEI	GFKGRYQLN
	10	20	30	40	50	60
	70	80	90	100	110	120
m219.pep	EDGVWTLSD	QSMSYDMIS	PFADRTVHI	DQYSGKILA	DIREDDYNP	FGKFMAASIA
a219	EDGVWTLSD	QSMSYDMIS	PFADRTVHI	DQYSGKILA	DIREDDYNP	FGKFMAASIA
	70	80	90	100	110	120
	130	140	150	160	170	180
m219.pep	LGWWSVL	ANVLFCL	AVIFIGIS	GCVMWVK	RRTGAVG	IVPPAQK
a219	LGWWSVL	ANVLFCL	AVIFIGIS	GCVMWVK	RPSGAVG	IVPPAQK
	130	140	150	160	170	180
	190	200	210			
m219.pep	ALLFPTS	LLAIAVI	WLLDTLL	LSRIPVL	RRLRWFK	X
a219	ALLFPTA	LLAIAVI	WLLDTLL	LSRIPVL	RRLRWFK	X
	190	200	210			

This corresponds to the amino acid sequence <SEQ ID 782; ORF 221.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 783>:

This corresponds to the amino acid sequence <SEQ ID 784; ORF 221>:

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 221 shows 87.6% identity over a 170 aa overlap with a predicted ORF (ORF 221.ng) from *N. gonorrhoeae*:

m221/g221

		10	20	30	40	50
m221.pep		MXVLMXRSLVRQAVNQIDADGFEP	RFARRIDDFGFFVTLD	DAVDRRLHFGVE		
		: :		:		:
g221		MHDHGAMDRRLPAFGSLMRR	VNXIDADGFEPCLTGGIDDFGFF	VALDAVD	CRLHFGVE	
		10	20	30	40	50
		60	70	80	90	100
m221.pep		ILNADAHAVEAESAEHEDGVAAD	FARVDFDGVFAGGD	XLEMFAYHAEDT	FDLFVAQKGA-	
				:	:	
g221		ILNADAHAVEAESAEHEDGVAAD	FARVDFDGI	FAGRYQFEMFADHAEDT	FDLFVAQKGR	
		70	80	90	100	110
		120	130	140	150	160
		170				

507

```

m221.pep    CPAEVQLGKLVPSVQMWSEQFHFFFKIFDVGIGAAAFVFGDDFVAAAVVADGVAERNVNVK
             |||||||
g221        AAAEVQLGKLVPSVQMWSEQFHFFFKIFDVGIGAAAFVFGDDFVAAAVVADGVAERNVNVK
             130      140      150      160      170      180

m221.pep    GKRFBX
             |||||
g221        GKRFBX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 785>:

```

a221.seq
1   ATGGTGGTTT TGATGCTCCG AAGTCTGGTG CGGCAGGCCG TAAATCAAAT
51  CGACGCTGAC GGATTTGAAC CCCGCTTCGC GCGCCGCATC GATGACTTCT
101 TTGGTTTCTT CGTAACTTTG GATGCGGTTG ACCGCCGCCT GCACTTTGGG
151 GTCGAAATCC TGAATGCCGA TGCTCATGCG GTTGAAGCCG AGTCTGCCGA
201 GCATGAGGAC GGTGTCGCGG CTGACTTTGC GCGGGTCGAT TTCGATGGAG
251 TATTCGCCGG TGGGGATTAA CTCGAAATGT TTGCGTATCA TCGGGAAGAC
301 ACGTTTCGATT TGGTCGTCGC TCAAAAAGGT CGCGTGCCG CCGCCGAAGT
351 GCAGTTGGGC AAGCTGGTGC CGTCCGTTCA GATGTGGAGC GAGCAGTTCC
401 ATTTCTTTTT CAAGAAATTC GATGTAGGCA TCGCGCGCGC TTTTGTCTTT
451 GGTGATGATT TTGTTGCAGC CGCAGTAGTA GCAGATGGTG TTGCAGAACG
501 GAATGTGAAT GTAAAGGGAA AGCGTTTGT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 786; ORF 221.a>:

```

a221.pep
1   MVVLMRLSLV RQAVNQIDAD GFEPRFARRI DDFGFFVTL DAVDRRLHFG
51  VEILNADAHA VEAESAHEHED GVAADFARVD FDGVFAGGD* LEMFAYHAED
101 TFDLVVAQKG RRAAAEVQLG KLVPSVQMW S EQFHFFFKF DVGIGAAAFV
151 GDDFVAAAVV ADGVAERNVN VKGKRFBV*

```

m221/a221 95.5% identity in 177 aa overlap

```

               10      20      30      40      50      60
m221.pep      MXVLMXRSLVRQAVNQIDADGFEPFRARRIDDFGFFVTLDAVDRRLHFGVEILNADAHA
               | | | | |
a221          MVVLMRLSLVRQAVNQIDADGFEPFRARRIDDFGFFVTLDAVDRRLHFGVEILNADAHA
               10      20      30      40      50      60

               70      80      90      100     110     119
m221.pep      VEAESAHEHEDGVAADFARVDFDGVFAGGD*LEMFAYHAEDTFDLFVAQKGA-CPAEVQLG
               | | | | |
a221          VEAESAHEHEDGVAADFARVDFDGVFAGGD*LEMFAYHAEDTFDLVVAQKGRRAAAEVQLG
               70      80      90      100     110     120

120      130      140      150      160      170
m221.pep      KLVPSVQMWSEQFHFFFKIFDVGIGAAAFVFGDDFVAAAVVADGVAERNVNVKGRFBX
               | | | | |
a221          KLVPSVQMWSEQFHFFFKIFDVGIGAAAFVFGDDFVAAAVVADGVAERNVNVKGRFBX
               130      140      150      160      170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 787>:

```

g223.seq
1   atggaattca ggcaccaggt agtggtagtt ggtgtcgaac catttggtca
51  ttctgatggc gaattggtct ttgttgccgc gcgccagttg gaagaattgt
101 tccaaaggca ggttttggct atcgaagccg aaacgggagg gaatcgcgcc
151 cgtggatact tgcaggtcga ggatgtgatg gtagaaagtg aaatcacgta
201 cagcaacgta atcagcggtt ggagcagctt ggtgtttcca gtttttctcg
251 cgcaggtctt tggcaacgtc gagcagctct tgttactga tctctttgcg
301 ccagtatttt tcttgggcga atttcaattc acggaaggcg ccgacacgcg
351 ggaagcctga

```

This corresponds to the amino acid sequence <SEQ ID 788; ORF 223.ng>:

g223.pep..

```
m223.seq
  1  GTGGAATTCA  GGCACCAAGT  AGTGGTAGTT  GGTGTCGAAC  CATTTGGTCA
 51  TTTTCGATAG  GAATTTGGTCT  TTGTTACCGC  CGGCCAGTTG  GAAGAATTGT
101  TCCAAAGACA  GGTTTTGGCT  GTCGAAGCCG  AAGCGGGCGG  GAATCGCGCT
151  GGTGCGCACT  TGCAGGTCGA  GGATGTGGTC  GTAGAAAGTG  AAATCsCTAC
201  GGCAACGAAA  TCGGCGTTGG  CAGCGACCTG  GTGTTTCCAG  TTTTCTCGC
251  GCAAGTCTTT  AGCAACAGCC  AGCAATTCTT  GCTCGCTGAT  TTCTTTGCGC
301  CAGTATTTTT  CTTGTGCGAA  TTTCAATTCT  CGGAAGGCGC  CGACACGCGG
351  GAAGCCTGA
```

```
m223.pep
  1  VEFRHQVVVV  GVEPFGHFDS  ELVFVTARQL  EELFQRQVLA  VEA EAGGNRA
 51  GGD LQVEDVV  VESEIXY GNE  IGVGSDLVFP  VFLAQVFSNS  QQFL LADFFA
101  PVFELCEFOF  AEGADTREA*
```

ORF 223 shows 80.7% identity over a 119 aa overlap with a predicted ORF (ORF 223.ng) from *N. gonorrhoeae*:

m223/g223

	10	20	30	40	50	60
m223.pep	VEFRHQVVVVGVPEFGHFDSELVFTARQLEELFQRQVLAVEAEAGGNRAGGDLQVEDVV					
g223	MEFRHQVVVVGVPEFGHFDGELVFVAARQLEELFQRQVLAEAEAGGNRARGYLQVEDVM					
	10	20	30	40	50	60
m223.pep	VESEIXYGNEIGVGS DLVFPVFLAQVFSNSQQFLLADFFAPVFFLCEFQFAEGADTREAX					
g223	VESEITYSNVISVRSSLVFPVFLAQVFGNVEQLLFTDLFAPVFFLGEFQFTEGADTREAX					
	70	80	90	100	110	120

a223.seq

1	GTGGAATTCA	GGCACCAAGT	AGTGGTAGTT	GGTGTCAAC	CATTGGTCA
51	TTTCGATAGC	GAATTGGTCT	TTGTTACCGC	GCGCCAGTTG	GAAGAATTGG
101	TCCAAGATA	GGTTTTGGCT	GTCGAAGCCG	AAGCGGGCGG	GAATCGCGCT
151	GGTGGCGACT	TGCAGGTCGA	GGATGTGGTC	GTAGAAAGTG	AAATCGCCTA
201	CGGCAACGTA	ATCGGCGTTG	GCAGCGGCCT	GGTGTTTCCA	GTTTTTCTCG
251	CGCAAGTCTT	TAGCAACAGC	CAGCAATTCT	TGCTCGCTGA	TTTCTTTGCG
301	CCAGTATTTT	TCTTGTGCGA	ATTTCAATTC	GCGGAAGCGA	CCGACACGCG
351	GGGAAGCTGA				

a223.pep

1	VEFRHQVVVV	GVEPFGHFDS	ELVFVTARQL	EELFQR*VLA	VEAEAGGNRA
51	GGDLQVEDVV	VESEIAYGNV	<u>IGVGSGLVFP</u>	<u>VFLAQVFSNS</u>	QQFLLADFFA
101	PVFFLCEFOF	AEGTDTREA*			

	10	20	30	40	50	60
m223.pep	VEFRHQVVVVGVPEFGHFDSELVFTARQLEELFORQVLAVEAEAGGNRAGGDLQVEDVV					
a223						
	10	20	30	40	50	60
	VEFRHQVVVVGVPEFGHFDSELVFTARQLEELFORQVLAVEAEAGGNRAGGDLQVEDVV					
	10	20	30	40	50	60
m223.pep	70	80	90	100	110	120
	VESEIXYGNIEIGVSGDLVFPVFLAQVFSNSQQFLLADFPVPVFLCEFQFAEGADTREAX					
a223						
	VESEIAYGNVIGVSGSLVFPVFLAQVFSNSQQFLLADFPVPVFLCEFQFAEGTDTREAX					

70 80 90 100 110 120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 793>:

```
g225.seq
1  atggattctt ttttcaaacc ggcagtttgg gcggttttgt ggctgatgtt
51  tgccgtccgc cccgcccttg cgcacgagtt gaccaacctg ctcagcagcc
101  gcgagcagat tctcagacag tttgccgaag acgaacagcc cgttttacc
151  gtcaaccgag ccccccggcg gcgggcgggc aatgccgacg aactcatcgg
201  cggcgcgatg gggcttaacg aacagcccgt tgtacgcgtc aaccgagccn
251  ccgcccggcg ggcgggcaat gccgacaaac tcatcggcag cgcgatcgcg
301  cttttgggta ttgcctaccg ctacggcggc acatcgggtg ctaccggttt
351  tgactgcagc ggattcatgc agcacatctt caaacgcgcc atgggcatca
401  acctgccgcg cacgtcggcg gaacaggcgc ggatgggagc acccgttgcc
451  cgaagcgaat tgcagcccgg ggatatggtg tttttccgca cgctcggcgg
501  cagccgcatt tcccatgtcg gactttatat cggcaacaac cgcttcaccc
551  acgcgcgcg caggggaaa aatatcgaaa tcaccagcct gagccacaaa
601  tattggagcg gcaaataatg gtctgccgcg cgggtcaaga aaaacgaccc
651  gtcacgcttt ctgaactga
```

This corresponds to the amino acid sequence <SEQ ID 794; ORF 225.ng>:

```
g225.pep
1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  VNRAPARRAG NADELIGGAM GLNEQPVVRV NRAXARRAGN ADKLIGSAMR
101  LLGIAYRYGG TSVSTGFDCS GFMQHIFKRA MGINLPRTSA EQARMGAPVA
151  RSELQPGDMV FFRTLGGSR I SHVGLYIGNN RFIHAPRTGK NIEITSLSHK
201  YWSGKYAFAR RVKKNPSRF LN*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 795>:

```
m225.seq (partial)
1  ..TTTCAAACC CGGCAGTTTG GCGGTTTTTG TGGCTGAwGT TTGCCGTCCG
51  CCCC GCCCTT GCCGACGAGT TGACCAACCT GCTCAGCAGC CGCGAGCAGA
101  TTCTCAGACA GTTTGCCGAA GACGAACAGC CCGTTTACC CATCAACCGA
151  GCCCCCGCCC GCGGGCGGG CAATGCCGAC GAACTCATCG GCAGCGCGAT
201  GGGGCTTAAC GAACAGCCCG TTTTACCCGT CAACCGAGTC CCCGCCCGGC
251  GGGCGGGCAA TGCCGACGAA CTCATCGGCA ACGCGATGGG GCTTAACGAA
301  CAGCCCGTTT TACCCGTCAA CCGAGCCCC GCGGCGGGG CGGGCAATGC
351  CGACGAACTC ATCGGCAACG CGATGGGACT TTTGGGTATT GCCTACCGCT
401  ACGGCGGCAC ATCGGTTTCT ACCGTTTTTG ACTGCAGCGG CTTTCATGCAG
451  CACATCTTCA AACGCGCCAT GGGCATCAAC CTGCCGCGCA CGTCGGCAGA
501  ACAGGCACGG ATGGGTACGC CGTTTGCCCG AAGCGAATTG CAGCCCGGAG
551  ATATGGTGTT TTTCCGACG CTCGGCGGCA GCCGCATTTC CCATGTTCGA
601  CTTTATATCG GCAACAACCG CTTTCATCCAC GCGCCGCGCA CGGGGAAAAA
651  TATCGAAATC ACCAGCCTGA GCCACAAATA TTGGAGCGGC AAATACGCGT
701  TCGCCCGCCG GGTCAGAAA AACGACCCGT CCCGCTTCT GAACTGA
```

This corresponds to the amino acid sequence <SEQ ID 796; ORF 225>:

```
m225.pep (partial)
1  ..FSNPAVWAVL WLXFAVRPAL ADELTNLLSS REQILRQFAE DEQVLPINR
51  APARRAGNAD ELIGSAMGLN EQVLPVNRV PARRAGNADE LIGNAMGLNE
101  QPVLPVNRAP ARRAGNADEL IGNAMGLLGI AYRYGGTSVS TGFDSCGFMO
151  HIFKRAMGIN LPRTSAEQAR MGTPVARSEL QPGDMVFFRT LGGSRISHVG
201  LYIGNNRFIH APRTGKNIEI TSLSHKYWSG KYAFARRVKK NDPSRFLN*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 225 shows 83.5% identity over a 248 aa overlap with a predicted ORF (ORF 225.ng) from *N. gonorrhoeae*:

m225/g225

```

          10      20      30      40      50
m225.pep  FSNPAVWAVLWLXFAVRPALADELTNLSSREQILRQFAEDEQVLPINRAPARRAG
          | : ||||| ||||| ||||| ||||| ||||| : |||||
g225      MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQVLPVNRAPARRAG
```

510

	10	20	30	40	50	60
m225 . pep	60	70	80	90	100	110
	NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA					
	: :					
g225	NADELIG-----			GAMGLNEQPVVVRVNRAXARRAGNA		
		70	80	90		
m225 . pep	120	130	140	150	160	170
	DELIGNAMGLLGIAIYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR					
	: : :					
g225	DKLIGSAMRLLGIAIYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGAPVAR					
	100	110	120	130	140	150
m225 . pep	180	190	200	210	220	230
	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR					
g225	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR					
	160	170	180	190	200	210
m225 . pep	240	249				
	VKKN D P S R F L N X					
g225	VKKN D P S R F L N					
	220					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 797>:

```

a225 . seq
1  ATGGATTCTT TTTTCAAACC GGCAGTTTGG GCGGTTTTGT GGCTGATGTT
51  TGCCGTCCGC CCCGCCCTTG CCGACGAGTT GACCAACCTG CTCAGCAGCC
101 GCGAGCAGAT TCTCAGACAG TTTGCCGAAG ACGAACAGCC CGTTTTACCC
151 ATCAACCGAN CCCCCGCCG GCGGGCGGGC AATGCCGACG AACTCATCGG
201 CAGCGCGATG GGGCTTAACG AACAGCCCGT TTTACCCGTC AACCANTCC
251 CCGCCCGGCG GCGGGGCAAT GCCGACNAAC TCATCGGCAA CGCGATGGGG
301 CTTAACGAAC AGCCCGTTTT ACCCGTCAAC CGAGTCCCG CCCGGCGGGC
351 GGGCAATGCC GACGAACTCA TCGGCAACGC GATGGGGCTT AACGAACAGC
401 CCGTTTTACC CGTCAACCGA GCCCCCGCCC GCGGGCGGG CAATGCCGAC
451 GAACTCATCG GCAACGCGAT GGGACTTTTG GGTATTGCCT ACCGCTACGG
501 CCGCACATCG ATTTCTACCG GTTTTGACTG CAGCGGCTTC ATGCAGACA
551 TCTTCAAACG CGCCATGGGC ATCAACCTGC CGCGCACGTC GGCAGAACAG
601 GCGCGGATGG GTACGCCGTG TGCCCGAAGC GAATTGCAGC CCGGGGATAT
651 GGTGTNTTTC CGCACGCTCG GCGGCAGCCG CATTTCCCAT GTCGGACTTT
701 ATATCGGCAA CAACCGCTTC ATCCACGCGC CGCGCACGGG GAAAAATATC
751 GAAATACCA GCCTGAGCCA CAAATATTGG AGCGGCAAAT ACGCGTTTCG
801 CCGCCGGGTC AAGAAAACG ACCCGTCCCG CTTTCTGAAC TGA

```

This corresponds to the amino acid sequence <SEQ ID 798; ORF 225.a>:

```

a225 . pep
1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQVLP
51  INRXPARRAG NADELIGSAM GLNEQPVLPV NRXPARRAGN ADXLIGNAMG
101 LNEQPVLPVN RVPARRAGNA DELIGNAMGL NEQPVLPVNR APARRAGNAD
151 ELIGNAMGLL GIAIYRYGGTS ISTGFDCSGF MQHIFKRAMG INLPRTSAEQ
201 ARMGTPVAR S ELQPGDMVXF RTLGGSRISH VGLYIGNNRF IHAPRTGKNI
251 EITSLSHKYW SGKYAFARRV KKNDPSRFLN *

```

m225/a225 87.4% identity in 277 aa overlap

	10	20	30	40	50
m225 . pep	FSNPAVWAVLWLXFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG				
	:				
a225	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRXPARRAG				
	10	20	30	40	50
	60	70	79	80	
m225 . pep	NADELIGSAMGLNEQPVLPVNR-----				VPARRAGNA

511

```

|||||
a225      NADELIGSAMGLNEQPVLPVNRXPARRAGNADXLIGNAMGLNEQPVLPVNRVPARRAGNA
              70      80      90      100      110      120

          90      100      110      120      130      140
m225.pep  DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF
          |||||
a225      DELIGNAMGLNEQPVLPVNRAPARRAGNADDELIGNAMGLLGIAYRYGGTSISTGFDCSGF
              130      140      150      160      170      180

          150      160      170      180      190      200
m225.pep  MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
          |||||
a225      MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVXFRTLGGSRISHVGLYIGNNRF
              190      200      210      220      230      240

          210      220      230      240      249
m225.pep  IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNLPSRFLNX
          |||||
a225      IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNLPSRFLNX
              250      260      270      280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 799>:

g225-1.seq

```

1  atggattctt ttttcaaacc ggcagtttgg gcggttttgt ggctgatgtt
51  tgcgcgtccg cccgcccttg ccgacgagtt gaccaacctg ctcagcagcc
101  gcgagcagat tctcagacag tttgccgaag acgaacagcc cgttttaccc
151  gtcaaccgag ccccgcccg gcgggcgggc aatgccgacg aactcatcgg
201  cggcgcgatg gggcttaacg aacagcccg tgtacgcgtc aaccgagccn
251  ccgcccgcg ggcgggcaat gccgacaaac tcacgagcag cgcgatgcgg
301  cttttgggta ttgcctaccg ctacggcggc acatcggtgt ctaccggttt
351  tgactgcagc ggattcatgc agcacatctt caaacgcgcc atggggcatca
401  acctgccgcg cactcggcg gaacaggcgc ggatgggcgc acccggtgcc
451  cgaagcgaat tgcagcccg ggatatggtg tttttccgca cgctcggcgg
501  cagccgcatt tcccatgtcg gactttatat cggcaacaac cgcttcatcc
551  acgcccgcg cagggggaaa aatatcgaaa tcaccagcct gagccacaaa
601  tattggagcg gcaaatatgc gttcgccgc cgggtcaaga aaaacgacct
651  gtcacgcttt ctgaactga

```

This corresponds to the amino acid sequence <SEQ ID 800; ORF 225-1.ng>:

m225-1.pep

```

1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  VNRAPARRAG NADELIGGAM GLNEQPVVRV NRAXARRAGN ADKLIGSAMR
101  LGLIAYRYGG TSVSTGFDCS GFMQHIFKRA MGINLPRTSA EQARMGAPVA
151  RSELQPGDMV FRTLGGSRIS SHVGLYIGNN RFIHAPRTGK NIEITSLSHK
201  YWSGKYAFAR RVKKNLPSRF LN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 801>:

m225-1.seq

```

1  ATGGATTCTT TTTTCAAACC GGCAGTTTGG GCGGTTTTGT GGCTGATGTT
51  TGCCGTCCTG CCCGCCCTTG CCGACGAGTT GACCAACyTG CTCAGCAGCC
101  GCGAGCAGAT TCTCAGACAG TTTGCCGAAG ACGAACAGCC CGTTTTACCC
151  ATCAACCGAG CCCCCGCCCC GCGGGCGGGC AATGCCGACG AACTCATCGG
201  CAGCGCGATG GGGCTTAACG AACAGCCCGT TTTACCCGTC AACCGAGTCC
251  CCGCCCGCGG GCGGGGCAAT GCCGACGAAC TCATCGGCAA CGCGATGGGG
301  CTTAACGAAC AGCCCGTTTT ACCCGTCAAC CGAGCCCCCG CCGGCGGGC
351  GGGCAATGCC GACGAAGTCA TCGGCAACGC GATGGGACTT TTGGGTATTG
401  CCTACCGCTA CGGCGGCACA TCGGTTTCTA CCGGTTTTGA CTGCAGCGGC
451  TTCATGCAGC ACATCTTCAA ACGCGCCATG GGCATCAACC TGCCGCGCAC
501  GTCGGCAGAA CAGGCACGGA TGGGTACGCC GGTGCCCCGA AGCGAATTGC
551  AGCCCGGAGA TATGGTGTTT TTCCGCACGC TCGGCGGCAG CCGCATTTCC
601  CATGTCGGAC TTTATATCGG CAACAACCGC TTCATCCACG CGCCGCGCAC
651  GGGGAAAAAT ATCGAAATCA CCAGCCTGAG CCACAAATAT TGGAGCGGCA
701  AATACGCGTT CGCCCGCCGG GTCAAGAAAA ACGACCCGTC CCGCTTCTG
751  AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 802; ORF 217>:

m225-1.pep

```

1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  INRAPARRAG NADELIGSAM GLNEQVLPV NRVPARRAGN ADELIGNAMG
101 LNEQVLPVNR RAPARRAGNA DELIGNAMGL LGIAYRYGGT SVSTGFDCSG
151 FMQHIFKRAM GINLPRTSAE QARMGTPVAR SELQPGDMVF FRTLGGSRIS
201 HVGLYIGNNR FIHAPRTGKN IEITSLSHKY WSGKYAFARR VKKNDPSRFL
251 N*

```

m225-1/g225-1 84.9% identity in 251 aa overlap

```

              10      20      30      40      50      60
m225-1.pep    MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g225-1        MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPVNRAPARRAG
              10      20      30      40      50      60

              70      80      90     100     110     120
m225-1.pep    NADELIGSAMGLNEQVLPVNRVPARRAGNADELIGNAMGLNEQVLPVNRAPARRAGNA
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g225-1        NADE-----LIGGAMGLNEQPVVRVNRAXARRAGNA
                      70      80      90

              130     140     150     160     170     180
m225-1.pep    DELIGNAMGLLGIAIYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
              |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g225-1        DKLIGSAMRLLGIAIYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGAPVAR
              100     110     120     130     140     150

              190     200     210     220     230     240
m225-1.pep    SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g225-1        SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
              160     170     180     190     200     210

              250
m225-1.pep    VKKNDPSRFLNX
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g225-1        VKKNDPSRFLNX
              220

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 803>:

a225-1.seq

```

1  ATGGATTCTT TTTTCAAACC GGCAGTTTGG GCGGTTTTGT GGCTGATGTT
51  TGCCGTCCGC CCCGCCCTTG CCGACGAGTT GACCAACCTG CTCAGCAGCC
101 GCGAGCAGAT TCTCAGACAG TTTGCCGAAG ACGAACAGCC CGTTTTACCC
151 ATCAACCGAN CCCC GCCCGC GCGGGCGGGC AATGCCGACG AACTCATCGG
201 CAGCGCGATG GGGCTTAACG AACAGCCCGT TTTACCCGTC AACCGANTCC
251 CCGCCCGGGC GCGGGGCAAT GCCGACNAAC TCATCGGCAA CGCGATGGGG
301 CTTAACGAAC AGCCCGTTTT ACCCGTCAAC CGAGTCCCCG CCCGGCGGGC
351 GGGCAATGCC GACGAACCTA TCGGCAACGC GATGGGGCTT AACGAACAGC
401 CCGTTTTACC CGTCAACCGA GCCCCGCGCC GCGGGCGGG CAATGCCGAC
451 GAACTCATCG GCAACGCGAT GGGACTTTTG GGTATTGCCT ACCGCTACGG
501 CGGCACATCG ATTTCTACCG GTTTTGACTG CAGCGGCTTC ATGCAGCACA
551 TCTTCAAACG CGCCATGGGC ATCAACCTGC CGCGCACGTC GGCAGAACAG
601 GCGCGGATGG GTACGCCGGT TGCCCGAAGC GAATTGCAGC CCGGGGATAT
651 GGTGTNTTTC CGCACGCTCG GCGGCAGCCG CATTTCCCAT GTCGGACTTT
701 ATATCGGCAA CAACCGCTTC ATCCACGCGC CGCGCACGGG GAAAAATATC
751 GAAATCACCA GCCTGAGCCA CAAATATTGG AGCGGCAAA AC CGCTTCG
801 CCGCCGGGTC AAGAAAAACG ACCCGTCCCG CTTTCTGAAC TGA

```

This corresponds to the amino acid sequence <SEQ ID 804; ORF 225-1.a>:

a225-1.pep

```

1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  INRXPARRAG NADELIGSAM GLNEQVLPV NRXPARRAGN ADXLIGNAMG
101 LNEQVLPVNR RVPARRAGNA DELIGNAMGL NEQVLPVNR APARRAGNAD
151 ELIGNAMGLL GIAYRYGGTS ISTGFDCSGF MQHIFKRAMG INLPRTSAEQ
201 ARMGTPVAR ELQPGDMVXF RTLGGSRISH VGLYIGNNRF IHAPRTGKNI
251 EITSLSHKYW SGKYAFARRV KKNDDPSRFLN *

```


513

a225-1/m225-1 88.6% identity in 280 aa overlap

	10	20	30	40	50	60
a225-1.pep	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRXPARRAG					
m225-1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG					
	10	20	30	40	50	60
	70	80	90	100	110	120
a225-1.pep	NADELIGSAMGLNEQPVLPVNRXPARRAGNADXLIGNAMGLNEQPVLPVNRVPARRAGNA					
m225-1	NADELIGSAMGLNEQ-----VLPVNRVPARRAGNA					
	70	80	90			
	130	140	150	160	170	180
a225-1.pep	DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLGIAYRYGGTSISTGFDCSGF					
m225-1	DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLGIAYRYGGTSVSTGFDCSGF					
	100	110	120	130	140	150
	190	200	210	220	230	240
a225-1.pep	MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVXFRTLGGSRISHVGLYIGNNRF					
m225-1	MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF					
	160	170	180	190	200	210
	250	260	270	280		
a225-1.pep	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLNX					
m225-1	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLNX					
	220	230	240	250		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 805>:

g226.seq

```

1  ATGAGCGAAA TCCTCAGGCA GCCCAGCGTT CTGCTTTTCC TCACGCTTGC
51  CGTGACGCG CTTGCGATTA TCGTGCGCAC GCGCACGGGC AATATCTTCT
101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC
151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAAT TCATTGATTT
201 TCGGCTGAAA cccGccgtCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC
251 GCCGTAAAAT CTTCAACCAG TGGCTGCCCG TCATCGTTTC GCAGCTTGCG
301 GGCAGCGTTA cggGCATTGT tacggggATG TATTTTgccg cttggctcgg
351 gccggatacc caattctcct tcccgcctcg tcttcaatat ctgttattta
401 caccctctgg aatcccaatt cacaccctgt atgcgcgggt tctcccacca
451 tttctgttgc ctccgcctct cctgccgcgc ctggccccgc atacattgcg
501 ccggttcaca atacttccaa aaaaactacg gccgtttaag cccctcctcc
551 cagttgtggt cctttctcct Ccgggcctcg cccctcccct cttataa

```

This corresponds to the amino acid sequence <SEQ ID 806; ORF 226.ng>:

g226.pep

```

1  MSEILRQPSV LLFLTLAVYA LAIIVRTRTG NIFCNPVLVS TIVLIAYLKI
51  LGIDYAVYHN AAQFIDFRLK PAVVVLAVPL YQNRKIFNQ WLPVIVSQLA
101 GSVTGIVTGM YFAAWLGPDT QFSFPRLQY LLFTPSGIPI HTLYARVLPP
151 FLLPPPLLPR LGPHTLRRFT ILPKKL RPFK PLLPVVVLSP PGLAPPLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 807>:

m226.seq

```

1  ATGAACGAAA TCCTCAGGCA GCCCAGCGTT CTGCTTTTCC TCACGCTTGC
51  CGTGACGCG CTTGCGATTA TCGTGCGCAC GCGCACGGGC AATATCTTCT
101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC
151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAAT TCATTGATTT
201 TTGGCTGAAA CCCGCCGTCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC
251 GCCGTAAAAT CTTCAACCAG TGGCTGCCCG TCATCGTTTC ACAGCTTGCG
301 GGCAGCGTTA CGGGCATTGT TACAGGGATG TATTTTGCCA AATGGCTGGG
351 CGCGGAACGC GAAGTCGTCC TCTCGCTCGC GTCCAAATCT GTTACCAACC
401 CCATCGCTAT TGAAATCACC CGCTCCATCG GCGGCATTCC CGCCATTACC
451 GCCGCCACCG TCATCATTGC CGGTCTGGTC GGACAGATTG CCGGTTACAA

```

m226 . pep

m226/g226

a226.seq

a226.pap

10 20 30 40 50 60

515

```

m226.pep  MNEILRQPSVLLFLTLAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN
|||||:|||||
a226      MNEILRQPSILLFLTLAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN
          10      20      30      40      50      60

          70      80      90      100     110     120
m226.pep  AAQFIDFWLKPAVVVLAVPLYQNRRIKFNQWLPVIVSQLAGSVTGIVTGMYFAKWLGAER
|||||
a226      AAQFIDFWLKPAVVVLAVPLYQNRRIKFNQWLPVIVSQLAGSVTGIVTGMYFAKWLGAER
          70      80      90      100     110     120

          130     140     150     160     170     180
m226.pep  EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVMPSSVG
|||||
a226      EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVMPSSVG
          130     140     150     160     170     180

          190     200     210     220     230
m226.pep  MSLGTASHAMGIAASLERSRMAAYAGLGLTFNGVLTALIAPLLIPVLGFX
|||||
a226      MSLGTASHAMGIAASLERSRMAAYAGLGLTFNGVLTALIAPLLIPVLGFX
          190     200     210     220     230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 811>:

```

g227.seq
1  atgaacatca tccgcgcgct cctcatcatc ctcggctgcc tcgccgcggg
51 cgaaaccgcc gttttcctag caggcatcaa actgcccgcc agcatcgctc
101 gcatgggcgt gctgtttgcg cttttgcagg cgggttggtc caaaacgtct
151 tggctgcaac agcttaccga cgcgctgatg gcaaacctga cgctgttctc
201 cgtgccgccc tgcgtggcgg tcatcagcta tttggatttg attgccgacg
251 attggttttc gatactggtt tccgcctccg ccagcacttt gtgcgtactg
301 ctggttacgg gcaaggttca ccgctggata cggagcatta tctga

```

This corresponds to the amino acid sequence <SEQ ID 812; ORF 227.ng>:

```

g227.pep
1  MNIIRALLII LGCLAAGETA VFLAGIKLPG SIVGMGVLFA LLQAGWLKTS
51  WLQQLTDALM ANLTLEFLVPP CVAVISYLDL IADDWFSILV SASASTLCVL
101 LVTGKVHRWI RSII*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 813>:

```

m227.seq (partial)
1  ..ACGTCTTkgc TGCAACAGCT TACCGACGCG CTGATGTCTGA ACCTGACGCT
51  GTtCCTCGTG CCgCC.TGCG TGGCGGTCAT CAGCTATTG GATTGATTG
101 CCGACGATTG GTTTTCGATA CTGGTTTCCG CCTCCGCCAG cACTTTGTGC
151 GTACTGCTGG TTACGGGCAA AGTCCACCGG TGGATACGGG GTATTATCCG
201 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 814; ORF 227>:

```

m227.pep (partial)
1  ..TSXLQQLTDA LMSNLTFLV PPCVAVISYL DLIADDWFSI LVSASASTLC
51  VLLVTGKVHR WIRGIIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 227 shows 95.5% identity over a 66 aa overlap with a predicted ORF (ORF 227.ng) from *N. gonorrhoeae*:

```

m227/g227

          10      20      30
m227.pep  TSXLQQLTDALMSNLTFLVPPCVAVISYL
          || |||||:|||||
g227      TAVFLAGIKLPGSIVGMGVLFALLQAGWLKTSWLQQLTDALMANLTFLVPPCVAVISYL
          20      30      40      50      60      70

          40      50      60

```

516

```

m227.pep      DLIADDWFSILVSASASTLCVLLVTGKVHRWIRGIIRX
               |||
g227          DLIADDWFSILVSASASTLCVLLVTGKVHRWIRSIIX
               80      90      100      110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 815>:

```

a227.seq
1  ATGAACATCA TCCGCGCGCT CCTCATCATC CTCGGCTGCC TCGCCACCGG
51 CGAAACCGCC GTTTTCCTAG CAGGCATCAA ACTGCCCGGC AGCATCGTCG
101 GCATGGGCGT ACTGTTTGCG CTTTTCGAGG CGGGTTGGGT CAAAACGTCT
151 TGGCTGCAAC AGCTTACCGA CGCGCTGATG GCGAATCTGA CGTTGTTTCT
201 CGTGCCGCCC TGCCTGGCGG TCATCAGCTA TTTGGATTG ATTGCCGACG
251 ATTGGTTTTC GATACTGGTT TCCGCCTCCG CCAGCACTTT GTGCGTACTG
301 CTGGTTACAG GCAAGGTTCA CCGCTGATA CGGAGCATT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 816; ORF 227.a>:

```

a227.pep
1  MNIIRALLII LGCLATGETA VFLAGIKLPG SIVGMGVLEA LLQAGWVKTS
51 WLQQLTDALM ANLTLFLVPP CVAVISYLDL IADDWFSILV SASASTLCVL
101 LVTGKVHRWI RSII*

```

m227/a227 95.5% identity in 66 aa overlap

```

m227.pep      TSXLQQLTDALMSNLTLFLVPPCVAVISYL
               |||
a227          TAVFLAGIKLPGSIVGMGVLFALLQAGWVKTSWLQQLTDALMANLTLFLVPPCVAVISYL
               20      30      40      50      60      70

m227.pep      DLIADDWFSILVSASASTLCVLLVTGKVHRWIRGIIRX
               |||
a227          DLIADDWFSILVSASASTLCVLLVTGKVHRWIRSIIX
               80      90      100      110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 817>:

```

m228.seq
1  ATGAAAAAAT TATTGATTGC CGCAATGATG GCGGCTGCCT TGGCAGCTTG
51 TTCGCAAGAA GCCAAACAGG AGGTAAAGGA AGCGGTTCAA GCCGTTGAGT
101 CCGATGTTAA AGACACTGCG GCTTCTGCCG CCGAGTCTGC CGCTTCTGCC
151 GTCGAAGAAG CGAAAGACCA AGTCAAAGAT GCTGCGGCTG ATGCAAAGGC
201 AAGTGCCGAG GAAGCTGTAA CTGAAGCCAA AGAAGCTGTA ACTGAAGCAG
251 CTAAAGATAC TTTGAACAAA GCTGCCGACG CGACTCAGGA AGCGGCAGAC
301 AAAATGAAAG ATGCCGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 818; ORF 228>:

```

m228.pep
1  MKLLIAAMM AAALAACSQE AKQEVKEAVQ AVESDVKDTA ASAAESAASA
51 VEEAKDQVKD AAADAKASAE EAVTEAKEAV TEAAKDTLNK AADATQEAAD
101 KMKDAAK*

```

Computer analysis of this amino acid sequence gave the following results:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 819>:

```

a228.seq
1  ATGAAAAAAT TATTGATTGC CGCAATGATG GCGGCTGCCT TGGCAGCTTG
51 TTCGCAAGAA GCCAAACAGG AGGTAAAGGA AGCGGTTCAA GCCGTTGAGT
101 CCGATGTTAA AGACACTGCG GCTTCTGCCG CCGAGTCTGC CGCTTCTGCC
151 GTCGAAGAAG CGAAAGACCA AGTCAAAGAT GCTGCGGCTG ATGCAAAGGC
201 AAGTGCCGAG GAAGCTGTAA CTGAAGCCAA AGAAGCTGTA ACTGAAGCAG
251 CTAAAGATAC TTTGAACAAA GCTGCCGACG CGACTCAGGA AGCGGCAGAC
301 AAAATGAAAG ATGCCGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 820; ORF 228.a>:

517

```

a228.pep
1   MKKLLIAAMM AAALAACSQE AKQEVKEAVQ AVESDVKDTA ASAAESAASA
51  VEEAKDQVKD AAADAKASAE EAVTEAKEAV TEAAKDTLNK AADATQEAAD
101 KMKDAAK*

```

m228/a228 100.0% identity in 107 aa overlap

	10	20	30	40	50	60
m228.pep	MKKLLIAAMMAAALAACSQEAKQEVKEAVQAVESDVKDTAASAAESAASAVEEAKDQVKD					
a228	MKKLLIAAMMAAALAACSQEAKQEVKEAVQAVESDVKDTAASAAESAASAVEEAKDQVKD					
	10	20	30	40	50	60
	70	80	90	100		
m228.pep	AAADAKASAE EAVTEAKEAVTEAAKDTLNKAADATQEAADKMKDAAKX					
a228	AAADAKASAE EAVTEAKEAVTEAAKDTLNKAADATQEAADKMKDAAKX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 821>:

```

g229.seq
1   atggctgccg ttcggtcgccg cgggtcggtc ttcctgataa tgcttcaca
51  tattgccgcg gttcagcgtc agccgccagc gttcgcccaa gcgtcgggag
101 aaatcgccat tgaagccgcc ggcgaaattg tatcggtgcg cgccaagag
151 gttttgcccg acaaacggca cggtgccgaa cgagcgcggt accgaacggt
201 tttgatggcc gaacgacagg cgcaggttct gttcgctgaa atctttgtta
251 tcccaataat gcacgcgcgc gctgatgccg ccgtagagga aatgatgcc
301 gcccgcattg atttcgcgcg acacgcccga gccgtagcgc aaaccgtgtg
351 ccttttgccg caggctgtcg gcggttttcg tccagcttct gcccgcaa
401 tcaatcgttt tttcggaaga agcgttggtt atagcggatt aacaaaaatc
451 aggacaaggc ggcgggccgc aggcagtacg gatggtacgg aaccggttcg
501 cccggtgctt ggacgcctta gggaaccggt ccctttgagc cggggcgggg
551 caaccggtac cgggttttgt tcatccgcca tattgtgttg a

```

This corresponds to the amino acid sequence <SEQ ID 822; ORF 229.ng>:

```

g229.pep
1   MAAVSGGGAV FLIMLPFIAR VQRQPPAFAQ ASGEIGIEAA GEIVSAAAEQ
51  VLPDKRHGAE RARYRTVLMA ERQAQVLF AE IFVIPIMHAA ADAAVEEMMP
101 ARIDFARHAQ AVAQTVCLLR QAVGGFRPAS ARKFNRFGR SVVYSGLTKI
151 RTRRRAAGST DGTEPVRPVL GRLREPFPLS RGGATRTGFC SSAILC*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 823>:

```

m229.seq (partial)
1   ..GCTCAAGCGT TGGGAGAAAT CGGCATTGAA GCCGCCGACG AAATTGTATC
51  GGCTGCCGCC TAAGAGGTTT TGCTCGACAA ACGGCACGAT GCCGAACGAG
101 CGCGTTACCG AACGGTTTTT ATAGCCGAAC GACAGGCGCA GGCTCTGTTC
151 GCTGAAATCT TTGTTATCCC AATAATGCAC GCCGCCGCCG CTGATGCCGC
201 CGTAGAGGAA ATGATGCCTG CCCGCATTGA TTTCGCGCGA CACGCCTAAG
251 CCCTAGCGCA AACCGTGTGC CTTTTCGCGC AGGCTGTGCG CGGTTTTTCGT
301 CCAGCTTCTG CCCGCAAATT CAATCGTTTT TTCGACGAA GCGTTGTTTA
351 TAGCGGATTA ACAAAAATCA GGACAAGGCA ACGAAGCCGC AGACAGTACA
401 AATAGTACGG AACCGATTCA CTTGGTGCTT CAGCACCTTA GAGAATCGTT
451 CTCTTTTTTG TTCATCCGCT ATATTGTGTT GA

```

This corresponds to the amino acid sequence <SEQ ID 824; ORF 229>:

```

m229.pep (partial)
1   ..AQALGEIGIE AADEIVSAAA XEVLLDKRHD AERARYRTVF IAERQAQALF
51  AEIFVIPIMH AAAADA AVEE MPPARIDFAR HAXALAQTV LRLQAVGGFR
101 PASARKFNRF FGRSVVYSL TKIRTRQSA DSTNSTEPIH LVLQHLRESR
151 SLFCSSAILC *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 229 shows 80.5% identity over a 169 aa overlap with a predicted ORF (ORF 229.ng) from *N. gonorrhoeae*:

m229/g209

```

                                10      20      30
m229.pep                      AQALGEIGIEAADEIVSAAAXEVLDDKRHDAE
                                ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g229      MAVSGGGAVFLIMLPHIARVQRQPPAFAQASGEIGIEAAGEIVSAAAEVLDPDKRHGAE
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m229.pep      RARYRTVFIAERQAQALFAEIVFVIPIMHAAAADA AVEEMMPARIDFARHAXALAQTVCLL
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g229      RARYRTVILMAERQAQVLF AEIVFVIPIMHAAA -DA AVEEMMPARIDFARHAQAVAQTVCLL
                                70      80      90      100     110

                                100     110     120     130     140
m229.pep      RQAVGGFRPASARKFNRFGRSVVYSGLT KIRTRQRSADSTNSTEPIHLVLQHLRE ---
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g229      RQAVGGFRPASARKFNRFGRSVVYSGLT KIRTRRRRAAGSTDGTEPVRPVLGRRLREPFPL
                                120     130     140     150     160     170

                                150     160
m229.pep      -----SRSLFCSSAILCX
                :|: ||| ||| |||
g229      SRGGATRTGFCSSAILC
                                180     190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 825>:

```

a229.seq (partial)
1  ATGGCTGTCTG TATCGGGCGG CGGTGCGGTC TTCCTGATAA CGCTTCCACA
51 TATTGCCCAC GTTCAGCGTC AGCCGCCA.. GTTCGCTCAA GCGTCGGGAG
101 AAATCGGCAT TGAAGCCGCC GACGAAATTG TATCGGCTGC CGCCTAAGAG
151 GTTTTGCTCG ATAAACGGCA CGATGCCGAA TGAGCGCGTT ACTGAACGGT
201 TTTTATAGCC GAGCGACAGG CGCAGGCTCT GTTCGCTGAA ATCTTTGTTA
251 TCCTAATAGT GCACGCCGCC GCCGCTGATG TCTCCGTAGA GGAATGATG
301 CCCGCCCGCA TTGATTTCGC GCGACACGCC CAAGCCGTAG CGCAAACCGT
351 GTGCCTTTTG CGGCAGGCTG TCGGCGGTTT TCGTCCAGCT TCTGCCTGCA
401 AATTC AATCG TTTTTCGGA CGAAGCGTTG TTTATAGCGG ATTAACAAAA
451 ATCAGGACAA GCGACGAAG CGCAGACAGT ACAGATAGTA CGGAACCGAT
501 TCACTTGGTG CTTACGACC TTAGAGAATC GTCTCTTTGA GCTAAGGCCA
551 GGCAACGCCG TACTGGTTT TGTTCATCCA CTATA

```

This corresponds to the amino acid sequence <SEQ ID 826; ORF 229.a>:

```

a229.pep (partial)
1  MAVVSGGGAV FLITLPHIAH VQRQPPXFAQ ASGEIGIEAA DEIVSAAA*E
51 VLLDKRHDAE *ARY*TVFIA ERQAQALFAE IFVILIVHAA AADVSV EEMM
101 PARIDFARHA QAVAQTVCLL RQAVGGFRPA SACKFNRFEG RSVVYSGLT K
151 ITRRRSADS TDSTEPIHLV LQHLRESSL* AKARQRTGF CSSTI

```

m229/a229 85.6% identity in 167 aa overlap

```

                                10      20      30
m229.pep                      AQALGEIGIEAADEIVSAAAXEVLDDKRHDAE
                                ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
a229      MAVVSGGGAVFLITLPHIAHVQRQPPXFAQASGEIGIEAADEIVSAAAXEVLDDKRHDAE
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m229.pep      RARYRTVFIAERQAQALFAEIVFVIPIMHAAAADA AVEEMMPARIDFARHAXALAQTVCLL
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
a229      XARYXTVFIAERQAQALFAEIVFVILIVHAAAADVSVEEMMPARIDFARHAQAVAQTVCLL
                                70      80      90      100     110     120

```

519

	100	110	120	130	140	149
m229.pep	RQAVGGFRPASARKFNRRFFGRSVVYSGLTKIRTRQRSADSTNSTEPIHLVLQHLRES---					
a229	RQAVGGFRPASACKFNRRFFGRSVVYSGLTKIRTRRRSADSTDSTEPIHLVLQHLRESSLX					
	130	140	150	160	170	180
	150	160				
m229.pep	-----RSLFCSSAILCX					
a229	AKARQRRRTGFCSSIT					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 827>:

g230.seq

1	atgttccatt	ccatcgaaaa	atacagaaca	cccgcccaag	tcttattagg
51	cctgattgca	ttactttttg	tgggttcg	cgtcagcacg	gtttcccatc
101	cgggcgccga	ctacatcgtc	caagtggg	acgaaaaaat	cagcgagcac
151	tcaatcaaca	acgccatgca	gaacgagcag	gcggacggcg	gcagcccttg
201	gcgcgacgcg	gtgttccaat	ccctgctgca	acgcgcctac	ctgaaacagg
251	gcgcgaagct	gatgggcatt	tcggtttctt	ccgaacaaat	caagcagatg
301	attgtggacg	atcccaattt	ccacgacgca	aacggcaaat	tcagtcacgc
351	gcttttgagt	caatacctgt	cgcaacgcca	tatgtctgaa	gaccagtttg
401	tcgaagaaat	ccgcgatcag	tttgccctgc	agaatttggt	aagcctcgtc
451	caaaacggcg	tattggtcgg	cgacgcgcag	gcggaacagc	tgatcaggct
501	gacgcaggct	aaccgcacca	tccgttcgca	cactttcaac	cccgcagagt
551	tcacgcccc	agtcaaaagc	tctgaagccg	atttgcagaa	attttataat
601	gcgaacaaaa	aagactatct	gctgcccgcg	gcgggtcaaat	tggaatatgt
651	cgccctgaat	ctgaaggatt	ttgcagacaa	gcagaccgtc	agtgaacagg
701	aagtgaaaaa	tgcgtttgaa	gagcgcgtgg	cgcgtttgcc	ggcacatgaa
751	gccaaacctt	ctttcgagca	ggaaaaagcc	gccgtcgaaa	acgaattgaa
801	aatgaaaaag	gcggttgccg	acttcaacaa	ggcaaaaagaa	aagctggggcg
851	acgatgcgtt	caatacatccc	tcttcgcttg	ccgaagccgc	caaaaacagc
901	ggtttgaaa	tggaaaccca	agaaacttgg	ctgagcaggc	aggacgcaca
951	aatgtccggc	atgcccgaaa	acctaataca	tgccgtattc	agcgacgacg
1001	tattgaagaa	aaaacacaa	tccgaagtgc	tgaccatcaa	cagcgaaacc
1051	gcgtgggtcg	tccgcgcca	agaagtccgc	gaagaaaaaa	acctactgtt
1101	tgaagaagcc	aaagatgcgg	tgcgtcaggc	ctatatccgt	accgaagccg
1151	ccaaactttt	gaaaacaatg	taa		

This corresponds to the amino acid sequence <SEQ ID 828; ORF 230.ng>:

g230.pep

1	MFHSIEKYRT	PAQVLLGLIA	LTFVGFVST	VSHPGADYIV	QVGDEKISEH
51	SINNAMQNEQ	ADGGSPWRDA	VFQSLQRAY	LKQGAKLMI	SVSSEIKQM
101	IVDDPNFHDA	NGKFSHALLS	QYLSQRHMSE	DQFVEEIRDQ	FALQNLVSLV
151	QNGVLVGDAQ	AEQLIRLTQV	NRTIRSHTFN	PDEFIAQVKA	SEADLQKFYN
201	ANKKDYLLPQ	AVKLEYVALN	LKDFADKQTV	SETEVKNAFE	ERVARLPAHE
251	AKPSFEQEKA	AVENELKMKK	AVADFNKAKE	KLGDDAFNHP	SSLAEAAKNS
301	GLKVETQETW	LSRQDAQMSG	MPENLINAVF	SDDVLKKKHN	SEVLINSET
351	AWVVRKEVR	EEKNLLFEEA	KDAVRQAYIR	TEAAKLLKTM	*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 829>:

m230.seq (partial)

1	ATGTTCCATT	CCATCGAAAA	ATACAGAACG	CCCGCCCAAG	TCCTTTTGGG
51	CCTGATTGCA	TTAACCTTCG	TGGGCTTCGG	GGTCAGCACG	GTATCCCATC
101	CGGGTGCCGA	CTACATCGTC	CAAGTGGGCG	ACGAAAAAaT	CAGCGACCAC
151	TCCATCAACA	ACGCCATACA	GAACGAACAG	GCGGACGGCG	GCGGCCCTTC
201	Gcc.GACGCG	GTGTTCCAAT	CCCTGCTGCA	ACGCGCTTAC	CTGAAACAGG
251	GCGCGAAGCT	GATGGGCATT	TCGGTTTCTT	CCGAACAAAT	CAAGCAAATT
301	ATCGTGGACG	ATCCCAATTT	CCACGACGCA	AACGGCAAAT	TCGACCACGC
351	GCTTTTAAAC	CGCTACCTTT	CCCAACGCCA	TATGTCTGAA	GACCAGTTTG
401	TCGAAGAAAT	CCGCGATCAG	TTTGCCTTGC	AGAATTTGGT	AAACCTCGTC

520

```

451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACACAGGTC AACCGCACCA TCCGTTTCGCA CACTTTCAAC CCCGACGAGT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 GCGAACAAAA AAGACTATCT GCTGCCGCAG gCGGTCAAAT TGGAATATGT
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAAACGg
701 AAGTGAAAAA TGCATTTGAA GAGCGCGTGG CGCGTTTGCC GGCAAATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAAGAA AAATTGGGCG
851 ACGATGC.GT cAACCATCCT TCyTCGCTTG CCGAAGCCGC CAAAAACAGC
901 GGTTTGAAAAG TCGAAACCCA AGAAACTTGG CTGAGTAGGC AGGACGCGCA
951 AATGTCCGGT ATGCCCGAAA ACCTGATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAA TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 TCGTGGGTCT TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACCTT...

```

This corresponds to the amino acid sequence <SEQ ID 830; ORF 230>:

```

m230.pep (partial)
  1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
 51 SINNAIQNEQ ADGGGSPDA VFQSLQRAY LKQGAQLMGI SVSSEQIKQI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSE DQFVEEIRDQ FALQNLNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAVNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVL TINSET
351 AWWVRAKEVR EEKTLPFMEA KDAVRQAYIR TEAAKL....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 230 shows 95.9% identity over a 386 aa overlap with a predicted ORF (ORF 230.ng) from *N. gonorrhoeae*:

m230/g230

	10	20	30	40	50	60
m230.pep	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
g230	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISEHSINNAMQNEQ					
	10	20	30	40	50	60
m230.pep	ADGGGSPSPDAVFQSLQRAYLKQGAQLMGISVSSEQIKQIIVDDPNFHDAANGKFDHALLN					
g230	ADGGSPWRDAVFQSLQRAYLKQGAQLMGISVSSEQIKQMIVDDPNFHDAANGKFSHALLS					
	70	80	90	100	110	120
m230.pep	RYLSQRHMSEDQFVEEIRDQFALQNLNLVQNGVLVGDAQAEQLIRLTQVNRRTIRSHTFN					
g230	QYLSQRHMSEDQFVEEIRDQFALQNLVSLVQNGVLVGDAQAEQLIRLTQVNRRTIRSHTFN					
	130	140	150	160	170	180
m230.pep	PDEFIAQVKVSEADLQKFYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE					
g230	PDEFIAQVKASEADLQKFYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE					
	190	200	210	220	230	240
m230.pep	ERVARLPANEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDDAVNHPSSLAEAAKNS					
g230	ERVARLPAHEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDDAFNHPSSLAEAAKNS					
	250	260	270	280	290	300

521

	310	320	330	340	350	360
m230.pep	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSVLTINSETAWVVRKEVR					
g230	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSVLTINSETAWVVRKEVR					
	310	320	330	340	350	360
	370	380				
m230.pep	EEKTLPFAEAKDAVRQAYIRTEAAKL					
	:					
g230	EEKNLLFEEAKDAVRQAYIRTEAAKLLKTM					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 831>:

a230.seq (partial)

```

1 ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCCAAG TCCTTTTGGG
51 CCTGATTGCA TTAACCTTCG TCGGCTTCGG GGTCAGCACG GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCGCGACGCG GTGTTCCAAT CCCTGCTACA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAGATT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCACGC
351 GCTTTTAAAC CGCTACCTTT CCCAACGTCA TATGTCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTGGT AAACCTCGTC
451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACGCAGGTC AACC GCACCA TCCGTTTCGCA CACTTTCAAC CCCGACGAAT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA GTTTTATAAC
601 GCAAACAAAA AAGACTACCT GCTTCCCAA GCGGTCAAAT TGGAATATGT
651 CGCCTTGAAT CTGAAAGACT TTGCAGACAA ACAGACCGTC AGCGAAACAG
701 AAGTGAAAAA TGCGTTTGAA GAGCGCGTGG CGCGTTTGCC GGCAAATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAATAA GGCAAAGAA AAGCTGGGCG
851 ATGACGCGTT CAACCATCCT TCCTCGCTTG CCGAAGCCGC CAAAACAGC
901 GGTTTGAAAG TCGAAACCCA AGAACTTGG CTGAGCAGGC AGGATGCGCA
951 AATGTCCGGT ATGCCCAGAA ACCTGATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACCTT

```

This corresponds to the amino acid sequence <SEQ ID 832; ORF 230.a>:

a230.pep (partial)

```

1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGPSRDA VFQSLQRAY LKQAKLMGI SVSSEQIKQI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSE DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPK AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHNS SEVLTINSET
351 AWWVVRKEVR EEKTLFPAEA KDAVRQAYIR TEAAKL

```

m230/a230 99.2% identity in 386 aa overlap

	10	20	30	40	50	60
m230.pep	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
a230	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m230.pep	ADGGGPSRDAVFQSLQRAYLKQAKLMGISVSSEQIKQIIIVDDPNFHDANGKFDHALLN					
a230	ADGGGPSRDAVFQSLQRAYLKQAKLMGISVSSEQIKQIIIVDDPNFHDANGKFDHALLN					
	70	80	90	100	110	120
	130	140	150	160	170	180

522

m230.pep	RYLSQRHMSEDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN
a230	RYLSQRHMSEDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN
	130 140 150 160 170 180
m230.pep	PDEFIAQVKVSEADLQKFYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE
a230	PDEFIAQVKVSEADLQKFYNANKKDYLLPKAVKLEYVALNLKDFADKQTVSETEVKNAFE
	190 200 210 220 230 240
m230.pep	ERVARLPANEAKPSFEQEKAAVENELKMKKAVADFNKAKEKLGDDAVNHPSSLAEAAKNS
a230	ERVARLPANEAKPSFEQEKAAVENELKMKKAVADFNKAKEKLGDDAFNHPSSLAEAAKNS
	250 260 270 280 290 300
m230.pep	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSVLTINSETAWVVRAKEVR
a230	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSVLTINSETAWVVRAKEVR
	310 320 330 340 350 360
m230.pep	EKKTLPFAEAKDAVRQAYIRTEAAKL
a230	EKKTLPFAEAKDAVRQAYIRTEAAKL
	370 380

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 833>:

g230-1.seq

```

1  ATGTTCCATT CCATCGAAAA ATACAGAACA CCCGCCCAAG TCTTATTAGG
51  CCTGATTGCA TTAACCTTTG TCGGCTTCGG CGTCAGCACG GTTTCCCATC
101 CGGGCGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGAGCAC
151 TCAATCAACA ACGCCATGCA GAACGAGCAG GCGGACGGCG GCAGCCCTTG
201 GCGCGACGCG GTGTTCCAAT CCCTGCTGCA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTCTT CCGAACAAAT CAAGCAGATG
301 ATTGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCAGTCACGC
351 GCTTTTGAGT CAATACCTGT CGCAACGCCA TATGCTGAA GACCAAGTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTTGGT AAGCCTCGTC
451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACGAGGTC AACCGCACCA TCCGTCGCA CACTTCAAC CCCGACGAGT
551 TCATCGCCCA AGTCAAAGCG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 CGGAACAAAA AAGACTATCT GCTGCCGCAG GCGGTCAAAT TGGAATATGT
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAAACGG
701 AAGTGAAAAA TGCGTTTGAA GAGCGCGTGG CGCGTTTGCC GGCACATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTGCGG ACTTCAACAA GGCAAAAGAA AAGCTGGGCG
851 ACGATGCGTT CAATCATCCC TCCTCGCTTG CCGAAGCCGC CAAAACAGC
901 GGTTTGAAAG TGGAAACCCA AGAACTTGG CTGAGCAGGC AGGACGCACA
951 AATGTCCGGC ATGCCCGAAA ACCTAATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAAAAAA ACCTACTGTT
1101 TGAAGAAGCC AAAGATGCGG TGCGTCAGGC CTATATCCGT ACCGAAGCCG
1151 CCAAACCTTG CAAAAACAAG GAAAAAGAAG TGCTTACCCA ACTGAACGGC
1201 GGCAAGGCAG TTGACGTGAA ATGCTCGGAA GTGTCCGTTT TGGGCGCGCA
1251 GCAGGCAAGG CAGTCCATGC CGCCCGAGGC TTATGCGGAA CTGCTGAAAG
1301 CAAAACCGGC AAACGGCAAA CCCGCCATG TCACTACTGAC CGGTCTGCCG
1351 GCACCCGTGA TTGTCGAGGC GCAGGCAGTC ACGCCTCCGG AGGATATTGC
1401 CGCACAGCTT CCTCCTGCGA AACAGGCTTT GGCACAACAG CAGTCTGCCA
1451 ATACTTTTGA CCTGCTGATC CGCTATTTC ACGGAAAAAT CAAACAGACT
1501 AAAGGAGCAC AATCGGTTGA CAACGGCGAT GGTCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 834; ORF 230-1.ng>:

g230-1.pep

```

1  MFHSIEKYRT PAQVLLGLIA LTFVFGVST VSHPGADYIV QVGDEKISEH
51  SINNAMQNEQ ADGGSPWRDA VFQSLQRAY LKQGAKLMI SVSSEIQKM
101 IVDDPNFHDA NGKFSHALLS QYLSQRHMSE DQFVEEIRDQ FALQNLVSLV

```

m230-1.seq

m230-1.ppt

1	MFHSIEKYRT	PAQVLLGLIA	LTfVFGfGVST	VSHPGADYIV	QVGDEKISDH
51	SINNAIQNEQ	ADGGGPPSRDA	VFQSLQRAY	LKQGAKLMGI	SVSSEQIKQI
101	IVDDPNFHDA	NGKFDHALLN	RYLSQRHMSE	DQFVEEIRDO	FALQNLVNLV
151	QNGVLVGDA	AEQLIRLTQV	NRTIRSHTFN	PDEFIAQKVQ	SEADLQKIFYN
201	ANKKDYLLPQ	AVKLEYVALN	LKDFADKQTV	SETEVKNAFE	ERVARLPANE
251	AKPSFEQZKA	AVENELKMKG	AVADFNKAKE	KLGGDADFNP	SSLAEAAKNS
301	GLKVETQETW	LSRQDAQMSK	MPENLINAVF	SDDDLKKKHN	SEVLTNINSET
351	AWVVRAKEVR	EKKTLPFAEA	KDAVRQYAIR	TEAAKLAENK	AKDVLTLQNG
401	GKAVDVKKSE	VSVLGAQQAR	QSMPPeAYAE	LLKAKPANGK	PAYVRLIGLP
451	APPIVEVQAV	TFPDDIAAQL	FLAKQALAAQ	QSANTFDLLI	RYFNGKIKQT
501	KGAOSVDNGD	GO*			

m230-1/g230-1 96.3% identity in 512 aa overlap

	10	20	30	40	50	60
m230-1.pep	MFHSIEKYRTPAQVLLGLIALT	FTVGFVGSTVSHPGADYIVQVG	DEKISDHSINNAIQNEQ			
g230-1	MFHSIEKYRTPAQVLLGLIALT	FTVGFVGSTVSHPGADYIVQVG	DEKISEHSINNAMQNEQ			
	10	20	30	40	50	60
m230-1.pep	ADGGGSPSRDAVFQSL	LQRAYLKQGA	KLMGISVSSE	QIKQIIVDDPN	FHDANGK	FDHALLN
g230-1	ADGGSPWRDAVFQSL	LQRAYLKQGA	KLMGISVSSE	QIKQIMIVDDPN	FHDANGKF	SHALLS
	70	80	90	100	110	120
m230-1.pep	RYLSQRHMS	EDQFVEEIR	DQFALQNL	VNLVQNGVL	VGDAOAEOLIR	LTOVNRTIRSH
g230-1	RYLSQRHMS	EDQFVEEIR	DQFALQNL	VNLVQNGVL	VGDAOAEOLIR	LTOVNRTIRSH
	130	140	150	160	170	180
m230-1.pep	RYLSQRHMS	EDQFVEEIR	DQFALQNL	VNLVQNGVL	VGDAOAEOLIR	LTOVNRTIRSH
g230-1	RYLSQRHMS	EDQFVEEIR	DQFALQNL	VNLVQNGVL	VGDAOAEOLIR	LTOVNRTIRSH

g230-1	:	:	:	:	:	:
	QYLSQRHMS	EDQFVEE	IRDQFAL	QNLVSLV	QNGVLVG	DAQAEQLIRLTQVNR
	130	140	150	160	170	180
m230-1.pep	PDEFIAQVKVSEADLQKFYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE					
g230-1	PDEFIAQVKASEADLQKFYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE					
	190	200	210	220	230	240
m230-1.pep	ERVARLPANEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDDAFNHPSSLAEAAKNS					
g230-1	ERVARLPAHEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDDAFNHPSSLAEAAKNS					
	250	260	270	280	290	300
m230-1.pep	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSVLTINSETAWVVRKEVR					
g230-1	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSVLTINSETAWVVRKEVR					
	310	320	330	340	350	360
m230-1.pep	EEKTLFFAEAKDAVRQAYIRTEAAKLAENKAKDVLTLQNGGKAVDVKWSEVSVLGAQQAR					
g230-1	EEKNLLFEEAKDAVRQAYIRTEAAKLAENKAKEVLTQNGGKAVDVKWSEVSVLGAQQAR					
	370	380	390	400	410	420
m230-1.pep	QSMPEAYAE LLKAKPANGKPAYVRLIGLPAPVIVEVQAVTPPDDIAAQLPLAKQALAAQQ					
g230-1	QSMPEAYAE LLKAKPANGKPAYVRLTGLPAPVIVEAQAVTPPEDIAAQLPPAKQALAAQQ					
	430	440	450	460	470	480
m230-1.pep	QSANTFDLLIRYFNGKIKQTKGAQSVDNGDGQX					
g230-1	QSANTFDLLIRYFNGKIKQTKGAQSVDNGDGQX					
	490	500	510			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 837>:

a230-1.seq

```

1   ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCAAG TCCTTTTGGG
51  CCTGATTGCA TTAACCTTCG TCGGCTTCGG GGTACGACAG GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCGCGACGCG GTGTTTCAAT CCCTGCTACA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAGATT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCACGC
351 GCTTTTAAAC CGCTACCTTT CCAACGTCA TATGCTGAA GACCAAGTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTTGGT AAACCTCGTC
451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACGACGGTC AACCGCACCA TCCGTTTCGA CACTTTCAAC CCCGACGAAT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA GTTTTATAAC
601 GCAAAACAAA AAGACTACCT GCTTCCCAA GCGGTCAAAT TGGAATATGT
651 CGCCTTGAAT CTGAAAGACT TTGCAGACAA ACAGACCGTC AGCGAAACAG
701 AAGTGAAAAA TGCCTTTGAA GAGCGCGTGG CGCCTTTGCC GGCAAATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAATAA GGCAAAAGAA AAGCTGGGCG
851 ATGACGCGTT CAACCATCCT TCCTCGCTTG CCGAAGCCGC CAAAACAGC
901 GGTTTGAAAG TCGAAACCCA AGAACTTGG CTGAGCAGGC AGGATGCGCA
951 AATGTCGGGT ATGCCCGAAA ACCTGATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCTG TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACCTGC CGAAAAAAG GCAAAAGACG TGCTTACCCA ACTGAACGGC
1201 GCGAAGGCTG TTGACGTGAA ATGGTCGGAA GTGTCCGTTT TGGGCGCACA
1251 GCAGGCAAGG CAGTCCATGC CGCCCGAGGC TTATGCGGAA CTGCTGAAAG
1301 CAAAACGGGC AAACGGCAAA CCCGCCTACG TCAGGCTGAT CGGTCTGCGG
1351 GCACCCGTGA TTGTCGAAGT ACAGGCTGTA ACCCCGCCGG ATGATATCGC
1401 CGCACAGCTT CCGCTTGCAA AACAGGCTTT GCGCAACAG CAGTCTGCCA
1451 ATACTTTCGA CTTGTTGATA CGTTATTTC ACGGCAAAAT CAAACAGACC
1501 AAAGGAGCGC AATCGGTCGA CAACGGCGAC GGTCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 838; ORF 230-1.a>:

a230-1.pep

```
1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGPSRDA VFQSLQRAY LKQGAKLMGI SVSSEQIKQI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSE DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPK AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLTINSET
351 AWVVRKEVR EEKTLPFAEA KDAVRQAYIR TEAAKLAENK AKDVLTLQNG
401 GKAVDVWSE VSVLGAQQAR QSMPEAYAE LLKAKPANGK PAYVRLIGLP
451 APVIVEVQAV TPDIDIAAQL PLAKQALAAQ QSANTFDLLI RYFNGKIKQT
501 KGAQSVNDGD GQ*
```

a230-1/m230-1 99.8% identity in 512 aa overlap

a230-1.pep	10	20	30	40	50	60
m230-1	10	20	30	40	50	60
a230-1.pep	70	80	90	100	110	120
m230-1	70	80	90	100	110	120
a230-1.pep	130	140	150	160	170	180
m230-1	130	140	150	160	170	180
a230-1.pep	190	200	210	220	230	240
m230-1	190	200	210	220	230	240
a230-1.pep	250	260	270	280	290	300
m230-1	250	260	270	280	290	300
a230-1.pep	310	320	330	340	350	360
m230-1	310	320	330	340	350	360
a230-1.pep	370	380	390	400	410	420
m230-1	370	380	390	400	410	420
a230-1.pep	430	440	450	460	470	480
m230-1	430	440	450	460	470	480
a230-1.pep	490	500	510			
m230-1	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 839>:

g231.seq

```

1  atgtcaaaac gaaaatccat aaaccgtccg tatcaaaaac cggcggaact
51  gccgccgttg caaaataatc cgccatttta ccgtaaaaac cgccgcctga
101 acttttttat cgcggcagac ggccggttgc cgtctccgca aaaatgcagg
151 gcgcgcggtt ttcagacggc atttgccgtt caaggccgtg cgggtgtctt
201 accaaatgcc caaccattcg cccacggaat ccatccaatc cttattgcc
251 ccgcgcgtcc tgccgtgccg gcggtacgcc cacggcgctt gcggattttt
301 agctttccac aatcctttgc gttcccttcc cgctgaatt tgagcgtcgg
351 catagtcggc aaaatccgcc ttatcctgct gttcttttagc ataactttta
401 taatgccacg ccgccccgtc ctgcacctgc atcaggttca aatcggtttt
451 gccggcggat acctgcgcca cttcgcgctg atagcggtcg gtttcaaaac
501 cacgtacact gactttccta ccctccgccg ccgcgcgcag gttgtcgcgc
551 gaacgtgtac cgtaagccctg tttcatctcc ggtgcgtcga tatacgccat
601 ccgaatttta tgtttcgcgc cgtcgcgcgtc gatgacgtga agggatcgcg
651 cgtcatagac tttggacacc gtgcctgtgt agctgtggcc ggatttcgcc
701 gatgcccgtc ggcgaacggg cgcgtcgaaa cccacgtccc ctgcagtgcc
751 gagtacgtcg agtacggcaa ccgccgtccg caccgcctca ctgtcatatc
801 ccgtataacc caacgcgccc aaaagcgaca gggcgacggg aagccatttc
851 atgatttttt taatctgcat atttttcaaa tgccgatgcc gtcgaacat
901 ctctga

```

This corresponds to the amino acid sequence <SEQ ID 840; ORF 231.ng>:

g231.pep

```

1  MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
51  ARGFQTAFV QGRAVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF
101 SFPQSFAFFP RLNLSVGIVG KIRLILLFFS ITFIMPRRPV LHLHQVQIGF
151 AGGYLRHFAL IAVGFKHTYT DFPTLRRRAQ VVARTCTVSL FHLRCVDIRH
201 PNFMFRAVAV DDVKGIIVID FGHRACVAVA GFRRCPSANG RVETHVPCSA
251 EYVEYGNRRP HRLTVISRIT QRAQKRQGDG KPFHDFNLH IFQMPMPSEH
301 L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 841>:

m231.seq (partial)

```

1  ATGTCAAAAC GAAAATCCAT AAACCGTCCG TATCAAAAAC CGGCGGAAC
51  GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGCGGCAGAC GGCGGTTGCG CGTCTCCGCA AAAATGCAGG
151 CCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CGGTGTCTTT
201 ACCAAATGCC CAACCATTCG GC....

```

This corresponds to the amino acid sequence <SEQ ID 842; ORF 231>:

m231.pep (partial)

```

1  MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
51  ARGFQTAFV QGRAVSLPNA QPFG....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 231 shows 98.6% identity over a 73 aa overlap with a predicted ORF (ORF 231.ng) from *N. gonorrhoeae*:

m231/g231

	10	20	30	40	50	60
m231.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV					
	:					
g231	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV					
	10	20	30	40	50	60
	70					
m231.pep	QGRAVSLPNAQPFG					
	:					
g231	QGRAVSLPNAQPFAHGIHPILIAPAAPACPAVRPRRLRIFSFPQSFAFFPRLNLSVGIVG					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 843>:

527

a231.seq (partial)

```

1 ATGTCAAAAC GAAAATCCAT AAACCGTCCG TATCAAAAAC CGGCGGAACT
51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCTGA
101 ACTTTTTTAT CGNGGCAGAC GGCGGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CGGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCC GCGGTACGCC CACGGCGCTT GCGGATTTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACTTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 GCCGACAGAA ACCTGCGCCA CTTGCGCTG GTAGCGGTCG GTGTGAACA
501 CGCGGACGCT GACTTTCCTG CCTTCCGCCG CCGCGCGCAG GTTGTGCGCG
551 GAACGCGTGC CGTAAGCCTG TTTCATCTCC GGCGCGTCGA TATACGCCAT
601 CCGGATTTTG TGTTCGCGC CGTCGCGGTC GATAACGTGA AGGGTGTGCG
651 CGTCATAGAC TTTGGACACC GTGCCTGTGT AGCGGTGGCC GGATTTTCGCC
701 GATGCTCGGC GCGGGGCGGG CGCGTCGAA CCCGCTCCC CTGCCGCGCC
751 GAGTACGTCG AGTACGGCAA CCGCGTCCG CACCGCTCG CTGCCGTACC
801 CCGTATAACC CAACGCACCC AAAAGCGACA AGGCGACGGG AAGCCATTTT
851 ATGATTTTTT TAATCTGCAT ATTTTTCAAA TGCCGATGCC GTCTGAACAT
901 ATC

```

This corresponds to the amino acid sequence <SEQ ID 844; ORF 217.a>:

a231.pep (partial)

```

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIXAD GGCASPQKCR
51 ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF
101 SFPQSFAFPF RLNLVSGIIG KIRLILLFFS ITFIMPRRPV LHLHQVQIGF
151 ADRNLRHFAL VAVGVEHADA DFPAFRRAQ VVARTRAVSL FHLRRVDIRH
201 PDFVFRAVAV DNVKGVAVID FGHRACVAVA GFRRCSAAGG RVGTRVPCRA
251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFNLH IFQMPMPSEH
301 I

```

m231/a231 98.6% identity in 73 aa overlap

	10	20	30	40	50	60
m231.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPOKCRARGFQTAFV					
a231	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIXADGGCASPOKCRARGFQTAFV					
	10	20	30	40	50	60
	70					
m231.pep	QSRVSLPNAQPFG					
a231	QSRVSLPNAQPFAHGIHPILIAPAAPACPAVRPRRLRIFSFPQSFAFPFRLNLVSGIIG					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 845>:

g231-1.seq

```

1 ATGTCAAAAC GAAAATCCAT AAACCGTCCG TATCAAAAAC CGGCGGAACT
51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCTGA
101 ACTTTTTTAT CGCGGCAGAC GGCGGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAGGCCGTG CGGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGAAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCC GCGGTACGCC CACGGCGCTT GCGGATTTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAGTCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACTTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 GCCGGCGGAT ACCTGCGCCA CTTGCGCTG ATAGCGGTCG GTTTCAAACa
501 CaCgTaCaat gagtttcgta ccctccGCCG ccgcgcgCAG GTTgtcgcGC
551 GAACgTGTAC CGTAagcgtg TTtcatctcc GGTGcgtcGA TATACGCCaT
601 cCgAATTTta tGtttcgcgc cgtcgcCgtc gATGACGTGA AGGGtatcGC
651 CgtcATAGAC TTTGGACACC Gtgcctgcgt AGctGTGGCC GGATttcgc

```

This corresponds to the amino acid sequence <SEQ ID 846; ORF 231-1.ng>:

g231-1.pep

```

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
51 ARGFQTAFV QGRAVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF

```

```
101 SFQSFAPFF RLNLVGIVG KIRLILFFS ITFIMPRRPV LHLHQVQIGF
151 AGGYLRHFAL IAVGFKHTYN EFRTLRRRAQ VVARTCTVSV FHLRCVDIRH
201 PNFMFRAVAV DDVKGIAVID FGHRACVAVA GFR
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 847>:

m231-1.seq

```
1 ATGTCAAAAC GAAAATCCAT AAACCGTCCG TATCAAAAC CGGCGGAAC
51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGCGGCAGAC GGCGGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CCGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCC
251 CCGCCGCTCC TGCCTGCTCG GCGGTACGCC CACGGCGCTT GCGGATTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCTGAATT TGAGCGTCGG
351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACTTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 GCCGACAGAA ACCTGCGCCA CTTCGCGCTG GTAGCGGTCG GTATCGAACA
501 CGCGCACGCT GACTTTCCTG CCTTCGCGCG CCGCGCGCAG GTTGTCGCGC
551 GAACGCGTGC CGTAAGCCTG TTTCATCTCC GGCGCGTCGA TATACGCCAT
601 CCGGATTTTG TGTTCGCGC CGTCGCGGTC GATAACGTGA AGGTGTCTGC
651 CGTCATAGAC TTTGGACACC GTGCTGTGT AGCGGTGGCC GGATTTCGCC
701 GATGCTCGGC GGGGGGCGGG CGGTCGGAA CCCGCGTCCC CTGCCGCGCC
751 GAGTACGTCG AGTACGGCAA CCGCCGTCG CACCGCTCG CTGCCGTACC
801 CCGTATAACC CAACGCACCC AAAAGCGACA GGGCGACGGG AAGCCATTTC
851 ATGATTTTTT TAATCTGCAT ATTTTCAA TGCCGATGCC GTCTGAACAT
901 ATCGGAATCG GATTTCAGAC GGCATCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 848; ORF 231-1>:

m231-1.pep

```
1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPOKCR
51 ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAAPACS AVRPRRLRIF
101 SFQSFAPFF RLNLVGIIIG KIRLILFFS ITFIMPRRPV LHLHQVQIGF
151 ADRNLRHFAL VAVGIEHAHA DFPAFRRRAQ VVARTRAVSL FHLRRVDIRH
201 PDFVFRAVAV DNVKGVAVID FGHRACVAVA GFRRC SAAG RVGTRVPCRA
251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFNHL IFQMMPMSEH
301 IGIGFQTAS*
```

g231-1/m231-1 87.0% identity in 262 aa overlap

	10	20	30	40	50	60
g231-1.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASFPQKCRARGFQTAFV					
m231-1	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASFPQKCRARGFQTAFV					
	10	20	30	40	50	60
g231-1.pep	QGRAVSLPNAQPFPAHGIHPILIAPAAPACPAVRPRRLRIFSFPQSFAFPFRLNLVGIVG					
m231-1	QSRVSLPNAQPFPAHGIHPILIAPAAPACSAVRPRRLRIFSFPQSFAFPFRLNLVGIIIG					
	70	80	90	100	110	120
g231-1.pep	KIRLILFFSITFIMPRRPVLHLHQVQIGFAGGYLRHFALIAVGFKHTYNEFRTLRRRAQ					
m231-1	KIRLILFFSITFIMPRRPVLHLHQVQIGFADRNLRFALVAVGIEHAHADFPFRRRAQ					
	130	140	150	160	170	180
g231-1.pep	VVARTCTVSVFHLRCVDIRHPNFMFRAVAVDDVKGIAVIDFGHRACVAVAGFRXCPSANG					
m231-1	VVARTRAVSLFHLRRVDIRHPDFVFRAVAVDNVKGVAVIDFGHRACVAVAGFRRC SAAGG					
	190	200	210	220	230	240
g231-1.pep	CVETHVPCSAEYVVXGNRRPHR					
m231-1	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQGDGKPFHDFNHLIFQMMPMSEH					
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 849>:

a231-1.seq

```
1 ATGTCAAAAC GAAAATCCAT AAACCGTCCG TATCAAAAC CGGCGGAAC
51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGCGGCAGAC GGCGGTTGCG CGTCTCCGCA AAAATGCAGG
```



```

151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CCGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCG GCGGTACGCC CACGGCGCTT GCGGATTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACTTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 GCCGACAGAA ACCTGCGCCA CTTGCGCTG GTAGCGGTCG GTGTCGAACA
501 CGCGGACGCT GACTTTCCTG CCTTCGCGCG CCGCGCGCAG GTTGTGCGCG
551 GAACGCGTGC CGTAAGCCTG TTTTCATCTC GCGCGCTCGA TATACGCCAT
601 CCGGATTTTG TGTTCGCGC CGTCGCCGTC GATAACGTGA AGGGTGTGCG
651 CGTCATAGAC TTTGGACACC GTGCCTGTGT AGCGGTGGCC GGATTTCGCC
701 GATGCTCGGC GCGGGCGGG GCGCTCGGAA CCCGCTCCC CTGCCGCGCC
751 GAGTACGTCG AGTACGGCAA CCGCCGTCG CACCGCTCG CTGCCGTACC
801 CCGTATAACC CAACGCACCC AAAAGCGACA AGGCGACGGG AAGCCATTTC
851 ATGATTTTTT TAATCTGCAT ATTTTTCAAA TGCCGATGCC GTCTGAACAT
901 ATCGGAATCG GATTTCAGAC GGCATCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 850; ORF 231-1.a>:

a231-1.pep

```

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
51 ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAACP AVRPRLRIF
101 SFQSFAPFP RLNLVSGIIG KIRLILFFS ITFIMPRPV LHLHQVQIGF
151 ADRNLRHFA VAVGEHADAD DFPFRRRAQ VVARTRAVSL FHLRRVDIRH
201 PDFVFRVAV DNVKGVAVID FGHRACVAVA GFRRCSAAG RVGTRVPCRA
251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFNLH IFQMPMPSEH
301 IGIGFQTAS*

```

a231-1/m231-1 99.0% identity in 309 aa overlap

	10	20	30	40	50	60
a231-1.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV					
m231-1	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV					
	10	20	30	40	50	60
a231-1.pep	70	80	90	100	110	120
	QSRVSLPNAQPFAHGIHPILIAPAACPAPVPRRLRIFSFQSFAPFRLNLVSGIIG					
m231-1	QSRVSLPNAQPFAHGIHPILIAPAACPASAVRPRRLRIFSFQSFAPFRLNLVSGIIG					
	70	80	90	100	110	120
a231-1.pep	130	140	150	160	170	180
	KIRLILFFSITFIMPRRPVLHLHQVQIGFADRNLRHFAVAVGEHADADFPFRRRAQ					
m231-1	KIRLILFFSITFIMPRRPVLHLHQVQIGFADRNLRHFAVAVGIEHADADFPFRRRAQ					
	130	140	150	160	170	180
a231-1.pep	190	200	210	220	230	240
	VVARTRAVSLFHLRRVDIRHPDFVFRVAVDQNVKGVAVIDFGHRACVAVAGFRRCASAGG					
m231-1	VVARTRAVSLFHLRRVDIRHPDFVFRVAVDQNVKGVAVIDFGHRACVAVAGFRRCASAGG					
	190	200	210	220	230	240
a231-1.pep	250	260	270	280	290	300
	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQGDGKPFHDFNLHIFQMPMPSEH					
m231-1	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQGDGKPFHDFNLHIFQMPMPSEH					
	250	260	270	280	290	300
a231-1.pep	310					
	IGIGFQTASX					
m231-1	IGIGFQTASX					
	310					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 851>:

g232.seq

```

1 atgatgggca acagcctgat tgaatccggt acgtttgtcg ccatecctgtt
51 tggtcagatt ttgggaacgg cggttgccgg cgcgccgct tatattgtcg
101 ggatactggt ttgctggtc gccgtcggag gaacggccgg cagcctgttt

```

530

```

151 atgccgtccg tacccgccaa ggctgccgat acccaaatcg agtgggaatat
201 tgtccgtggt aaaaaatccc tgctgcgtga aacgggtgcg cacaatcccc
251 tttttaccgc cattatcggc atctcgtggt tttggtttgt cggcgcggtt
301 tataccacgc aactgccgac ctttacccaa atccatttgg gcggcaacga
351 taatgttttt aacctgatgc ttgctttggt ttccatcggt attgccgccc
401 gtccggtact gtgtgccaaag ttcggcaggg aacggctgat gttggcttgg
451 gtaacggttg gtgcgttggg ttcgacggtt tgcggcctgg ttttggtgtg
501 gctgacgcac ggacaccggt ttgaagggct gaacggcatt ttttggtttt
551 tatcgcaagg atgggcatac cccgtgatgg cggtgatgac gctgatcggc
601 tttttcggcg gattttttctc cgttccgctc tatacctggc tgcaaacgcg
651 cagcagcgag actttccgcg cccgcgcgct tgccgccaac aatatcgtta
701 acggcatctt tatggtttcc gccgcgctt tgagcgcggt attgctgttt
751 ttgtttgaca gcatttccct gctgtatctg attgtcgctt tgggcaatat
801 tccgttggcg gtatttttga ttaagcgca aaggcggttt ttaggcgcgg
851 cggcaatcag gaaaaaacct tga

```

This corresponds to the amino acid sequence <SEQ ID 852; ORF 232.ng>:

g232.pep

```

1 MMGNSLIESG TFVAILFGQI LGTAVAGAPP YIVGILVLLV AVGGTAGSLF
51 MPSVPAKAAD TQIEWNIVRG TKSLLRETVR HNPVFTAIIG ISWFWFVGAV
101 YTTQLPTFTQ IHLGGNDNVF NLMLALFSIG IAAGSVLCAK FGRERLMLAW
151 VTVGALGSTV CGLVLVWLTH GHRFEGLNGI FWFLSQGWAY PVMAMVTLIG
201 FFGGFFSVPL YTWLQTASSE TFRARAVAN NVNGIFMVSA AAVLSAVLLF
251 LFDSISLLYL IVALGNIPLA VFLIKRERRF LGAAAIRKKP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 853>:

m232.seq

```

1 ATGATGGGCA ACAGCCTGAT TGAATCGGGT ACGTTTGTCTG CCATCCTGTT
51 CCGTCAGATT TTGGGAACGG CCGTGGCAGG TGTACCGCCT TATATTGTCTG
101 GGATACTGGT TTTGCTGGTC GCCGTCGGAG GCACGGTCGG CAGCCTGTTT
151 ATGCCGTCCG TACCCGCCAA GGCTGCCGAT ACACAAATTG AGTGAATAT
201 TGTCCGTGGC ACAAATCCCC TGCTGCGTGA AACGGTGCGG CACAAGCCCG
251 TTTTACC GC CATTATCGGT ATTTCTGTTG TTTGGTTTGT CGGCGCGGTT
301 TATACCACGC AACTGCCGAC CTTTACCCAA ATCCATCTGG GCGGCAACGA
351 CAATGTTTTC AACCTGATGC TTGCTCTGTT TTCCATCGGT ATTGCCGCCG
401 GTTCGGTACT GTGTGCCAAG TTCAGCAKGG AACGCCTGAT GTTGCTTGG
451 GTAACGGTTG GTGCGTTGGG TTTGACGGTT TCGGCTTGG TTTTGGTGTG
501 GCTGACGCAC GGACACCGTT TTGAAGGGCT GAACGGCATT TTTTGTGTTT
551 TATCGCAAGG ATGGGCATAT CCCGTGATGG CCGTGATGAC GCTGATCGGC
601 TTTTTCGGCG GATTTTTTCTC CGTTCCGCTC TATACCT (g) TG CAAACCGCCA
651 TAGCGAGaTT TCCGCGCCCG GCCGTTGCCG CCAACAATAT CGTTAACGGT
701 ATTTTATG TTTCCGCTGC CGTTTTGAGC GCGGTGTTGC TGTTTTGTG
751 TGACAGCATT TCCTTGTGTT ATCTGATTGT CGCTTTGGGC AATATTCCGT
801 TGTCGTATT TTTGATTAA GCGGAAAGGC GGTTTTTAGG CGCGCGCGCA
851 ATCAGGAAAA AACCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 854; ORF 232>:

m232.pep

```

1 MMGNSLIESG TFVAILFGQI LGTAVAGVPP YIVGILVLLV AVGGTVGSLF
51 MPSVPAKAAD TQIEWNIVRG TKSLLRETVR HKPVFTAIIG ISWFWFVGAV
101 YTTQLPTFTQ IHLGGNDNVF NLMLALFSIG IAAGSVLCAK FSXERLMLAW
151 VTVGALGLTV CGLVLVWLTH GHRFEGLNGI FXFLSQGWAY PVMAMVTLIG
201 FFGGFFSVPL YTVQTAIARF PRPAVAANNI VNGIFMVSA VLSAVLLFLF
251 DSISLLYLIV ALGNIPLSVF LIKRERRFLG AAAIRKKP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 232 shows 94.1% identity over a 290 aa overlap with a predicted ORF (ORF 232.ng) from *N. gonorrhoeae*:

m232/g232

```

          10      20      30      40      50      60
m232.pep  MMGNSLIESGTFVAILFGQILGTAVAGVPPYIVGILVLLVAVGGTVGSLFMPSVPAKAAD
          |||||:|||||:|||||:|||||:|||||:|||||:
g232      MMGNSLIESGTFVAILFGQILGTAVAGAPPYIVGILVLLVAVGGTAGSLFMPSVPAKAAD

```

531

	10	20	30	40	50	60
	70	80	90	100	110	120
m232.pep	TQIEWNIVRGTKSLLRETVRHKPVFTAIIGISWFWFVGAVYTTQLPTFTQIHLGGNDNVF					
g232	TQIEWNIVRGTKSLLRETVRHNPFVFTAIIGISWFWFVGAVYTTQLPTFTQIHLGGNDNVF					
	130	140	150	160	170	180
m232.pep	NLMLALFSIGIAAGSVLCAKFSXERLMLAWVTVGALGLTVCGLVLVWLTHGHRFEGLNGI					
g232	NLMLALFSIGIAAGSVLCAKFRERLMLAWVTVGALGSTVCGLVLVWLTHGHRFEGLNGI					
	190	200	210	220	230	
m232.pep	FXFLSQGWAYPVMAMVTLIGFFGGFFSVPLYT-VQTAIARFPRP-AVAANNIVNGIFMVS					
g232	FWFLSQGWAYPVMAMVTLIGFFGGFFSVPLYTWLQTASSETFRARAVAANNIVNGIFMVS					
	240	250	260	270	280	289
m232.pep	AAVLSAVLLFLFDSISLLYLIALGNIPLSVFLIKRERRFLGAAAIRKKPX					
g232	AAVLSAVLLFLFDSISLLYLIALGNIPLAFLIKRERRFLGAAAIRKKP					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 855>:

```

a232.seq
1  ATGTACGCTA AAAAAGGCGG TTTGGGACTG GTTAAAGCC GCCGTTTCGC
51  ACCTCTTTTC GCTACGCAGT TTCTCGGCGC GTTCAACGAC AATGTGTTCA
101 AAACCGCGCT GTTTGTGATG ATTGGGTTTT ACGGTTTGGG GCAAAACGGC
151 TTCTTGCCCTG CCGGACAGAT GTTGAAGTTG GGCGCGTTGC TGTATTATTT
201 GCCGTATTTC CTGTTTTCCCT CGCTGTCGGG GCAGTTGGGT AACAAATTCG
251 ACAAGGCCGT TTTGGCGCGT TGGGCCAAGG TGCTGGAAAT GATCATTATG
301 GCGGTGGCGG CATACGGGTT TTATATCCGG TCTGCCCGCG TGCTTTTGGC
351 GTGTCTGTTT TGCATGGGCG CGCAATCGAC GCTGTTTCGG CCGCTGAAAT
401 ACGCCATCCT GCCCGATTAT CTCGACGACA AAGAGTTGAT GATGGGCAAC
451 AGCCTGATTG AATCGGGTAC GTTTGTCCGC ATCCTGTTCC GTCAGATACT
501 GGGGACTGCG GTGGCAGGTG TACCGCCTTA TATTGTCGGG ATACTGGTTT
551 TGCTGGTCGC CGTAGGAGGC ACGGTCGGCA GCCTGTTTAT GCCGTCCGTA
601 CCCGCCAAGG CTGCCGATAC ACAAATTGAG TGGAATATTG TCCGGGGTAC
651 AAAATCCCTG CTGCGTGAAA CCGTGCGGCA CAAGCCCGTT TTTACCGCCA
701 TTATCGGTAT TTCGTGGTTT TGGTTTGTGC GCGCGGTTTA TACCACGCAA
751 CTGCCGACCT TTACCCAAAT CCATCTAGGC GGCAACGACA ATGTTTTCAA
801 CCTGATGCTT GCCCTGTTTT CCATCGGTAT TGCCGCCGGT TCGGTACTGT
851 GTGCCAAGTT CAGCAGGGAA CGGCTGAGGT TGGCTTGGGT AACGGTTGGT
901 GCGTTGGGTT TGACGGTTTG CGGCTTGGTT TTGGTGTGGC TGACGCACGG
951 ACACCGTTTT GAAGGGCTGA ACGGCATTTT TTGGTTTTTA TCGCAAGGAT
1001 GGGCATATCC CGTGATGGCG GTGATGACGC TGATCGGCTT TTTCGGCGGA
1051 TTTTCTCCG TTCCGCTCTA TACCTGGCTG CAAACCGCCA GTAGCGAGAC
1101 TTTCCGCGCC CGCGCCGTTG CCGCCAACAA TATCGTTAAC GGTATTTTAA
1151 TGGTTTCCGC TGCCGTTTTG AGCGCGGTGT TGCTGTTTTT GTTTGACAGC
1201 ATTTCTTGT TGTATCTGAT TGTGCTTTG GGCAATATTC CGTTGTCCGT
1251 ATTTTGTGAT AAGCGCGAAA GCGGTTTTTT AGGCGCGGCG GCAATCAGGA
1301 AAAAACCTTG A

```

This corresponds to the amino acid sequence <SEQ ID 856; ORF 232.a>:

```

a232.pep
1  MYAKKGGLGL VKSRRFAPLF ATQFLGAFND NVEKTALFVM IGFYGLGQNG
51  FLPAGQMLNL GALLFILPYF LFSSLSGQLG NKFDKAVLAR WAKVLEMIIM
101 AVAAYGFYIR SAPLLIACLF CMGAQSTLFG PLKYAILPDY LDDKELMMGN
151 SLIESGTFA ILFGQILGTA VAGVPPYIVG ILVLLVAVGG TVGSLEMPSPV
201 PAKAADTQIE WNIVRGTKSL LRETVRHKPV FTAIGISWF WFGAVYTTQ
251 LPTFTQIHLG GNDNVFNML ALFSIGIAAG SVLCAKFSRE RLRLAWVTVG

```

532

301 ALGLTVCGLV LVWLTHGHRF EGLNGIFWFL SQGWAYPVMA VMTLIGFFGG
 351 FFSVPLYTWL QTASSETFRA RAVAANNIVN GIFMVSAAVL SAVLLFLFDS
 401 ISLLYLIVAL GNIPLSVFLI KRERRFLGAA AIRKKP*

m232/a232 95.9% identity in 290 aa overlap

m232.pep					10	20	30
					MMGNSLIESGTFVAILEFGQILGTAVAGVPP		
a232	ACLFCMGAQSTLFGPLKYAILPDYLDKELMMGNSLIESGTFVAILEFGQILGTAVAGVPP						
	120	130	140	150	160	170	
m232.pep		40	50	60	70	80	90
		YIVGILVLLVAVGGTVGSLFMPSVPAKAADTQIEWNIVRGTKSLLRETVRHKPVFTAIIG					
a232		YIVGILVLLVAVGGTVGSLFMPSVPAKAADTQIEWNIVRGTKSLLRETVRHKPVFTAIIG					
		180	190	200	210	220	230
m232.pep		100	110	120	130	140	150
		ISWFWFVGAVYTTQLPTFTQIHLGGNDNVFNLMMLALFSIGIAAGSVLCAKFSXERLMLAW					
a232		ISWFWFVGAVYTTQLPTFTQIHLGGNDNVFNLMMLALFSIGIAAGSVLCAKFSRERLRLAW					
		240	250	260	270	280	290
m232.pep		160	170	180	190	200	210
		VTVGALGLTVCGLVLVWLTHGHRFEGLNGIFXFLSQGWAYPVMAVMTLIGFFGGFFSVPL					
a232		VTVGALGLTVCGLVLVWLTHGHRFEGLNGIFWFLSQGWAYPVMAVMTLIGFFGGFFSVPL					
		300	310	320	330	340	350
m232.pep		220	230	240	250	260	
		YT-VQTAIARFPRP-AVAANNIVNGIFMVSAAVLSAVLLFLFDSISLLYLIVALGNIPLS					
a232		YTWLQTASSETFRARAVAANNIVNGIFMVSAAVLSAVLLFLFDSISLLYLIVALGNIPLS					
		360	370	380	390	400	410
m232.pep		270	280	289			
		VFLIKRERRFLGAAAIRKKPX					
a232		VFLIKRERRFLGAAAIRKKPX					
		420	430				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 857>:

g233.seq

```

1  atgaaacgca aaaatatcgc gctgattccc gccgccggca tcgggggtgcg
51  tttcggtgcg gacaaaccca agcaatatgt cgaaatcgga agcaaaaccg
101 ttttagaaca tgtacttggg atttttgaac ggcattgaggc cgtcgatttg
151 accgtcgttg tcgtctcgcc cgaagacacg tttgccgata aggttcagac
201 ggcatttcca caggttcggg tgtggaaaaa cgggtggacag acccgcgccg
251 aaactgtccg caacgggtgtg gcaaaactgt tggaaaccgg tttggcggcg
301 gaaaccgaca atattctggt acacgatgcc gcccgctgct gcctgccgtc
351 tgaagctctg gcgcggttga tagaacaggc gggcaacgcc gccgaaggcg
401 ggattttggc agttcccgtt gccgatacgc tcaagcgcgc agaaagcgga
451 caaatcagtg caactgtcga ccgttcgggg ctttggcagg cgaaacgcc
501 gcagcttttt caagcggggtt tgctgcaccg cgcattggct gcggaaaact
551 tgggcggcat taccgatgaa gcgtccgccg tggaaaaact ggggtgtcgt
601 ccgctactga tacagggcga cgcgcgcaat ttgaaactga cgcagccgca
651 ggacgcatac atcgtcaggc tgctgctcaa tgccgtctga
```

This corresponds to the amino acid sequence <SEQ ID 858; ORF 233.ng>:

g233.pep

```

1  MKRKNIALIP AAGIGVRFGA DKPKQYVEIG SKTVLEHVLG IFERHEAVDL
51  TVVVVSPEDT FADKVQTAFP QVRVWKNNGQ TRAETVRNGV AKLLETGLAA
101 ETDNILVHDA ARCCLPSEAL ARLIEQAGNA AEGGILAVPV ADTLKRAESG
```

```
m233.seq (partial)
```

1	ATGAAGCGCA	AAAATATCGC	GCTGATTCCC	GCCGCCGGCA	TCGGGGCGCG
51	TTTCGGTGCG	GACAAACCCA	AGCAATATGT	CGAAATCGGA	AGCAAAACCG
101	TTTTAGAACA	TACGATTGGG	ATTTTTGAAC	GGCATGAGGC	CGTCGATTTG
151	ACCGTCGTG	TCGTCTCGCC	CGAAGACACG	TTTGCCGATA	AGGTTCAGAC
201	GGCATTTCGA	CAGGTTCCGG	TGTGGAAAAA	CGGCGGACAG	ACCCGCGCCG
251	AAACCGTCCG	CAACGGGTGTG	GCAAAACTGT	TGGAAAACCGG	TTTGCGCGCG
301	GAAACCGACA	ATATTCTGGT	ACACGATGCC	GCGCGTTGCT	GCCTGCCGTC
351	TGAAGCTTGC	ACGCGTTTGA	TAGAACAGGC	GGGCAACGCC	GCCGAAGGGC
401	GGATTTTGG	AATTCCCAT	GCCGATACGC	TCAAGTGCGC	GGACGTTGGG
451	AACATT				

m233.pep (partial)

```

1  MKRKNIALLIP AAGIGARFGA DKPKQYVEIG SKTVLEHTIG IFERHEAVDL
51  TVVVVSPEDT FADKVQTAFP QVRVWKNGGQ TRAETVRNGV AKLLETGLAA
101 ETDNILVHDA ARCCLPSEAL TRLIEQAGNA AEGGILAIPI ADTLKCADGG
151 NI....

```

Homology with a predicted ORF from *N. gonorrhoeae*

m233/g233

		10	20	30	40	50	60
m233.pep		MKRKNIALIPAAIGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT					
		:					
g233		MKRKNIALIPAAIGIGVRFGADKPKQYVEIGSKTVLEHVLGIFERHEAVDLTVVVVSPEDT					
		10	20	30	40	50	60
		70	80	90	100	110	120
m233.pep		FADKVQTAFPPQVRVWKNKGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL					
g233		FADKVQTAFPPQVRVWKNKGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL					
		70	80	90	100	110	120
		130	140	150			
m233.pep		TRLIEQAGNAAEGGILAIPIADTLKCADGGNI					
		: : : : :					
g233		ARLIEQAGNAAEGGILAVPADTLKRAESGQISATVDRSGLWQAQTPQLFQAGLLHRLALA					
		130	140	150	160	170	180

a233.seq

1	ATGAAGCGCA	AAAATATCGC	GCTGATTCCC	GCCGCCGGCA	TCGGGGCGCG
51	TTTCGGTGCG	GACAAACCCA	AGCAATATGT	CGAAATCGGA	AGCAAAACCG
101	TTTTAGAACA	TACGATTGGG	ATTTTTGAAC	GGCATGAGGC	CGTCGATTTG
151	ACCGTCGTTG	TCGTCCTCGC	CGAAGACAGC	TTTGCCGATA	AGGTCAGAC
201	GGCATTTCCA	CAGGTTCCGG	TGTGGA AAAA	CGCGGAGACAG	ACCCCGCGCG
251	AAACTGTCCG	CAACGGGTGTG	GCAAAATTGT	TGGA AACCGG	TTTGCGCGCG
301	GAAACCGACA	ATATTCTGTT	ACACGATGCC	GCGCGTTGCT	GCCTCCCGTC
351	TGAAGCTTTG	ACGCGGTTGA	TAGAACAGGC	GGCGCAACGCT	GCCGAAGGTG
401	GGATTTTGGC	AATTCCCGTT	CGCGATACGC	TCAAGTGC GC	GGACGCTGGG
451	AACATTAGTG	CAACCGTCGA	GCGGACGAGC	CTTTGGCAGG	CGCAAACGCC
501	GCAGCTTTTC	CGCGCCGGGC	TGCTGCAACG	CGCATTGGCT	GCGGAAAAC T
551	TGGACGGCAT	TACCGATGAA	CGCTCCGCCG	TGGA AAAATT	GGGCATCCGC
601	CCTTTGCTGG	TGCAGGCGCA	GCGCGCAATT	TTGAAACTGA	CGCAGCCGCA
651	GGACGCATAC	ATCGTCAGGC	TGCTGTCTGA	TGCCCTCTGA	

This corresponds to the amino acid sequence <SEQ ID 862; ORF 233.a>:

```
a233.pep
  1 MKRKNIALIP AAGIGARFGA DKPKQYVEIG SKTVLEHTIG IFERHEAVDL
 51 TVVVVSPEDT FADKVQTAFF QVRVWKNNGGQ TRAETVRNGV AKLLETGLAA
101 ETDNILVHDA ARCCLPSEAL TRLIEQAGNA AEGGILAIPIV ADTLKCADGG
151 NISATVERTS LWQAQTPQLF RAGLLHRLA AENLDGITDE ASAVEKLGIR
201 PLLVQGDARN LKLTQPQDAY IVRLLLDAV*
```

m233/a233 99.3% identity in 152 aa overlap

```

              10      20      30      40      50      60
m233.pep      MKRKNIALIP AAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT
              |||||||
a233           MKRKNIALIP AAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT
              10      20      30      40      50      60

              70      80      90      100     110     120
m233.pep      FADKVQTAFFQVRVWKNNGGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL
              |||||||
a233           FADKVQTAFFQVRVWKNNGGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL
              70      80      90      100     110     120

              130     140     150
m233.pep      TRLIEQAGNA AEGGILAIPIADTLKCADGGNI
              |||||||
a233           TRLIEQAGNA AEGGILAIPIVADTLKCADGGNISATVERTSLWQAQTPQLFRAGLLHRLA
              130     140     150     160     170     180

a233           AENLDGITDEASAVEKLGIRPLLQGDARNLKLTQPQDAYIVRLLLDAVX
              190     200     210     220     230
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 863>:

```
g234.seq
  1 atgaaaaccg tttccgcgcg catcgctttt gccgcgcgctg ccgtttcact
 51 gaccggctgt gcgaccgagt cctcacgcag cctcgagggt gcaaaagtcg
101 cctcctgcaa tacgcaatat cacggtgttc gcaccccgat ttccgtcgga
151 acattcgaca accgctccag cttccaaaaa ggcattttct ccgacagtga
201 agaccgtctg ggcagccagg caaaaacat cctggtaaca cacctgcaac
251 aaaccaaccg cttcaacgta ctgaaccgca ccaaccttag cgcattgaaa
301 caggaatccg gcatttcgag caaagcgag aacctgaaag gcgcagatta
351 tgctggtacc ggcgatgtaa ccgaattcgg acgcagagat gtcggcgatc
401 atcagctctt cggcattttg ggctcgcgga aatcgcaaat cgcctatgca
451 aaagtggctc tgaatatcgt caacgtcaat acttccgaaa tcgtctattc
501 cacacagggc gcggcggaat acgcactttc caaccgcgaa atcatcggtt
551 tcggcggcac ttccggctac gatgcgactt tgaacggcaa agttttagac
601 ttggcaatcc gcgaagcgt cgacaacttg gttcaggctg tcgacaacgg
651 cgcattggcaa tccaaccgtt aa
```

This corresponds to the amino acid sequence <SEQ ID 864; ORF 234.ng>:

```
g234.pep
  1 MKTVSAAIAF AAAVSLTGC ATESSRSLEV AKVASCNTQY HGVRTPISVG
 51 TFDNRSSFQK GIFSDSEDRL GSQAKTILVT HLQQTNRFNV LNRNTLSALK
101 QESGISGKAQ NLKGADYVVT GDVTEFGRRD VGDHQLFGIL GRGKSQIAYA
151 KVALNIVNVN TSEIVYSTQG AGEYALSRE IIGFGGTSY DATLNGKVLN
201 LAIREAVDNL VQAVDNGAWQ SNR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 865>:

```
m234.seq (partial)
  1 ...GGCGCGGCG AATACGCACT TTCCAACCGT GAAATCATCG GTTTCGGCGG
 51 CACTTCCGGC TACGATGCGA CTTTGAACGG CAAAGTTTTA GACTTGGCAA
101 TCCGCGAAGC .gTCAACAGC CTGGTTCAGG CTGTTGACAA CGGCGCATGG
151 CAACCAACC GTTAA
```

This corresponds to the amino acid sequence <SEQ ID 866; ORF 234>:

535

m234.pep (partial)
 1 ..GAGEYALSNR EIIGFGGTSG YDATLNGKVL DLAIREAVNS LVQAVDNGAW
 51 QPNR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 234 shows 94.4% identity over a 54 aa overlap with a predicted ORF (ORF 234.ng) from *N. gonorrhoeae*:

m234/g234

					10	20	30
m234.pep					GAGEYALSNREI	IGFGGTSGY	DATLNGKVL
g234	LGRGKSQIAYAK	VALNIVNVNT	SEIVYSTQ	GAGEYALSNREI	IGFGGTSGY	DATLNGKVL	
	140	150	160	170	180	190	

		40	50
m234.pep	DLAIREAVNSLVQ	AVDNGAWQ	PNRX
g234	DLAIREAVDNLVQ	AVDNGAWQ	SNRX
	200	210	220

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 867>:

a234.seq (partial)
 1 AACCGCACCT ATTTGAACGC ATTAAACAG GAATCCGGCA TTTCCGGCAA
 51 AGCGCATAAC CTGAAAGGCG CAAATTATGT CGNNACCGGC GATGTAACCG
 101 AATTCGGACG CANAGATGTC GGCGATCATC AGCTCTTCGG CATTTTGGGT
 151 CGCGGCAAAT CGCAAATCGC CTATGCAAAA GTGGCTCTGA ATATCGTCAA
 201 CGTCAATACT TCCGAAATCG TCTATTCCGC ACAGGGCGCG GGCGAATACG
 251 CACTTTCCAA CCGTGAAATC ATCGGTTTCG GCGGCACTTC CGGCTACGAT
 301 GCGACTTTGA ACGGCAAAGT TTTAGACTTG GCAATCCGCG AAGCCGTCAA
 351 CAGCCTGGTT CAGGCTGTTG ACAACGGCGC ATGGCAACCC AACCGTTAA

This corresponds to the amino acid sequence <SEQ ID 868; ORF 234.a>:

a234.pep (partial)
 1 NRTYLNALKQ ESGISGAHN LKGANYVXTG DVTEFGRXDV GDHQLFGILG
 51 RGKSQIAYAK VALNIVNVNT SEIVYSAQGA GEYALSNREI IGFGGTSGYD
 101 ATLNGKVLDL AIREAVNSLV QAVDNGAWQP NR*

m234/a234 100.0% identity in 54 aa overlap

					10	20
30						
m234.pep					GAGEYALSNREI	IGFGGTSGYD
a234	LGRGKSQIAYAK	VALNIVNVNT	SEIVYSAQGA	GAGEYALSNREI	IGFGGTSGYD	DATLNGKVL
	50	60	70	80	90	100

		40	50
m234.pep	DLAIREAVNSLVQ	AVDNGAWQ	PNRX
a234	DLAIREAVNSLVQ	AVDNGAWQ	PNRX
	110	120	130

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 869>:

g235.seq

g235.pep

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 871>:

m235.seq

This corresponds to the amino acid sequence <SEQ ID 872; ORF 235>:

m235 . pep

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 235 shows 96.7% identity over a 215 aa overlap with a predicted ORF (ORF 235.ng) from *N. gonorrhoeae*:

m235/q235

	10	20	30	40	50	60
m235.pep	MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGV	LAST				
g235	MKPLILGLAAVLALSACQVRKAPDLDYTSFKESKPASILVVPPLNESPDVNGTWG	MLAST				
	10	20	30	40	50	60
	70	80	90	100	110	120
m235.pep	AAPLSEAGYVVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVAVLYITVTEY	GTS				
g235	AAPLSEAGYVVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVAVLYITVTEY	GTS				
	70	80	90	100	110	120
	130	140	150	160	170	180

537

```

m235.pep      YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
               ||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||
g235          YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVGAVVNQIANSLT
               130      140      150      160      170      180

               190      200      210
m235.pep      DRGYQVSKTAAYNLLSPYSHNGILKGPRFVVEEQPKX
               ||||||||||||||||||||:|||||||||||||||||
g235          DRGYQVSKTAAYNLLSPYSRNGILKGPRFVVEEQPKX
               190      200      210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 873>:

```

a235.seq
1  ATGAAACCTT TGATTTTAGG GCTTGCCGCC GTGTTGGCGC TGTCTGCCTG
51 CCAAGTCAA AAAGCGCCCG ATTTGCGACT CACGTCATTC AAGGAAAGCA
101 AACCGGCTTC AATTTTGGTG GTTCCGCCGC TGAACGAATC GCCCGATGTC
151 AACGGAACAT GGGGTGTACT GGCTTCGACC GCCGCGCCGC TTTCCGAAGC
201 CGGCTATTAC GTCTTCCCGC CCGCAGTCGT GGAGGAAACC TTCAAACAA
251 ACGGCTTGAC CAATGCCGCC GATATTCACG CCGTCCGGCC GGAAAACTG
301 CATCAGATTT TCGGCAATGA TCGGGTTTTG TACATTACGG TTACCGAATA
351 CGGCACTTCA TATCAAATTT TAGACAGCGT GACGACCGTA TCCGCCAAAG
401 CACGGCTGGT CGATCCCCGC AACGGAAG AGTTGTGGTC GGGTTCGGCC
451 AGCATCCGCG AAGGCAGCAA CAACAGCAAC AGCGGCCTGT TGGGGGCTTT
501 GGTCAAGCGA GTGGTCAATC AGATTGCCAA CAGCCTGACC GACCGCGGTT
551 ATCAGGTTTC TAAACCGCC GCATACAACC TGCTGTCGCC CTATTCTCAC
601 AACGCATCT TGAAAGGTCC GAGATTGCTC GAAGAGCAGC CCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 874; ORF 235.a>:

```

a235.pep
1  MKPLILGLAA VLALSACQVQ KAPDFDYTSF KESKPASILV VPPLNESPDV
51 NGTWGVLAST AAPLSEAGYY VFPAAVVEET FKQNGLTNAA DIHAVRPEKL
101 HQIFGNDAVL YITVTEYGTS YQILDSVTTV SAKARLVDSR NGKELWSGSA
151 SIREGSNNSN SGLLGALVSA VVNQIANSLT DRGYQVSKTA AYNLLSPYSH
201 NGILKGPRFV EEQPK*

```

m235/a235 100.0% identity in 215 aa overlap

```

               10      20      30      40      50      60
m235.pep      MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
               |||||||||||||||||||||||||||||||||||||||||||
a235          MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
               10      20      30      40      50      60

               70      80      90      100     110     120
m235.pep      AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIAVRPEKLHQIFGNDAVLYITVTEYGTS
               |||||||||||||||||||||||||||||||||||||||||||
a235          AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIAVRPEKLHQIFGNDAVLYITVTEYGTS
               70      80      90      100     110     120

               130     140     150     160     170     180
m235.pep      YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
               |||||||||||||||||||||||||||||||||||||||||||
a235          YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
               130     140     150     160     170     180

               190     200     210
m235.pep      DRGYQVSKTAAYNLLSPYSHNGILKGPRFVVEEQPKX
               ||||||||||||||||||||:|||||||||||||||||
a235          DRGYQVSKTAAYNLLSPYSHNGILKGPRFVVEEQPKX
               190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 875>:

g236.seq

```

1  ATGGCGCGTT TCGCCTTCTC CGCCGACATT CTCCGCACAG CGTTTGCAGA
51  CGGTTTCATA ACCTGCAACC GCGCCACAT CCGGGGTGTA ATGCCAGCAG
101 CGTTCGCATT TTTCGCCGTC GCTGGCTTTG GCGGCAACGG CAAGTTCATC
151 ACCGACTTTC ACTTCTGCTT TAGACACCAG CAGGGCAAAG CGCAATTCCT
201 CGCCCAAAGC ATTCAGATAG CCGGCCATTT CTCCGGCGC AGTAATTTCTG
251 GCTTCCGCCCT GCAAaggacga accgacagTT TTGTcggcGC GCAAAGGCTC
301 GAtagcggcg gTtACTGCTT CGCGCGCTTC GCGGATTGCC GTCCATTTTT
351 TCACCAGTTC GGCTTCGGCT TTTCGTTGA TGGCCGGAA CTCGTGCCAA
401 GTATGGAAGA GGACGCTGTC TTCTTCGCCG CCGCCGATGA TGTCCACGC
451 TTCTTCGCCG GTGAAGCACA AAATCGGTGC AATCAAGAGA ACCAGGCTGC
501 GCGTGATGTG GTACAGGGCG GTTTCGCGC TCGGCGGGC GCGGCTGTCTG
551 GCTTTGGTGG TGTAGAGGCG GTCTTTCAGG ATGTCGAGGT AGAACGCGCC
601 CAAGTCTTCC GAGCAGAAAG AAACAATGTC TTTCACGGCG AAGTGAAGG
651 CATAGCGCGG ATAGTAACCG CCTGCCAAAC GCTCTTGCA CCGCCGCGCC
701 AATACCAAGG CGTAGCGGTC GATTTCCACC ATATCCGCC TTTGCACGGC
751 ATCTTCAATC GGATTAAAGT CGCTCAAATT GGCAAacagG AAGCTCAAGG
801 TATTGCGGAT GCGGCGGTAG CTTTCGGTAA CGCGTTTGAG GATTTCTTTG
851 GAAatcgCCA ATtcgccgct gTAATCGGTG GATCCGCCC ACAGGCGCAG
901 GATGTCCGCG CCGAATTCGT TATAGACTTC CTGCGGCGCG ACGACGTTGC
951 CGATGGATT TCGACATTTTG CGGCCGTTTT GGTCAACCAC GAAACCGTGG
1001 GTCAGCAGCT GTTTATACGG TCGCGTCCC ATGGATGA

```

This corresponds to the amino acid sequence <SEQ ID 876; ORF 236.ng>:

g236.pep

```

1  MARFAFSADI LRTAFADGFI TCNRAHIAGV MPAAFAFFAV AGFGGNGKFI
51  TDFHFCFRHQ QGKAQFFAQ IQIAGHFFRR GNFGFRLQGR TDSFVGAQRL
101 DSGGYCFARF ADCRPFFHQF GFGFFVDGRE LVPSMEEDAV FFAAADVPR
151 FFAGEAQNRC NQENQAARDV VQGLLRAAG AAVGFGGVEA VFQDVEVERA
201 QVFRAERNNV FHGEVEGIAR IVTACQTLQ PPRQYQGVAV DFHHIRLLHG
251 IFNRIKVAQI GKQEAQGIAD AAVAFGNAFE DFFGNRQFAA VIGGCRPQAG
301 DVRAEFVIDF LRRDDVADGF RHFAAVLVNH ETVGQQLFIR CASHG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 877>:

m236.seq (partial)

```

1  ..TTGCACGGAC GAACCGACGG TTTTGTCCGC GCGCAAAGGC TCGATGGCGG
51  CGGTTACCGC TTCGCGGGCT TCGCGGATTG CCGTCCATT TTTACCAGT
101 TCGGCTTCGG TTTTTCGTT GATGGTCGGG AACTCGTGCC AAGTATGGAA
151 GAGGACGCTG TcKtCTTCGC CGCCGCCGwT GAYGTCCAC GCTTCTTCGC
201 CGGTGAAGCA CAAAATCGGT GCAATCAAGA GAACCAAAC TCGTGTGATG
251 TGATACAGGG CAGTTTGTGC GCTGCGGCGT GCATGGCTGT CTGCTTTGGT
301 GGTGTAGAGG CGGTCTTTCA GGATGTCGAG GTAGAACGCA CCCAAGTCTT
351 CCGAGCAGAA AGAAACAATG TCTTTTACGG CAAAGTGGaA kGCATAACGC
401 GGATAGTAAT CGCCTGCCAG ACACCTTGC AGCTGACGTG CCAATACCAC
451 GGCGTAGCGG TCGATTCCA CCATATCCGC CTGTTGCACG GCATCTTCAA
501 TCGGATTAAA GTCGCTCAAG TTGGCAAACA AAAAGCTCAA GGTATTGCGG
551 ATACGGCGGT AgCTTTCGGT TACGCGTTTG AGGATTCTT TGGAAATCGC
601 CAATTCGCCG CTGTAATCGG TAGATGCCG CCACAGGCGC AGGATGTCTG
651 CGCCGAATTC GTTATAAACC TCTTGCGGTG CAACGACGTT GCCGATGGAT
701 TTCGACATTT TTTTGCCTTC GCCGTCGACA ACGAAACCAT GGGTCAGCAG
751 CTGTTTATAC GGCGCGCGAC CCATTGA

```

This corresponds to the amino acid sequence <SEQ ID 878; ORF 236>:

m236.pep (partial)

```

1  ..LHGRTDGFVG AQRLDGGGYR FAGFADCRPF FHQFGFGFFV DGRELVPSME
51  EDAVXFAAAX DVPRFFAGEA QNRCNQENQT ACDVIQSLC AAACMAVCFG
101 GVEAVFQDVE VERTQVFAE RNxVfYgKVE XiTRIVIAcQ TLLQLTcQYH
151 GVAVDFHHIR LLHGIFNRIK VAQVGKQKAQ GIADTAVAFG YAFEDFFGNR
201 QFAAVIGRCR PQAQDVCAEF VINLLRCNDV ADGFRHFFAF AVDNETMGQQ
251 LFIRRATH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 236 shows 82.9% identity over a 258 aa overlap with a predicted ORF (ORF 236.ng) from *N. gonorrhoeae*:

m236/g236

[illegible]

a236.seq

1	ATGGCGCGTT	TCGCCTTCTC	CGCCGACATT	CTCTGCACAG	CGTTTGCA
51	CGGTTTCATG	GCCTGCAACC	GCGCCCACAT	CGCGGGTGTA	GTGCCAGCAG
101	CGTTTCGATT	TTTCACCATT	ACTGGCTTTA	GCGGCAACGG	CAAGTTCGCT
151	GCCTACTTTT	ACTTCTGCTT	TAGACACCAG	CAAAGCAAAG	CGCAATTCTT
201	CGCCCAAAGC	ATTACAGATAG	CCGGCCATTT	CTTCCGGCGC	GGTAATTTTCG
251	GCTTCGGCTT	GCAAGGACGA	ACCGACGGTT	TTGTTCGGCGC	GCAAAGGCTC
301	GATGGCGGCG	GTTACCGCTT	CGCGGGCTTC	GCGGATTGCC	GTCCATTTTT
351	TCACCAGTTC	GGCTTCGGCT	TTTTCTGTTGA	TGGTCCGGAA	CTCGTGCCAA
401	GTATGGAATA	GCACGTGTCT	TTCTCGCGCC	CCGCCGATGA	TGTCCACGCG
451	TTCTTCGCCG	GTAAGACACA	AAATCGGTGC	AATCAAGAGA	ACCAGGCTGC
501	GCGTGATGTG	GTACAGGGCG	GTTTGCGCGC	TGCGGCGGGC	GCGGCTGTCTG
551	GCTTTGGTGG	TATAGAGGCG	GTCTTTTAGG	ATATCGAGGT	AGAACGCGCC
601	CAAGTCTTCC	GAGCAGAAAG	AAACCATTTC	TTTCACGGCA	AAGTGGAAGG
651	CATAACGCGG	ATAAAATCA	CCGGCAACGC	GTTCTTGCGA	CCGCCTTGCC
701	AACACCAAGG	CATAGCGTCT	GATTTCCACC	ATATCCGCCT	CTTGACGCGC
751	ATCTTCAATA	GGATTGAAGT	CGCTCAAGTT	GGCAAACAAA	AAGCTCAAGG
801	TATTGCGGAT	ACGGCGGTAG	CTTTCGGTTA	CGCGCTTGAG	GATTTCCTTG
851	GAAATCGCCA	ATTTCGCGCT	GTAATCGGTG	GATGCCGCC	ACAGGCGCAG
901	GATGTCCGCG	CCGAACCTCGT	TATACACTTC	TTGCGGCGCG	ACGACGTTGC
951	CGATGGATT	CGACATTTTG	CGCCCGTTTT	GATCCACCAC	GAAACCATGG
1001	GTCAGCAGCT	GTGTTGACGG	CGCGCGACCC	ATTGA	

a236.pep						
1	MARFAFSADI	LCTAFADGFM	ACNRAHIAGV	VPAAFAFFT I	TGFSGNGKFA	
51	AYFHFCFRHQ	QSKAQFFAQ S	IQIAGHFRR	GNFGFGLQGR	TDGFVGAQRL	
101	DGGGYRFAGF	ADCRPFHQF	GQGFVVDGRE	LVPSMEKHAV	FCAAADDVPR	
151	FFAGEAQNRC	NQENQAARDV	VQGGLRAAAG	AAVGFGGIEA	VFQDIEVERA	
201	QVFRAERNHF	FHGKVEGTR	IKITGNAFLQ	PPCQHQGIAA	DFHHIRLLHG	
251	IFNRIEVAQV	GKQKAQGIAD	TAVAFGYALE	DEFGNRQFAV	VIGGCRVPAQ	
301	DVRAELVIHF	LRRDDVDAGF	RHFAPVLIHH	ETMGQOLFVR	RATH*	

m236/a236 81.0% identity in 258 aa overlap

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 881>:

This corresponds to the amino acid sequence <SEQ ID 882; ORF 237.ng>:

g237.pep
1 MRDKVGGNIA LPAPRIFDSN IGKLRKNFKH ILADKLGHTR RIVDKFVILT
51 AEQPAVRAE AVIIIONMAVV AYCHIVADKP FCARAOGFGG NNGGADGNRL

541

```

101 AFQRPEYRVQ TDISIDGIDH IFTLDAAFGR VNQPTVLIRF DARHRGLEN
151 LRAGFGSGAG NTQRVIERMK MPQGQIELCA LVHIAVKLLF QLGFIPKLIM
201 TRTVMPLGVF MPLLQLFPML RTDGNRGITA LPITIDGMFA DAFVHQFDRL
251 QRLLPKPLRL LQADLFFNFP HTAGVVADNL PATPAGRAEA DTCGFQNDGF
301 MSVFRQRQCG TQTAQTAADN AGFGFQTALE FRINSMRINR TKIIRRQIFL
351 KIRANHCVCF IGYIFGRNDT DCRAISSXQK IG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 883>:

m237.seq

```

1 ATGCGGGACA AGGTTGGCGG TAATGTCGCA CTCCCCGCCC CACGAATATT
51 CGATTTTGAC ATCGGCAAGC TGCGGAAAAA CTTTAAGCAT ATCTTGGCGG
101 ACAAGCTCGG TCATaCGCTC AGGATTGTCTG ATAAACTCGT TATCCTTACC
151 GCCGAAAAGC AGTCTGCCGT CCGCGCTGAG GCGGTAATAA TCCAAAATAT
201 GGCGGTTGTC GCATACTGCC ATATTGTTAC GGATAAGCCC TTTGCGCGC
251 GCCCCCAAGG GTTCGGTCTGC AATAATAAAG GTGCTGACAG CAATCGCCTT
301 GCGTTCCAAA GGCCGGAATA TCGGGTTCAA ACCTGCATAA GTATTGACAG
351 CATAGACCAC ATTTTTCAC TCGACGCTGC CTTGCGGCGT GTAAACCAGC
401 CAACCGTTTT GATGCGGTTT GATGCACGTC ATCGGGGATT GCTCGAAAAAT
451 CTGCGCACCG GCTTCGGCAG CCGCACGAGC GATGCCCAAA GTGTAAGTGA
501 GCGGATGCAG GTGTCCGGAT AAGGGGTCGA ATTGTGCCCC TTGGTACATA
551 TCGCTGTCAA GCTGCTGTTT CAACTCGGCT TTATCCCAA GTGTACATG
601 ACTCGCACCG TAATGCCGTT GGGCGTGTTC ATGCCACTGC TGCAACTCTT
651 CCAATGCTG CGGACGGACG GCAACCGTGG CATAACCGCG CTGCCAATCA
701 CAATCGACGG CATGTTTGCG GACGCGTTCG TCCACCAGTT CGACCGCCTG
751 CAAAGACTGT TGCCAAAACC ATTGCGCCTG CTCCAAGCCG ACCTGTTTTT
801 CAATTTCCCC CATACCGCAG nCGTAATCGC TGATAACCTG CCCGCCACTC
851 CGTCCCAGC CGCCGAAACC GATACGCGCG GCTTCCAACA CAACCGTTTC
901 ATGTCCCTGC TCCGCCAAGG GCAATGCAGT GCACAAACCA CCAATCCGC
951 CGCCGATGAT ACAGGTATCG GTTTTCAGAC GGCATTGAAG TTtCGGATAA
1001 ACAGTATGAG GATTAACCGA ACTGAAATAA TAAGAAGGCA GATATTCTTG
1051 AAAATCAGGG CGAATCATTT TGTTTGCTTT ATCAGGTGTA TTTTCGGACG
1101 GAATGATACA GGCTGTCGGG CCATATCGTC CAwACAGAAA ATCGGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 884; ORF 237>:

m237.pep

```

1 MRDKVGGNVA LPAPRIFDFD IGKLRKNFKH ILADKLGHTL RIVDKLVILT
51 AEKQSAVRAE AVIIQNMAVV AYCHIVTDKP FCARPQGFGR NNGGADSNRL
101 AFQRPEYRVQ TCISIDSIDH IFALDAAFGR VNQPTVLMRF DARHRGLEN
151 LRTGFGSGTS DAQSVSERMQ VSGXGVELCP LVHIAVKLLF QLGFIPKLIM
201 TRTVMPLGVF MPLLQLFPML RTDGNRGITA LPITIDGMFA DAFVHQFDRL
251 QRLLPKPLRL LQADLFFNFP HTAXVIADNL PATPSRRAET DTRGFQHNRF
301 MSLLRQGQCS AQTTSQAADD TGIGFQTALK FRINSMRINR TEIIRRQIFL
351 KIRANHCVCF IRCIFGRNDT GCRAISSXQK IG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 237 shows 86.1% identity over a 382 aa overlap with a predicted ORF (ORF 237.ng) from *N. gonorrhoeae*:

m237/g237

	10	20	30	40	50	60
m237.pep	MRDKVGGNVALPAPRIFDFDIGKLRKNFKHILADKLGHTLRIVDKLVILTAEKQSAVRAE					
	: :					
g237	MRDKVGGNIALPAPRIFDSNIGKLRKNFKHILADKLGHTRRIVDKFVILTAEQPAVRAE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m237.pep	AVIIQNMAVVAYCHIVTDKPF CARPQGFGRNNGGADSNRLAFQRPEYRVQTCISIDSIDH					
	: : : :					
g237	AVIIQNMAVVAYCHIVADKPF CARAQFGGNNKGADGNRLAFQRPEYRVQTDISIDGIDH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m237.pep	IFALDAAFGRVNQPTVLMRFDARHRGLENLRTGFGSGTSDAQSVSERMQVSGXGVELCP					

[illegible]

```
a237.seq
1    ATGCGGGACA AGGTTGGCGG TAATGTCGCA CTCCCCGCC CACGAATATT
51   CGATTTTGAC ATCGGCAAGC TGCGGAAAAA CTTTAAGCAT ATCTTGGCGC
101  ACAAGCTCGG TCATACGCGC GGGATTGTGC ATAAACTCGT TATCCTTACC
151  GCCGAAAAGC AGTCTGCCGT CCGCGCTGAG CGGGTAATAA TCCAAAATAT
201  GACGGTTGTC GCATACTGCC ATATTGTTGC GGATAAGCCC TTTTGCACGC
251  GCGCCCAAGG GTTCTGTGGC AATAATAAAG GTGCTGACAG CAATCGCCTT
301  GCGCTCCAAA GGCTTGAATA TCGGATTCAA ACCGGCATAA GTATTGACGG
351  CGTACACCAG ATTTTTCGAT TCGACGCTGC CTTGCGGGGT GTAAACCAGC
401  CAACCGTTTT GATAAGGTTT AATGCGTATC ATGGGAGAAT GCTCAAAAAT
451  CTTCGTACCA GCTTCGGCAG CGGCGCGGGC GATGCCCAAC GTGTAATTGA
501  GCGGATGGAG ATGCCCGGAC AAGGGATCGA ACTGTGCGCC TTGGTACATA
551  TCGCTGTCAA GCTGCTGGCT CAGTTCAGTG TTAATCCAGA GTTGATAATG
601  AGTTGCACCG TAATATTTTT GGGCGTGCTC ATGCCATTGT GTCAATTCCT
651  CCAATGCTG CGAACGGATG GCAACCGTGG CATAACCGCG CTGCCAATCG
701  CAATCAATGG CATGTTTGCG GACGCGTTCG TCCACCAGTT CGACCGCCTG
751  CAAAGACTGT TGCCAAAACC ATTGCGCTTG CTCCAAACCG ACCTGTTTTT
801  CAATTTCCTC CATACCGCAG GCGTAATCGC TGATAACCTG CCCGCTACTC
851  CGTCCCGACG CGCCGAAACC GATACGCGCG GCTTCCAACA CACCGGTTTC
901  ATGTCCCTGC TCCGCCAAGG GCAATGCAGT GCACAAACCA CTCAATCCGC
951  CGCCGATGAT ACAGGTATCG GTTTTCAGAC GGCAATTGAAG TTTCGGATAA
1001 ACAGTATGAG GATTAACCGA ACTGAAATAA TAAGAAGGCA GATATTCTTG
1051 AAAATCAGGG CGAATCATTG TGTTTGCTTT ATCGGGTATA TTTTCGGACG
1101 GAATGATACA GGCTGTCTGAG CCATATCGTC CAAACAGAAA ATCGGTTGA
```

a237.pap

1	MRDKVGGNVA	LPAPRIFDFD	IGKLRLNFKH	ILADKLGHTR	GIVDKLVILT
51	AEKQSAVRAE	AVIIONMTVV	AYCHIVADPK	FCTRAQGFCC	NNKGADSNRL
101	ALQRLEYRIQ	TGISIDNGVHQ	IFAFDAADAFG	VNQPTVLIRF	NYHGRMLNL
151	LRTSFGSGAG	DAQRVIERME	MPGQGIELCA	LVHIAVKLLL	QFSVIPELIM
201	<u>SCTVIFLGLV</u>	<u>MPLLQFFPML</u>	RTDGNRGITA	LPIAINGMFA	DAFVHQFDRL
251	QRLLPKPLRL	LQTDLFFNFL	HTAGVIADNL	PATPSRAAET	DTRGFQHNRF
301	MSLLRQGCQS	AQTQTSAADD	TGIGFQTALK	FRINSMRINR	TEIIRRQIFL
351	KIRANHCVCF	IGYIFGRNDT	GCRAISSKQK	IG*	

543

m237/a237 85.6% identity in 382 aa overlap

	10	20	30	40	50	60
m237.pep	MRDKVGGNVALPAPRIFDFDIGKLRKNFKHILADKLGHTLRIVDKLVILTAEKQSAVRAE					
a237	MRDKVGGNVALPAPRIFDFDIGKLRKNFKHILADKLGHTRGIVDKLVILTAEKQSAVRAE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m237.pep	AVIIQNMAVVAYCHIVTDKPFPCARQGFGRNNKGADSNRLAFORPEYRVQTCISIDSIDH					
a237	AVIIQNMTVVAYCHIVADKPFCTRAQGFSGNNKGADSNRLALQRLRYRIQTGISIDGMVHQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m237.pep	IFALDAAFGRVNQPTVLMRFDARHRLLENLRTGFGSGTSDAQSVSERMQVSGXGVELCP					
a237	IFAFDAAFGGVNQPTVLIRFNAYHGRMLKNLRTSFGSGAGDAQRVIERMEMPGQGIELCA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m237.pep	LVHIAVKLLFQLGFIPKLIMTRTVMPLGVFMPLQLFPMRLTDGNRGITALPITIDGMFA					
a237	LVHIAVKLLQLFSVIPELIMSCTVIFLGVLMPLQLFFPMRLTDGNRGITALPIAINGMFA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m237.pep	DAFVHQFDRLQRLPKPLRLLQADLFFNFPHTAXVIADNLPATPSRRAETDTRGFQHNRF					
a237	DAFVHQFDRLQRLPKPLRLLQDLFFNFLHTAGVIADNLPATPSRRAETDTRGFQHNRF					
	250	260	270	280	290	300
	310	320	330	340	350	360
m237.pep	MSLLRQGQCSAQTTQSAADDTGIGFQTALKFRINSMRINRTEIIRRQIFLKIRANHCVCF					
a237	MSLLRQGQCSAQTTQSAADDTGIGFQTALKFRINSMRINRTEIIRRQIFLKIRANHCVCF					
	310	320	330	340	350	360
	370	380				
m237.pep	IRCFGRNDTGCRAISSXQKIGX					
a237	IGYIFGRNDTGCRAISSXQKIGX					
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 887>:

g238.seq

1	atgaatttgc	ctattcaaaa	attcatgatg	ctgttggcag	cggcaatatc
51	gatgctgcat	atccccatta	gtcatgcgaa	cggtttggat	gcccgtttgc
101	gcgatgatat	gcaggcaaaa	cactacgaac	cggttgga	ataccatctg
151	tttggtaatg	ctcgcgag	tgtaaaaaat	cggtttgag	ccgtccaaac
201	atttgatgca	actgcggtcg	gccccatact	gcctattaca	cacgaacgga
251	caggatttga	aggtgttatc	ggctatgaaa	cccatTTTTc	aggacacgga
301	cacgaagtac	acagtccggt	cgataatcat	gattcaaaaa	gcacttctga
351	tttcagcggc	ggcgtagacg	gcggttttac	cgtttaccac	cttcactcga
401	cagggtcgga	aatacatccc	gcagacggat	atgacgggcc	cacaaggcggc
451	ggttatccgg	aaccacaagg	ggcaagggat	atatacagct	accatatcaa
501	aggaacttca	acaaaaacaa	agataaacac	tggtccgcaa	gccccttttt
551	cagaccgctg	gctaaaagaa	aatgccggtg	ccgcttccgg	ttttctcagc
601	cgtgcggatg	aagcaggaaa	actgatatgg	gaaaacgacc	ccgataaaaa
651	ttggcgggct	aaccgtatgg	atgatattcg	cggcatcgtc	caagggtcgg
701	ttaatccttt	tttaacgggt	tttcaagggt	tagggattgg	ggcaattaca
751	gacagtgcgg	taagcccggg	cacagataca	gccgctcagc	agactctaca
801	aggtattaat	gatttaggaa	atttaagtcc	ggaagcacia	cttgccgccc

544

```

851 cgagcctatt acaggacagt gcctttgcgg taaaagacgg catcaattcc
901 gccagacaat gggctgatgc ccatccgaat ataacagcaa cagcccaaac
951 tgcccttgcc gtagcagagg ccgcaggtag gggttggcgc ggtaaaaaag
1001 tagaacttaa cccgaccaa tgggattggg taaaaatac cggctataaa
1051 aaacctgctg cccgccatat gcagactgta gatggggaga tggcaggggg
1101 gaatagaccg cctaaatcta taacgtcggg aggaaaagct aatgctgcaa
1151 cctatcctaa gttggttaat cagctaaatg agcaaaactt aaataacatt
1201 gcggctcaag atccaagatt gagtctagct attcatgagg gtaaaaaaaa
1251 ttttccaata ggaactgcaa cttatgaaga ggcagataga ctaggtaaaa
1301 tttgggttgg tgagggtgca agacaaacta gtggaggcgg atgggttaagt
1351 agagatggca ctcgacaata tcggccacca acagaaaaaa aatcacaatt
1401 tgcaactaca ggtattcaag caaattttga aacttatact attgattcaa
1451 atgaaaaaag aaataaaatt aaaaatggac atttaaatat taggtaa

```

This corresponds to the amino acid sequence <SEQ ID 888; ORF 238.ng>:

g238.pep

```

1 MNLPIQKFMM LLAAAI SMLH IPISHANGLD ARLRDDMQAK HYPEPGKYHL
51 FGNARGSVKN RVCAVQTFDA TAVGPILPIT HERTGFEGVI GYETHFSGHG
101 HEVHSPFDNH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP ADGYDGPQGG
151 GYPEPQGARD IYSYHIKGTs TKTKINTVPQ APFSDRWLKE NAGAASGFLS
201 RADEAGKLIW ENDPDKNWRA NRMDDIRGIV QGAVNPFLTG FQGVGIGAIT
251 DSAVSPVTDt AAQQTlQGIN DLGNLSPEAQ LAAASLLQDS AFAVKDGINS
301 ARQWADAHPN ITATAQTALA VAEAAGTVWR GKKVELNPTK WDWVKNTRYK
351 KPAARHMQTV DGEMAGGNRP PKSITSEGKA NAATYPKLVN QLNEQNLNNI
401 AAQDPRLSLA IHEGKKNFPI GTATYEEADR LGKIWVGEGA RQTSGGGWLS
451 RDGTRQYRPP TEKKSQFATT GIQANFETYt IDSNEKRNI KNHNLNIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 889>:

m238.seq

```

1 ATGAATTTGC CTATTCAAAA ATTCATGATG CTGTTTGcAG CAGCAATATC
51 GTTGCTGCAA ATCCCCATTA GTCATGCGAA CGGTTTGGAT GCGCGTTTGC
101 GCGATGATAT GCAGGCAAAA CAcTACGAAC CGGGTGGTAA ATACCATCTG
151 TTTGGTAATG CTCGCGGCAG TGTTAAAAAG CGGGTTTACG CCGTCCAGAC
201 ATTTGATGCA ACTGCGGTCA GTCCTGTACT GCCTATTACA CACGAACCGA
251 CAGGGTTTGA AGGTGTTATC GGTTATGAAA CCCATTTTTC AGGGCACGGA
301 CATGAAGTAC ACAGTCCGTT CGATCATCAT GATTCAAAA GCACTTCTGA
351 TTTcAGCGGC GGTGTAGACG GCGGTTTtAC TGTTTACCAA CTTCATCGAA
401 CAGGGTCGGA AATCCATCCG GAGGATGGAT ATGACGGGCC GCAAGGCAGC
451 GATTATCCGC CCCCcGGAGG AGCAAGGGAT ATATACAGCT ATTATGTCAA
501 AGGAACtTCA ACAAAAACAA AGACTAATAT TGTCCCTCAA GCGCCATTTT
551 CAGACCGTTG GCTAAAAGAA AATGCCGGTG CCGCCTCTGG TTTTTTCAGC
601 CGTGCGGATG AAGCAGGAAA ACTGATATGG GAAAGCGACC CCAATAAAAA
651 TTGGTGGGCT AACCGTATGG ATGATGTTCG CGGCATCGTG CAAGGTGCGG
701 TTAATCCTTT TTTAATGGGT TTTCAAGGAG TAGGGATTGG GGCAATTACA
751 GACAGTGCAG TAAGCCCGGT CACAGATACA GCCGCGCAGC AGACTCTACA
801 AGGTATTAAT GATTtTAGGAA AATTAAGTCC GGAAGCACA CTTGCTGCCG
851 CGAGCCTATT ACAGGACAGT GCTTTTGCGG TAAAAGACGG TATCAACTCT
901 GCCAAACAAT GGGCTGATGC CCATCCAAAT ATAACAGCTA CTGCCCCAAC
951 TGCCCTTTCC GCAGCAGAGG CCGCAGGTAC GGTTTGGAGA GGTAaaaaag
1001 TAGAACTTAA CCCGACTAAA TGGGATTGGG TTAAAAATAC CGGTTATAAA
1051 AAACCTGCTG CCCGCCATAT GCAGACTTTA GATGGGGAGA TGGCAGGTGG
1101 GAATAAACCT ATTAATCTT TACCAAAACAG TGCCGCTGAA AAAAGAAAAC
1151 AAAATTTTGA GAAGTTTAAT AGTAACTGGA GTTCAGCAAG TTTTGATTCA
1201 GTGCACAAAA CACTAACTCC CAATGCACCT GGTATTTTAA GTCCTGATAA
1251 AGTTAAACT CGATACACTA GTTTAGATGG AAAAATTACA ATTATAAAAG
1301 ATAACGAAAA CAACTATTTT AGAATCCATG ATAATTCACG AAAACAGTAT
1351 CTTGATTCAA ATGGTAATGC TGTGAAAACC GGTAAATTAC AAGGTAAGCA
1401 AGCAAAAGAT TATTtTACAAC AACAAACTCA TATCAGGAAC TTAGACAAAT
1451 GA

```

This corresponds to the amino acid sequence <SEQ ID 890; ORF 238>:

m238.pep

```

1 MNLPIQKFMM LFAAAISLLQ IPISHANGLD ARLRDDMQAK HYPEPGKYHL
51 FGNARGSVKK RVYAVQTFDA TAVSPVLPIT HERTGFEGVI GYETHFSGHG
101 HEVHSPFDHH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP EDGYDGPQGS

```


Homology with a predicted ORF from *N. gonorrhoeae*

m238/g238

m238.pep	MNLPIQKFMMLFAAAISLLQIPI	SHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKK			
g238	MNLPIQKFMMLLAAAISMLHIPI	SHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKN			
m238.pep	RVYAVQTFDATAVSPVLPITHERTGFEGVIGYETHFSGHGHEVHSPFDHHD	SKSTSDFSG			
g238	RVCAVQTFDATAVGPILPITHERTGFEGVIGYETHFSGHGHEVHSPFDNH	DSKSTSDFSG			
m238.pep	GVDGGFTVYQLHRTGSEIHPEDGYDGPQGS	DYPPPGGARDIYSYVVKGTSTKTKTNIVPQ			
g238	GVDGGFTVYQLHRTGSEIHPADGYDGPQGGGYEPQGARDIYSYHIKGTSTKTKINTVPQ				
m238.pep	APFSDRWLKENAGAASGFFSRADEAGKLIWESDPNKNWWANRMD	DVRGIVQGA	VNPFLMG		
g238	APFSDRWLKENAGAASGFLSRADEAGKLIWENDPDKNWRANRMD	DIRGIVQGA	VNPFLTG		
m238.pep	FQGVGIGAITDSAVSPVTD	TAAQQTLOGINDLGKLSPEAQLAAASLLQDS	SAFAVKD	GINS	
g238	FQGVGIGAITDSAVSPVTD	TAAQQTLOGINDLGNLSPEAQLAAASLLQDS	SAFAVKD	GINS	
m238.pep	AKQWADAHPNITATAQTALSA	AEAAAGTVWRGKKVELNPTKWDWVKNTGYKKPAARHMQTL			
g238	ARQWADAHPNITATAQTALAVAEAAAGTVWRGKKVELNPTKWDWVKNTGYKKPAARHMQTV				
m238.pep	DGEMAGGNKPIKSLPNSAAEKRKQNF	EKFNSNWSSASFDSVHKLTLPNAPGILSPDKVKT			
g238	DGEMAGGNRPPKSI-TSE	GKANAAATYPKLVNQLNEQNLNNIAAQDPRLSLAIHEGKKNFP			
m238.pep	RYTSLDGKITIIKDNENNYFRI	HDNSRKQYLD	SNGNAVKTGNLQ	GKQAKDY	LQQQTHIRN
g238	IGTATYEEADRLGKI	WVGEGARQTS	GGGWL	SRDGRQYRPPTEKKSQFATTGIQANFETY	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 891>:

```

a238.seq (partial)
  1 ATGAATTTGC CTATTCAAAA ATTCATGATG CTGTTTGCAG CAGCAATATC
 51 GTTGCTGCAA ATCCCATTA GTCATGCGAA CGGTTTGGAT GCCCGTTTGC
101 GCGATGATAT GCAGGCAAAA CACTACGAAC CGGGTGGTAA ATACCATCTG
151 TTTGGTAATG CTCGCGGCAG TGTTAAAAAT CGGGTTTACG CCGTCCAAAC
201 ATTTGATGCA ACTGCGGTCG GCCCATACT GCCTATTACA CACGAACGGA
251 CAGGATTTGA AGGCATTATC GGTTATGAAA CCCATTTTTC AGGACATGGA
301 CATGAAGTAC ACAGTCCGTT CGATAATCAT GATTCAAAAA GCACTTCTGA
351 TTTCAGCGGC GGCCTAGACG GTGGTTTTAC CGTTTACCAA CTTCATCGGA
401 CAGGGTCGGA AATCCATCCG GAGGATGGAT ATGACGGGCC GCAAGGCAGC
451 GATTATCCGC CCCCAGGAG AGCAAGGGAT ATATACAGCT ACTATGTCAA
501 AGGAACCTCA ACAAAAACAA AGAGTAATAT TGTTCCCCGA GCCCATTTT
551 CAGACCGCTG GCTAAAAGAA AATGCCGGTG CCGCCTCTGG TTTTTCAGC
601 CGTGCTGATG AAGCAGGAAA ACTGATATGG GAAAGCGACC CCAATAAAAA
651 TTGGTGGGCT AACCCTATGG ATGATATTCG CGGCATCGTC CAAGGTGCGG
701 TTAATCCTTT TTTAATGGGT TTTCAAGGAG TAGGGATTGG GGCAATTACA
751 GACAGTGCGAG TAAGCCCGGT CACAGATACA GCCGCGCAGC AGACTCTACA
801 AGGTATTAAT CATTTAGGAA ATTTAAGTCC CGAAGCACAA CTTGCGGCTG
851 CAACCGCATT ACAAGACAGT GCTTTTGCGG TAAAAGACGG TATCAATTCC
901 GCCAGACAAT GGGCTGATGC CCATCCGAAT ATAAGTCAA CAGCCCAAAC
951 TGCCCTTGCC GTAGCAGAGG CCGCAACTAC GGTTTGGGGC GGTAAAAAAG
1001 TAGAACTTAA CCCGACCAA TGGGATTGGG TTAAAAATAC CGGCTATAAA
1051 ACACCTGCTG TTCGCACCAT GCATACTTTG GATGGGGAAA TGGCCGGTGG
1101 GAATAGACCG CCTAAATCTA TAACGTCCAA CAGCAAAGCA GATGCTTCCA
1151 CACAA

```

This corresponds to the amino acid sequence <SEQ ID 892; ORF 238.a>:

```

a238.pep (partial)
  1 MNLPIQKEMM LFAAAISLLO IPISHANGLD ARLRDDMQAK HYPEGGKYHL
 51 FGNARGSVKN RVYAVQTFDA TAVGPILPIT HERTGFEGII GYETHFSGHG
101 HEVHSPFDNH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP EDGYDGPQGS
151 DYPPPGGARD IYSYVKGTS TKTKSNIVPR APFSDRWLKE NAGAASGFFS
201 RADEAGKLIW ESDPNKNWWA NRMDDIRGIV QGAVNPFLMG FQGVGIGAIT
251 DSAVSPVTD TAAQQTLOGIN HLGNSPEAQ LAAATALQDS AFAVKDGINS
301 ARQWADAHFN ITATAQTALA VAEAATTVWG GKVELNPTK WDWVKNTGYK
351 TPAVRTMHTL DGEMAGGNRP PKSITSNSKA DASTQ

```

m238/a238 91.9% identity in 385 aa overlap

	10	20	30	40	50	60
m238.pep	MNLPIQKFMMLFAAAISLLQIPISHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKK					
a238	MNLPIQKFMMLFAAAISLLQIPISHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKN					
	10	20	30	40	50	60
m238.pep	RVYAVQTFDATAVSPVLPITHERTGFEGVIGYETHFSGHGHEVHSPFDHHD	SKSTSDFSG				
a238	RVYAVQTFDATAVGPILPITHERTGFEGIIGYETHFSGHGHEVHSPFDNH	DSKSTSDFSG				
	70	80	90	100	110	120
m238.pep	GVDGGFTVYQLHRTGSEIHPEDGYDGPQGS	DYPPPGGARDIYSYVKG	TSTKTKTNIVPQ			
a238	GVDGGFTVYQLHRTGSEIHPEDGYDGPQGS	DYPPPGGARDIYSYVKG	TSTKTKSNIVPR			
	130	140	150	160	170	180
m238.pep	APFSDRWLKENAGAASGFFSRADEAGKLIWESDPNKNWWANRMD	DVRGIVQGAVNPFLMG				
a238	APFSDRWLKENAGAASGFFSRADEAGKLIWESDPNKNWWANRMD	DIRGIVQGAVNPFLMG				
	190	200	210	220	230	240
m238.pep	FQGVGIGAITDS	AVSPVTD	TAAQQTLOGINDL	GKLSPEAQ	LAAASLLQDS	SAFAVKDGINS
a238	FQGVGIGAITDS	AVSPVTD	TAAQQTLOGINDL	GKLSPEAQ	LAAASLLQDS	SAFAVKDGINS
	250	260	270	280	290	300
m238.pep	FQGVGIGAITDS	AVSPVTD	TAAQQTLOGINDL	GKLSPEAQ	LAAASLLQDS	SAFAVKDGINS
a238	FQGVGIGAITDS	AVSPVTD	TAAQQTLOGINDL	GKLSPEAQ	LAAASLLQDS	SAFAVKDGINS

547

```

|||||
a238      FQGVGIGAITDSAVSPVTDTAQQTLQGINHLGNLSPEAQLAAATALQDSFAVKGINS
          250      260      270      280      290      300

          310      320      330      340      350      360
m238.pep  AKQWADAHPNITATAQTALSAEEAAGTVVRGKKVELNPTKWDWVKNTGYKKPAARHMQTL
          |||||
a238      ARQWADAHPNITATAQTALAVAEAATTVWGGKKVELNPTKWDWVKNTGYKTPAVRTMHTL
          310      320      330      340      350      360

          370      380      390      400      410      419
m238.pep  DGEMAGGNKPIKSLP-NSAAEKRKQNFEFNSNWSSASFDSVHKTLTPNAPGILSPDKVK
          |||||
a238      DGEMAGGNRPPKSITSNSKADASTQ

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 893>:

```

g239.seq
1  atgttccacc ataaaggat tgcccgaaac cggcgatgg aggttttgtt
51  tttctgccgc cgccctgat gcttcgtgat tcgccaaac cgctgttgc
101 agcctcattt ggcataatc ctgctccaag gcgatttcct gttttttcgc
151 cttgtccaaa gctgtgaagt tgagcctgta ctgggttttc tgcatacaca
201 cggaaaaagc ggaaacgcac accgcaagca gcagaaagaa attcgatttg
251 ttcattgccg ttcagacgtt tttctctgtt attattccgg tatcgaccgc
301 gcagtcgctt ccgcccacac caaaactgcg ctctctcgcc tcgggttggc
351 ggcaatttcc gcttcaccgc gctttaatgc cctgcccacg attttcaggg
401 gcggatcggg caaatccgct tctctgaccg ccgcccagct cggcaggggc
451 tcgtgttgcg aatatttttt gacaaactgc ttcacaatgc ggtcttccaa
501 cgaatggaaa gcaatgacgc ccaaacgccc gccctctttc agacggcaca
551 tgacctgcgc caataccgcc cctacttctt caagctcgcg gttataaag
601 atgcggattg cctggaaggc gcgcgtcgca ggatcctgcc cccgctcgcg
651 agtacggacg ttttgtgcca cgatctgcgc cagcttgcgc gttgtatcga
701 ttggactttc cgcccgttgc gcgacaatgg cgcgcacaat ctggcggcta
751 aaccgctctt caccataa

```

This corresponds to the amino acid sequence <SEQ ID 894; ORF 239.ng>:

```

g239.pep
1  MFHHKGIARN RRMEVLFFCR RPDRFVIRQT RLLQPHLRII LLQGDFFFR
51  LVQSCEVEPV LVLLHHNGKS GNAHRKQKKE IRFVHCRSDV FLCYSGIGP
101 AVRSATRKTA LLALGLAAIS ASPGFNALPT IFRGGSGKSA SLTAAQLGRG
151 SCCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRHMTCGNTA PTSSSSRLIK
201 MRIAWKVRVA GSCPRSRVRT FCATICASLR VVSIGLSARC ATMARTIWR
251 NRSSP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 895>:

```

m239.seq
1  ATGCTCCACC ATAAAGGTmy kGCCCCGAAAC CGGCKGATGG AGGTTTTGT
51  TTTCTGCCGC CGCCCTGATC GCTTCGTGGT TCGCCAAACG CGCCTGTTGC
101 AGCCTCATTT GCGCATAATC CTGCTCCAAG GCGATTTCCT GTTTTTTCGC
151 CTTATCCAAA GCTGTGAAAT TGAGCCTGTA CTGGTTTTGC TGCATCACA
201 CGGAAAAAGC GGAAACGCAC ACCGCAAGCA GCAGAAGGAA ATTC AATTG
251 TTCATTGCCA TTCAGACGTT TTTCTCTGTG ATTGTTCCGG TATCGGACCG
301 GCAGTCCGCT CCGCCACACG CAAAACGCA CTTCTCGCCC TCGGATTGGC
351 GGCAATTTCC GCCTCACCAG GCTTTAATGC CCTGCCACG ATTTTCAGGG
401 GCAGCTCGGG CAAATCCGCT TCCCTGACCG CCGCCAGCG CGGCAGGGG
451 GCGTGTGCG AATATTTTTC GACAAACTGC TTCACAATGC GATCTTCCAA
501 CGAATGGAAA GCAATGACCG CCAAACGTCC GCCCTCTTTC AGACGACACA
551 TGACCTGCGG CAATACTGCC CTA CTCTT CAAGCTCGCG GTTAATAAAG
601 ATGCGGACCG CCTGGAAGGT GCGCGTCGCA GGATCTGCC CCCGCTCGCG
651 AGTACGACG TTTTGTGCCA CGATCTGCGC CAGCTTGCAG GTTGTATCGA
701 TTGGACTTTC CGCCC GTTGC GCAACAATGG CGCGCGCAAT cCGGCGGCTa
751 AACCGCTCTT cACCATAA

```

This corresponds to the amino acid sequence <SEQ ID 896; ORF 239>:

m239.pep
 1 MLHHKGXARN RXMEVLFFCR RPDRFVVRQT RLLQPHLRRI LLQGDFLFFR
 51 LIQSCEIEPV LVLLHHNGKS GNAHRKQOKE IQFVHCHSDV FLCDCSGIGP
 101 AVRSATRKTAL LALGLAAIS ASPGFNALPT IFRGSSGKSA SLTAAQRGRG
 151 ACCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRHMTCGNTA PTSSSSRLIK
 201 MRTAWKVRVA GSCPRSRVRT FCATICASLR VVSIIGLSARC ATMARAIIRRL
 251 NRSSP*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 239 shows 93.7% identity over a 255 aa overlap with a predicted ORF (ORF 239.ng) from *N. gonorrhoeae*:

m239/g239

m239.pep	10	20	30	40	50	60
	MLHHKGXARNRXMEVLFFCRRPDRFVVRQTRLLQPHLRRIILLQGDFLFFRLIQSCEIEPV					
g239	MFHHKGIARNRRMEVLFFCRRPDRFVIRQTRLLQPHLRRIILLQGDFLFFRLVQSCEVEPV					
	10	20	30	40	50	60
m239.pep	70	80	90	100	110	120
	LVLLHHNGKSGNAHRKQOKEIQFVHCHSDVFLCDCSGIGPAVRSATRKTALLALGLAAIS					
g239	LVLLHHNGKSGNAHRKQOKEIRFVHCRSDVFLCYYSIGIGPAVRSATRKTALLALGLAAIS					
	70	80	90	100	110	120
m239.pep	130	140	150	160	170	180
	ASPGFNALPTIFRGSSGKSASLTAAQRGRGACCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
g239	ASPGFNALPTIFRGSSGKSASLTAAQLGRGSCCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
	130	140	150	160	170	180
m239.pep	190	200	210	220	230	240
	RRHMTCGNTAPTSSSSRLIKMRTAWKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC					
g239	RRHMTCGNTAPTSSSSRLIKMRIA WKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC					
	190	200	210	220	230	240
m239.pep	250					
	ATMARAIIRRLNRSSPX					
g239	ATMARTIWRLNRSSPX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 897>:

a239.seq
 1 ATGCTCCACC ATAAAGGTAT TGCCCGAAAC CGGCGGATGG AGGTTTTGTT
 51 TTTCTGCCGC CGCCCTGATC GCTTCGTGGT TCGCCAAACG CGCCTGTTGC
 101 AGCCTCATTT GCGCATAATC CTGCTCCAAG GCGATTTCTT GTTTTTTCGC
 151 CTTATCCAAA GCTGTGAAGT TGAGCCTGTA CTGGTTTTGC TGCATCACAA
 201 CGGAAAAAGC GGAAACGCAC ACCGCAAGCA GCAGAAGGAA ATTCAATTTG
 251 TTCATTGCCA TTCAGACGTT TTTCTCTGTG ATTGTTCCGG TATCGGACCG
 301 GCAGTCCGCT CCGCCACACG CAAAACGCA CTTCTCGCCC TCGGATTGGC
 351 GGCAATTTCC GCCTCACCCG GCTTTAATGC CCTGCCCGCG ATTTTCAGGG
 401 GCGGCTCGGG CAAATCCGCT TCCCTGACCG CCGCCAGCG CGGCAGGGGC
 451 GCGTGTGCG AATATTTTTT GACAACTGC TTCACAATGC GGTCTTCCAA
 501 CGAATGGAAA GCAATGACCG CCAAACGTCC GCCCTCTTTC AGACGACACA
 551 TGACCTGCGG CAATACTGCC CCTACTTCTT CAAGCTCGCG GTTAATAAAG
 601 ATGCGGATTG CCTGGAAGGT GCGCGTCGCA GGATCCTGCC CCCGCTCGCG
 651 AGTACGGACG TTTTGTGCCA CGATCTGCGC CAGCTTGCAG GTTGATATCGA
 701 TTGGACTTTC CGCCCGTTGC GCAACAATGG CGCGCGCAAT CTGGCGGCTA
 751 AACCCTCTT CACCATAA

This corresponds to the amino acid sequence <SEQ ID 898; ORF 239.a>:

```
a239.pep
  1 MLHHKGIARN RRMEVLFFCR RPDRFVVRQT RLLQPHLRRI LLQGDFLFFR
 51 LIQSCEVEPV LVLLHHNGKS GNAHRKQQKE IQFVHCHSDV FLCDCSGIGP
101 AVRSATRKTA LLALGLAAIS ASPGFNALPA IFRGGSGKSA SLTAAQRGRG
151 ACCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRHMTCGNTA PTSSSRLIK
201 MRIAWKVRVA GSCPRSRVRT FCATICASLR VVSIGLSARC ATMARAIWRL
251 NRSSP*
```

m239/a239 97.3% identity in 255 aa overlap

	10	20	30	40	50	60	
m239.pep	MLHHK	GXARNR	XMEVLFFCR	RPDRFVVRQT	RLLQPHLRRI	LLQGDFLFFR	LIQSCEIEPV
a239	MLHHK	GIARNR	RRMEVLFFCR	RPDRFVVRQT	RLLQPHLRRI	LLQGDFLFFR	LIQSCEVEPV
	70	80	90	100	110	120	
m239.pep	LVLLHHNGKSG	NAHRKQQKEIQFVHCHSDV	FLCDCSGIGPAVRSATRKT	TALLALGLAAIS			
a239	LVLLHHNGKSG	NAHRKQQKEIQFVHCHSDV	FLCDCSGIGPAVRSATRKT	TALLALGLAAIS			
	130	140	150	160	170	180	
m239.pep	ASPGFNALPTIFR	GSSGKSASLTAAQRGRG	ACCEYFLTNCFTMRSSNEWK	AMTAKRPPSF			
a239	ASPGFNALPAIFR	GSSGKSASLTAAQRGRG	ACCEYFLTNCFTMRSSNEWK	AMTAKRPPSF			
	190	200	210	220	230	240	
m239.pep	RRHMTCGNTAPTSSSR	LIKMR	TAWKVRVAGS	CPRSRVRTFCATICASLR	VVSIGLSARC		
a239	RRHMTCGNTAPTSSSR	LIKMR	TAWKVRVAGS	CPRSRVRTFCATICASLR	VVSIGLSARC		
	250						
m239.pep	ATMARAI	RRLNRSSPX					
a239	ATMARAI	WRLNRSSPX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 899>:

```
g240.seq
  1 atgatagaag tcatacat ttt cttcggcgcc gaaacgcgca gacagtttgc
 51 ttgtgccgac gttggacgat ttctgcataa tgccgcgcac atccaaagag
101 gggtaaacaat gggatcatc gcgcacggga gacggtccga ttttataagg
151 ctgcgtattc agccgttcgt tcaaatacgg tttgcccgcga tccaatgcct
201 tcgcaatcac gaacggtttg attgccgaac caggttcgat catatcggtt
251 acggcacggg tgcgcgcgtg ttcgctgtct gcccggccgg gtctgttggg
301 atcgtaggcg ggcgtattgg ccaaggcgag gatttcccc gtgcgggcat
351 ccaaaaccac caccgttcgg gcttttgcct gatggtattc gaccgccttg
401 ttcaactctt cataggccaa ggtctgaatc ctctgatcga gggaaaggat
451 gatgtctttg ccgttttgcg gtgctttatt gcgcggggag tccaagctgt
501 ccacaatatt gccctgccgg tcccgcacaaa caacttcgcg gccgtcttcg
551 ccatacaggc tgtcttcaag cgaaagttcc aaaccttcct gacctttgcc
601 gtcaatatcg gtaaatccga tgacgtgtgc aaacaggttg cccatcgggg
651 aatggcggtt taa
```

This corresponds to the amino acid sequence <SEQ ID 900; ORF 240.ng>:

```
g240.pep
  1 MIEVIHFFGA ETRRQFACAD VGRFLHNAAH IQRGVNMGII AHGRRSDFIR
 51 LRIQPFVQIG FARIQCLRNH ERFDCRTRFD HIGYGTVA PL FAVCPAGSVG
101 IVGGRIGQGE DFPRAGIQNH HRS GFCLMV F DRLVQLFIGQ GLNPLIEGKD
151 DVFAVLRCFI ARGVQAVHNI ALPVPQNNFR AVFAIQAVFK RKFQTFLTFA
```

550

201 VNIGKSDDVC KQVAHRVMAF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 901>:

m240.seq

```

1   ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
51  TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTCA AATCGGTTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCCGCTGTTC GCTGTCTGCC CGGCCGGGCC TGTGGGATC
301 GTAGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCGTG CGGCATCCA
351 AACCACCAC CGTCCCGCT TTTGCCTGAT GGTATTCGAC CGCCTGTTC
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTCGGGG CTTTAKTGCG CGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGTCC CGCAAACGA CTTCCGCGCC GTCTCGCCA
551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAA CAGGTTGCC ATCGGGTAAT
651 GCGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 902; ORF 240>:

m240.pep

```

1   MIEVIHFFGT ETRRQFACAD VGRFLHDAAH IQRGVNMGIA HGRRSDFIRL
51  RIQPFVQIGF ARIQCLRNHK RFDCRTGFDH IGYGTVAPLF AVCPAGPVGI
101 VGGRIQGED FPRAGIQXHH RSGFCLMVFD RLVQLFIGQG LNPLIEGKDD
151 VFAVFRGFXA RGVQAVHNIA LPVPQNDFRA VFAMQAVFKR KFQTLFTFAV
201 NIGKSDDVCK QVAHRVMAF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 240 shows 94.5% identity over a 220 aa overlap with a predicted ORF (ORF 240.ng) from *N. gonorrhoeae*:

m240/g240

	10	20	30	40	50	59
m240.pep	MIEVIHFFGTETRRQFACADVGRFLHDAAH IQRGVNMGIAHGRRSDFIRLRIQPFVQIG					
	: : : : :					
g240	MIEVIHFFGAETRRQFACADVGRFLHNAAH IQRGVNMGIIAHGRRSDFIRLRIQPFVQIG					
	10	20	30	40	50	60
m240.pep	60	70	80	90	100	119
	FARIQCLRNHKRFDCRTGFDHIGYGTVAPLFAVCPAGPVGIVGGRIQGEDFPRAGIQXH					
	: : : : :					
g240	FARIQCLRNHERFDCRTRFDHIGYGTVAPLFAVCPAGSVGIVGGRIQGEDFPRAGIQNH					
	70	80	90	100	110	120
m240.pep	120	130	140	150	160	179
	HRSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFXARGVQAVHNIALPVPQNDFR					
	: : : : :					
g240	HRSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVLRCFIARGVQAVHNIALPVPQNNFR					
	130	140	150	160	170	180
m240.pep	180	190	200	210	220	
	AVFAMQAVFKRKQTLFTFAVNIGKSDDVCKQVAHRVMAFX					
	: : : : :					
g240	AVFAIQAVFKRKQTLFTFAVNIGKSDDVCKQVAHRVMAF					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 903>:

a240.seq

```

1   ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
51  TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTCA AATCGGTTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG

```

551

```

251 GCACGGTTGC GCCGCTGTTC GCTGTCTGCC CGGCCGGGCC TGTGGGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCCGTG CGGGCATCCA
351 AAACCACCAC CGTTCGGGCT TTTGCCTGAT GGTATTTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTTCGGGG CTTTATTGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAGGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAAA CAGGTTGCCC ATCGGGTAAT
651 GGCGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 904; ORF 240.a>:

```

a240.pep
  1 MIEVIHFFGT ETRRQFACAD VGRFLHDAAH IQRGVNMGIA HGRRSDFIRL
  51 RIQPFVQIGF ARIQCLRNHK RFD CRTGFDH IGYGTVAPLF AVCPAGPVGI
 101 VGGRIGQGED FPRAGIQNH RSGFCLMVFD RLVQLFIGQG LNPLIEGKDD
 151 VFAVFRGFIA RGVQAVHNIA LPVPQND FRA VFAMQAVFKR KFQTFLTFAV
 201 NIGKSDDVCK QVAHRVMAF*

```

m240/a240 99.1% identity in 219 aa overlap

```

              10      20      30      40      50      60
m240.pep      MIEVIHFFGTETRRQFACADVGRFLHDAAH IQRGVNMGIAHGRRSDFIRLRIQPFVQIGF
                ||||||||||||||||||||||||||||||||||||||||||||||||||||
a240           MIEVIHFFGTETRRQFACADVGRFLHDAAH IQRGVNMGIAHGRRSDFIRLRIQPFVQIGF
              10      20      30      40      50      60

              70      80      90     100     110     120
m240.pep      ARIQCLRNHKRFD CRTGFDHIGYGTVAPLFAVCPAGPVGIVGGRIGQGEDFPRAGIQXHH
                ||||||||||||||||||||||||||||||||||||||||||||||||||||
a240           ARIQCLRNHKRFD CRTGFDHIGYGTVAPLFAVCPAGPVGIVGGRIGQGEDFPRAGIQNH
              70      80      90     100     110     120

              130     140     150     160     170     180
m240.pep      RSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFXARGVQAVHNIALPVPQND FRA
                ||||||||||||||||||||||||||||||||||||||||||||||||||||
a240           RSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFIARGVQAVHNIALPVPQND FRA
              130     140     150     160     170     180

              190     200     210     220
m240.pep      VFAMQAVFKRK FQTF LTF AVNIGKSDDVCKQVAHRVMAFX
                ||||||||||||||||||||||||||||||||||||||||||||||||||||
a240           VFAMQAVFKRK FQTF LTF AVNIGKSDDVCKQVAHRVMAFX
              190     200     210     220

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 905>:

```

g241.seq
  1 ATGATAGAAG TCATACATTT CTTCCGGCACC GAAACGCGCA GACAGTTTGC
  51 TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
 101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
 151 CGTATTCAGC CGTTCGTTCA AATCGGTTTT GCCCGCATCC AATGCCTTCG
 201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
 251 GCACGGTTGC GCCGCTGTTC GCTGTCTGCC CGGCCGGGCC TGTGGGGATC
 301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCCGTG CGGGCATCCA
 351 AACCACCAC CGTTCGGGCT TTTGCCTGAT GGTATTTCGAC CGCCTTGTTT
 401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
 451 GTCTTTGCCG TTTTTCGGGG CTTTaktGCG CGGGGAGTCC AAGCTGTCCA
 501 CAATATTGCC CTGCCGGTCC CGCAAAACGA CTTCCGCGCC GTCTTCGCCA
 551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
 601 AATATCGGTA AATCCGATGA CGTGTGCAAA CAGGTTGCCC ATCGGGTAAT
 651 GGCGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 906; ORF 241.ng>:

```

g241.pep
  1 MPTRPTRAAN PPTPTTWLQT AYCPRPPYRP PSVQTHTPHE PASSTCAAKS

```

552

```

51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPSQ RQSVVMTVR
101 TVDMTVCDFL IGCIAHAFNR SFKADFHACQ RMVAVVHRLA VGNIGYTIDD
151 NIAGFRIVRF KHHTDLDFNR ERARIFNTDQ LRIMLTERIV GRKRHFDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFI QKLIVGIIHL IMQRNHGIFC
251 NSHICPFRNS RLITGAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 907>:

m241.seq (partial)

```

1  ..CGGCAATCAG TGGTGGTGAT GACCGTGC GG GCCGTGGACA TGACCGTGTG
51  CGATTTTCCTC ATCGGATGCA TCGCGCACGC TTTCAACTGT AGCCTTAAAG
101 CGGATTTTCA TGCCTGCCAA AGGATGGTTG CCGTCCACCA CCGCCTTGCC
151 GTCGGCAACA TCGGTTACAC GATAGACGAC AACATCGCCG GTTTCAGGAT
201 CGTCGGCTTC AAACATCATG CCGACTTCGA CTTCAACAGG GAACACGCCC
251 GCATCTTCGA TACGGACCAA CTCCGGATCC TGCTCGCCA ACGCATCGTC
301 GGGCGACAGC GCCACATCGA CCGTATCGCC GGCATCCTTA CCGTGCAACG
351 CCTCTTCCAC CAAAGGGAAA ATGCCGTCGT AACCGCCGTG CAGATACGCA
401 ATCGGTTCTT CGGTTTTGTC CAAAAGCTGA TTGTTGGCAT CATACTCTC
451 ATAATGCAGC GAAACCACGG AATTTTTCAC GATAGCCATA TTTGTCCTTT
501 CAGGAACAGC AGATTAATTA CAGGCGCATT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 908; ORF 241>:

m241.pep (partial)

```

1  ..RQSVVMTVR AVDMTVCDFL IGCIAHAFNC SLKADFHACQ RMVAVVHRLA
51  VGNIGYTIDD NIAGFRIVGF KHHADDFNR EHARIFDTDQ LRILLAERIV
101 GRQRHIDRIA GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL
151 IMQRNHGIFH DSHICPFRNS RLITGAF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 241 shows 91.5% identity over a 177 aa overlap with a predicted ORF (ORF 241.ng) from *N. gonorrhoeae*:

m241/g241

m241.pep				10	20	30
				RQSVVMTVR	AVDMTVCDFL	IGCIAHAFNC
g241	QPTYLLHPSN	KMPSETEQTL	FRRHQIPPSQ	RQSVVMTVR	TVDMTVCDFL	IGCIAHAFNR
	70	80	90	100	110	120
m241.pep		40	50	60	70	80
		SLKADFHACQ	RMVAVVHRLA	VGNIGYTIDD	NIAGFRIVGF	KHHADDFNR
g241	SFKADFHACQ	RMVAVVHRLA	VGNIGYTIDD	NIAGFRIVRF	KHHTDLDFNR	ERARIFNTDQ
	130	140	150	160	170	180
m241.pep		100	110	120	130	140
		LRILLAERIV	GRQRHIDRIA	GILTVQRLFH	QRENAVVTAV	QIRNRFFGFV
g241	LRIMLTERIV	GRKRHFDRIA	GILTVQRLFH	QRENAVVTAV	QIRNRFFGFI	QKLIVGIIHL
	190	200	210	220	230	240
m241.pep		160	170			
		IMQRNHGIFH	DSHICPFRNS	RLITGAFX		
g241	IMQRNHGIFC	NSHICPFRNS	RLITGAFX			
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 909>:

a241.seq

```

1  ATGCCAACAC GTCCAACCTG CGCCGCAAAG CATCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC
101 AAACGCATAC ACCGCATGAA CCGGCTTCCT CAACCTGCGC GGCAAAATCA
151 GCGAACCACG GGGAAAATTT TCATAATGCC CAACGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAATGGA ACAAACCCTT TTCAGACGGC

```


553

```

251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGCGG
301 ACCGTGGACA TGACCGTGTG CGATTTCTCT ATCGGATGCA TCGCGCACAC
351 TTTCAACCGT AGCCTTAAAG CGGATTTTCA TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTACC GTCGGCAACA TCGGTTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCC GCATCTTCAA TACGGACCAA CTCCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGAAAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTTCCAC CAAAGGGAAA ATGCCGTCGT
651 AACCGCCGTG CAGATACGCA ATCGGTTCTT CGGTTTTGTC CAAAAGCTGA
701 TTGTTGGCAT CATACTCTC ATAATGCAGC GAAACCACGG AATCTTTCAC
751 GATAGCCATA TTTGTCCTTT CAGGAACAGC AGATTAATTA CAGGCGCATT
801 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 910; ORF 241.a>:

```

a241.pep
  1 MPTRPTRAAK HPTPPTWLQT AYCPRPPYRP PSVQTHTPHE PASSTCAAKS
 51 ANRRENFHNA QPTYLLHPSN KMPSEMEQTL FRRHQIPPSC RQSVVMTVR
101 TVDMTVCDFL IGCIAHTFNR SLKADFHACQ RMVAVHRLT VGNIGYTIDD
151 NIAGFRIVGF KHHADFDENR EHARIFNTDQ LRILLAERIV GRKRHIDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL IMQRNHGILH
251 DSHICPFRNS RLITGAF*

```

m241/a241 96.0% identity in 177 aa overlap

```

                                10      20      30
m241.pep                                RQSVVMTVRAVDMTVCDFLIGCIAHAFNC
                                |||||:|||||:|||||:||
a241      QPTYLLHPSNKMPSMEQTLFRRHQIPPSCRQSVVMTVRTVDMTVCDFLIGCIAHTFNR
              70      80      90      100     110     120

              40      50      60      70      80      90
m241.pep      SLKADFHACQRMVAVHRLAVGNIGYTIDNIAAGFRIVGFKHHADFDENREHARIFDQ
              |||||:|||||:|||||:|||||:|||||:||
a241      SLKADFHACQRMVAVHRLTVGNIGYTIDNIAAGFRIVGFKHHADFDENREHARIFDQ
              130     140     150     160     170     180

              100     110     120     130     140     150
m241.pep      LRILLAERIVGRQRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL
              |||||:|||||:|||||:|||||:|||||:||
a241      LRILLAERIVGRKRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL
              190     200     210     220     230     240

              160     170
m241.pep      IMQRNHGIFHDSHICPFRNSRLITGAFX
              |||||:|||||:|||||:||
a241      IMQRNHGILHDSHICPFRNSRLITGAFX
              250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 911>:

```

g241-1.seq
  1 ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
 51 TTGTGCCGAC GTTGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTCA AATCGGTTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCCGCTGTTT GCTGTCTGCC CGGCCGGGCC TGTGGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCCGTG CGGGCATCCA
351 AACCACCAC CGTTCCGGCT TTTGCTGAT GGTATTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGG AAAGGATGAT
451 GTCTTTGCCG TTTTTCGGGG CTTTaktGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAA CAGGTTGCC ATCGGGTAAT
651 GCGTTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 912; ORF 241-1.ng>:

554

g241-1.pep

```

1  MPTRPTRAAN PPTPTTWLQT AYCPRPYPYR PSVQTHTPHE PASSTCAAKS
51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPSQ RQSVVVMVTR
101 TVDMTVCDL IGCIAHAFNR SFKADFHACQ RMVAVHHRLA VGNIGYTIDD
151 NIAGFRIVRF KHHTDLDFNR ERARIFNTDQ LRIMLTERIV GRKRHFDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFI QKLIVGIIHL IMQRNHGIFC
251 NSHICPFRNS RLITGAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 913>:

m241-1.seq

```

1  ATGCCAACAC GTCCAACCTG CGCTGCAAAC CCTCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC
101 AAACGCGTAC ACCGCGTGAA CCGGCTTCCT CAACCTGCGC GGCAAAATCA
151 GCGAACCGAC GGGAAAATTC TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAACGGA ACAAACCCTT TTCAGACGGC
251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGCGG
301 GCCGTGGACA TGACCGTGTG CGATTTCTCT ATCGGATGCA TCGCGCACGC
351 TTTCAACTGT AGCCTTAAAG CGGATTTTCA TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTGCC GTCGGCAACA TCGGTTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCC GCATCTTCGA TACGGACCAA CTCCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGACAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTTCCAC CAAAGGGAAA ATGCCGTCGT
651 AACC GCCGTG CAGATACGCA ATCGGTCTT CGGTTTGTG CAAAGCTGA
701 TTGTTGGCAT CATACTCTC ATAATGCAGC GAAACCACGG AATTTTTCAC
751 GATAGCCATA TTTGTCTTT CAGGAACAGC AGATTAAATTA CAGGCGCATT
801 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 914; ORF 241-1>:

m241-1.pep

```

1  MPTRPTRAAN PPTPTTWLQT AYCPRPYPYR PSVQTRTPRE PASSTCAAKS
51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPSQ RQSVVVMVTR
101 AVDMTVCDL IGCIAHAFNC SLKADFHACQ RMVAVHHRLA VGNIGYTIDD
151 NIAGFRIVGF KHHADDFDNR EHARIFDQDQ LRILLAERIV GRQRHIDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL IMQRNHGIFH
251 DSHICPFRNS RLITGAF*

```

m241-1/g241-1 93.3% identity in 267 aa overlap

	10	20	30	40	50	60
m241-1.pep	MPTRPTRAANPPTPTTWLQTAYCPRPPYRPPSVQTRTPREPASSTCAAKSANRRENSHNA					
g241	MPTRPTRAANPPTPTTWLQTAYCPRPPYRPPSVQTHTPHEPASSTCAAKSANRRENSHNA					
	10	20	30	40	50	60
m241-1.pep	QPTYLLHPSNKMPSSETEQTLFRRHQIPPSQSVVVMVTRAVDMTVCDLIGICIAHAFNC					
g241	QPTYLLHPSNKMPSSETEQTLFRRHQIPPSQSVVVMVTRVDMTVCDLIGICIAHAFNR					
	70	80	90	100	110	120
m241-1.pep	SLKADFHACQRMVAVHHRLAVGNIGYTIDNIAAGFRIVGFKHHADDFDNRERARIFDQ					
g241	SFKADFHACQRMVAVHHRLAVGNIGYTIDNIAAGFRIVRFKHHADDFDNRERARIFDQ					
	130	140	150	160	170	180
m241-1.pep	LRILLAERIVGRQRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL					
g241	LRIMLTERIVGRKRHFDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL					
	190	200	210	220	230	240
m241-1.pep	IMQRNHGIFHDSHICPFRNSRLITGAFX					
g241	IMQRNHGIFCNSHICPFRNSRLITGAFX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 915>:

a241-1.seq

```

1  ATGCCAACAC GTCCAACCTG CGCCGCAAAG CATCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC

```

101	AAACGCATAC	ACCGCATGAA	CCGGCTTCCT	CAACCTGCGC	GGCAAAATCA
151	GGCAACCGAC	GGGAAAAATT	TCATAATGCC	CAACCGACAT	ACCTTCTCTCA
201	TCCATCAAAA	AAATCGCGT	CTGAAATGGA	CAAAACCCCT	TTACAGACGGC
251	ATCAGATACC	TCCAAGCTGC	CGGCAATCAG	TGGTGGTGAT	GACCGTGCGG
301	ACCGTGAGCA	TGACCGTGTG	CGATTTCCTC	ATCGGATGCA	TGCGGCACAC
351	TTTCAACCGT	AGCCTTAAAG	CGGATTTCCT	TGCTTGCCAA	AGGATGGTTG
401	CCGTCCACCA	CCGCCTTACC	GTCGGCAACA	TCGGTTACAC	GATAGACGAC
451	AACATCGCCG	GTTCTCAGAT	CGTCGGCTTC	AAACATCATG	CCGACTTCGA
501	CTTCAACAGG	GATACAGCCC	GCATCTTCAA	TACGGACATG	TTCCGGATCG
551	TGCTCGCCGA	ACGCATCGTC	GGGCGAAAGC	GCCACATCGA	CCGTATCGCC
601	GGCATCTCTA	CCGTGCAACG	CCTCTTCCAC	CAAAAGGAAA	ATGCGCTCGT
651	AACCGCCGTG	CAGATACGCA	ATCGGTTCTT	CGGTTTGTG	CAAAAGCTGA
701	TGTATTGGCAT	CATACATCTC	ATAATGCAGC	GAAACACGG	AATTCTTCAC
751	GATAGCCATA	TTTGTCTCTT	CAGGAACAGC	AGATTAAATA	CAGGCGCAT
801	CTAA				

a241-1.pep

1	MPTRPTRAAR	HPTPPTWLQT	AYCPRPPYP	PSVQTHTPHE	PASSTCAAKS
51	ANRRNFHNA	LGTILHLPSN	KMPSEMEQTL	FRRHQIIPSC	RQSVVVMVTR
101	TVDMTQCDFL	IGCIAHTFNR	SLKADFAQCL	RMVAVHHRLC	VGNIGYITDD
151	NIAGFIRVGF	KHHADFDFNR	EHARIENTDQ	LRILLAERIV	GRKRHRIDRIA
201	GILTVQRLFH	QRENAVVTAV	QIRNREFGFV	<u>QKLIVGIHL</u>	<u>IMQRNHGILH</u>
251	DSHICPRFNS	RLITGAF*			

	10	20	30	40	50	60
m241-1.pep	MPTRPTRAANPPTPPTWLQTAYCPRPPYRPPSVQTRTPREPASSTCAAKSANRRENSHNA					
a241	MPTRPTRAAKHPTPPTWLQTAYCPRPPYRPPSVQTHPHEPASSTCAAKSANRRENFHNA					
	10	20	30	40	50	60
m241-1.pep	QPTYLLHPSNKMPSETEQTFLRRHQIPPSCRQSVVVMTVRAVDMTVCDFLIGCIAHAFNC					
a241	QPTYLLHPSNKMPSEMEQTFLRRHQIPPSCRQSVVVMTVRVTVDMTVCDFLIGCIAHTFNR					
	70	80	90	100	110	120
m241-1.pep	SLKADFHACQRMVAVHHRLAVGNIGYTIIDNNIAGFRIVGFKHHADFDENREHARIFDTDQ					
a241	SLKADFHACQRMVAVHHRLTVGNIGYTIIDNNIAGFRIVGFKHHADFDENREHARIFNTDQ					
	130	140	150	160	170	180
m241-1.pep	LRILLAERIVGRQRHIDRIAGILTVQRLFHQRENAVVTAVQIRNREFFGFVQKLIVGIIHL					
a241	LRILLAERIVGRKRHIDRIAGILTVQRLFHQRENAVVTAVQIRNREFFGFVQKLIVGIIHL					
	190	200	210	220	230	240
m241-1.pep	IMQRNHGIFHDSHICPFRNSRLITGAFX					
a241	IMQRNHGILHDSHICPFRNSRLITGAFX					
	250	260				

g242.seq

1	atgatcggcg	aacttgttgt	tttgtctgtg	atcgagcact	tcaagcaacg
51	cgctggcggg	atcgccccga	aagtcgctgc	ccaatttgtc	gatttcgtcg
101	agcaggaaca	acgggtttct	tacgcctgct	tttgccatat	tctgcaaaat
151	cttgccgggc	atagagccga	tataggtacg	gcggtgcccg	cggatttcgc
201	tttcgtcgcg	cacgccgccc	aaggccatac	ggacatattt	ccgcccgtt
251	gctttggcga	tggattcgcc	caaagagggt	ttgcccacgc	ccggagggcc
301	gaccaaacac	agaatcggac	ctttgagctt	gtccatacgt	ttttggacgg
351	cgaggtattc	caaaatccgt	tctttgactt	tttccaggcc	gtagtggattc
401	gcatccagca	ccagtcgcgc	tttggcgatg	tctttgtgta	cgcgggattt
451	tttcttccac	ggcagtccca	gcaggggtgc	gatgtagttg	cgtcacgcgc

501	tggattcggc	agacatcggc	ggcatcattt	tgagtttttt	cagttcggac
551	aggcattttt	cttcgcgttc	tttggtcata	ccgccttttt	tgatgcctgc
601	ctccaaggca	tccaagtcgc	cgttttcgtc	ttcttcgccc	aattctttgt
651	gtatcgcttt	aatctgttcg	ttcagataat	attcgcggtg	ggatttttcc
701	atttggcggt	tgacgcgttc	gcgtatgcgt	ttttcggcct	gcataatgtc
751	gagttcggat	tccagctttg	ccagcaggaa	ttccatccgt	ttgccgattt
801	cgggaatctc	caaaatctgt	tggcgttcgc	ccagtttcaa	ctgcaaatgc
851	gctgcgaccg	tatcgggttag			

g242.pwp

m242.seq

m242 . pep

m242/g24290.3% identity in 289 aa overlap

	10	20	30	40	50	60
m242 . pep	MIGKLVVLF	FGIEHF	EQRAGGI	ASEVVTQ	FVDFVE	QEQGVFHAGFCHILQNL
	:	:	:		:	:
g242	MIGELVVLF	VEHFQ	RAGGIAP	KVAAQ	FVDFVE	QEQRVSYACFCHILQNL
	10	20	30	40	50	60
	70	80	90	100	110	120
m242 . pep	AVSPDFAF	VAHAAQ	SHADIF	PPRCFG	DGFGA	QRGFAHARRADQAQNRAFEFVHTFLDGEVF
			:			: :
g242	AVPADFAF	VAHAAQ	GHTDIF	PPRCFG	DGFGA	QRGFAHARRADQTQNRTEFLVHTFLDGEVF
	70	80	90	100	110	120

	130	140	150	160	170	180
m242 . pep	QNPFFDFFQAVVVG	IQHSGFGDVFADAGFF	LPRLQEQSV	DVVAYDGGFRR	RRWHHFFELF	
g242	QNPFFDFFQAVVVG	IQHSGFGDVFADAGFF	LPRLQEQSV	DVVAYDGGFRR	RRHHFFEFF	
	130	140	150	160	170	180
	190	200	210	220	230	240
m242 . pep	QFGQAFFFRFFGH	TRLFDICFQGIQFA	VVFVFFAQFFVY	RNFLFVQIIIFAL	GFFHLAFDAS	
g242	QFGQAFFFRFFGH	TRLFDACLOGIQFA	VVFVFFAQFFVY	RNFLFVQIIIFAL	GFFHLAFDAS	
	190	200	210	220	230	240
	250	260	270	280	290	
m242 . pep	AYAFFGLHNVEFG	QLCQQEFHFPADF	GNLQNLALRQFQ	LQMRCDRIGX		
g242	AYAFFGLHNVEFG	QLCQQEFHFPADF	GNLQNLALRQFQ	LQMRCDRIGX		
	250	260	270	280		

```
a242.seq
1  ATGATCGGCG AACTTGTTGT TTTGCTCGGG ATCAAGCACT TCGAGCAACG
51  CGCTGGCGGG ATCGCCCCGG AAGTCGCTAN CCAATTTGTC GATTTCGTCG
101 AGCAGGAACA ATGGGTTTTT TACGCGGGCT TTTGCCATACT TCTGCAAAAT
151 CTTACCGGGC ATGGAGCCGA TATAGGTGCG GCGGTGTCCC CGGATTTGCG
201 TTTCGTCGCG CACGCCGCCC AAAGCCATGC GGACATATTT CCGCCCCGTT
251 GCTTTGGCGA TGGATTCGCC CAAAGAGGTT TTGCCACGCG CTGGAGGGCC
301 GACCAGGCAC AGAATCGGGC CTTTGAGTTT GTCCATACGT TTTTGACGG
351 CGAGGTATTC CAAATCCGT TCTTTGACTT TTTCCAGGCC GTAGTGGTCG
401 GTATCCAGCA CCAATCCGCG TTTGGCGATG TCTTTGCTGA CGCGGGATTT
451 TTTCTTCCAC GGCAGTTCGA GCAGGGTGTC GATGTAGTTG CGTACGACGG
501 TGGATTCGGC AGACATCGGC GGCATCATT TGA GCTTTT CAGTTCGGAC
551 AGGCATTTTT CTTCCGCTTC TTTGGTCATA CCCGCCTTTT TGATATCTGC
601 TTCCAAGGCA TCCAGTTCGC CGTTTTCGTC TTCTTCGCCC AGTCTTTGT
651 GTATCGCTTT AATCTGTTCC TTCAGATAAT ATTGCGCGTG GGATTTTTTC
701 ATTTGGCGTT TGACGCGTCC GCGTATGCGT TTTTCGGCCT GCATAATGTC
751 GAGTTCGGAT TCCAGCTGTG CCAGCAGGAA TTCCATCGT TTGCCGATTT
801 CGGGAATTT CAAAATCTGT TGGCGTTGCG CCAGTTTCAA CTGCAAATGC
851 GCTGCGACCG TATCGGTTAG
```

a242.pep

1	MIGELVLLG	IKHFEQRAGG	IAPEVAXQFV	DFVEQEQWVF	YAGFCHILQN
51	LTGHGADIGA	AVSPDFAFVA	HAAQSHADIF	PPRCFGDGFA	QRGFAHAWRA
101	DQQRNRAFEF	VHTFLDGEVF	QNPFDFDQFA	VVVGIQHQS	FGDVFADAGF
151	FLPRQFEQGV	DVVAYDGGGF	RHRRHHFELE	QFGQAFFERF	FGHTRLEFDC
201	<u>FQGIQFAVFV</u>	<u>FFAQFFVYRF</u>	<u>NLFVQIIFAL</u>	<u>GGFHAFDAS</u>	<u>AYAFFGLHN</u>
251	EGFGOLCOOE	FHPFADGNGF	ONLLALROFO	LOMRCRDIG*	

	10	20	30	40	50	60
m242.pep	MIGKLVVLF	GLGIEHFEQRAGGI	ASEVVTQFVDFVEQE	QGVFHAGFCHILQ	NLTGHRADIGA	
a242	MIGELVVLL	GLGIKHFEQRAGGI	APEVAXQFVDFVEQE	QWVFYAGFCHILQ	NLTGHGADIGA	
	10	20	30	40	50	60
	70	80	90	100	110	120
m242.pep	AVSPDFAFV	AHAAQSHADIFPP	RCFGDGFQAQ	RGFAHARRADQ	AQNRAFEFV	HTFLDGEVF
a242	AVSPDFAFV	AHAAQSHADIFPP	RCFGDGFQAQ	RGFAHAWRADQ	AQNRAFEFV	HTFLDGEVF
	70	80	90	100	110	120
	130	140	150	160	170	180
m242.pep	QNPFFDFFQ	AVVVGIQHQS	GFGDVFADAGF	FLPRQLEQS	VDVVAYDGG	FRRHRWHHFFELF

558

```

a242      QNPFDFQAVVVGIIHQSGFGDVFADAGFFLPRQFEQQGVDDVAYDGGFGRHRRHHFELF
           130      140      150      160      170      180
           190      200      210      220      230      240
m242.pep  QFGQAFFFRFFGHTRLFDICFQGIQFAVFVFFAQFFVYRENLFVQIIIFALGFFHLAFDAS
           |||||
a242      QFGQAFFFRFFGHTRLFDICFQGIQFAVFVFFAQFFVYRENLFVQIIIFALGFFHLAFDAS
           190      200      210      220      230      240
           250      260      270      280      290
m242.pep  AYAFFGLHNVEFGFQLCQQEFHFFADFGNFQNLALRQFQLQMRCDRIGX
           |||||
a242      AYAFFGLHNVEFGFQLCQQEFHFFADFGNFQNLALRQFQLQMRCDRIGX
           250      260      270      280      290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 923>:

```

g243.seq
1  ATGGTaatcg tctGGTTGcC cgAGTTaccg CCGATGCCGG CGACGATGGG
51  CATCAGCGCG GCGAGTGCGA CGATTTTTTC gatactgcCT TCAAACGCGC
101 CGATGACGCG GCTGGCGAGG AAGGCGGTGC AGAGGTTGAC GGCGAGCCAC
151 ATCCAGCGGT TTTTGACGGA ATCCAAGACG GGGGCGAACA GGTCTTCCTC
201 TTCCTGCAAA CCTGCCATGT TCAACATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATCTCGTCG ATGGTAATcc tgCCGATGAG CTTTTTGTTT
301 TCATCAACGA CGGGCGCGGT AACCAAGTCG TAG

```

This corresponds to the amino acid sequence <SEQ ID 924; ORF 243.ng>:

```

g243.pep
1  MVIVWLPELP PMPATMGISA ASATIFSILP SNAPMTRLAR KAVQRLTASH
51  IQRFLTESKT GANRSSSSCK PAMFNISASD SSRITSTISS MVILPMSFLF
101 SSTTGAVTKS *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 925>:

```

m243.seq
1  ATGGTAATCG TCTGGTTGCC CGAGTTACCG CCTATGCCGG CGACGATGGG
51  CATCAGCGCG GyGAGTGCGA CGATTTTTTC GATGCTGCCT TCAAACGCGC
101 CGATAACACG GyTGGCGAGG AAGGCGGTGC AGAGGTTGAC GGCGAGCCAC
151 ATCCAGyGGT TTTTACCGA ATCCCACACG GGGGCGAAyA GGTCTTCCTC
201 TTCCTGCAAA CCCGCCATAT TCAGCATATC CGCTTCCGAT TCTTCGCGGA
251 TCACGTCCAC CATCTCGTCG ATGGTAATCC TGCCGATGAG CTTTTTGTTT
301 TCATCGACGA CGGGCGCGGT AACCAAGTCG TAG

```

This corresponds to the amino acid sequence <SEQ ID 926; ORF 243>:

```

m243.pep
1  MVIVWLPELP PMPATMGISA XSATIFSMLP SNAPITRLAR KAVQRLTASH
51  IQXFFTESHT GANRSSSSCK PAIFSIASD SSRITSTISS MVILPMSFLF
101 SSTTGAVTKS *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 243 shows 92.7% identity over a 110 aa overlap with a predicted ORF (ORF 243.ng) from *N. gonorrhoeae*:

```

m243/g243
           10      20      30      40      50      60
m243.pep  MVIVWLPELPMPMPATMGISAXSATIFSMLPSNAPITRLARKAVQRLTASHIQXFFTESHT
           |||||
g243      MVIVWLPELPMPMPATMGISAASATIFSILPSNAPMTRLARKAVQRLTASHIQRFLTESKT
           10      20      30      40      50      60
           70      80      90      100     110
m243.pep  GANRSSSSCKPAIFSIASDSSRITSTISSMVILPMSFLFSSTTGAVTKSX
           |||||
g243      GANRSSSSCKPAMFNISASDSSRITSTISSMVILPMSFLFSSTTGAVTKSX

```

559

70 80 90 100 110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 927>:

```
a243.seq
1 ATGGTAATCG TCTGGTTGCC CGAGTTACCG CCTATGCCGG CGACGATGGG
51 CATCAGCGCG GCGAGTGCGA CGATTTTTC GATGCTGCCT TCAAACGCGC
101 CGATAACACG GCTGGCGAGG AAGGCGGTGC AGAGGTTGAC GGCAGGCCAC
151 ATCCAGCGGT TTTTGACGGA ATCCAAGACG GGGGCGAATA AGTCTTCCTC
201 TTCTTGCAA CCCGCCATAT TCAACATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATTTCGTCA ACGGTCACCC TGCCGATGAG CTTTTTGT
301 TCATCGACGA CGGCGCGGT AACCAAGTCA TAG
```

This corresponds to the amino acid sequence <SEQ ID 928; ORF 243.a>:

```
a243.pep
1 MVIVWLPELP PMPATMGISA ASATIFSMLP SNAPITRLAR KAVQRLTASH
51 IQRFLTESKT GANKSSSSCK PAIFNISASD SSRITSTISS TVTLMSFLF
101 SSTTGAVTKS *
```

m243/a243 92.7% identity in 110 aa overlap

	10	20	30	40	50	60
m243.pep	MVIVWLPELPPMPATMGISAXSATIFSMLPSNAPITRLARKAVQRLTASHIQXFFTESHT					
a243	MVIVWLPELPPMPATMGISAASATIFSMLPSNAPITRLARKAVQRLTASHIQRFLTESKT					
	10	20	30	40	50	60
	70	80	90	100	110	
m243.pep	GANKSSSSCKPAIFNISASDSSRITSTISSMVILPMSFLFSSTTGAVTKSX					
a243	GANKSSSSCKPAIFNISASDSSRITSTISSTVTLPMSFLFSSTTGAVTKSX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 929>:

```
g244.seq
1 atgccgcctg aagcccgccg ggcgggttca gacggcattg ccgctttact
51 tcgatcggtt tatacgcaaa acgcgcttca ggaaataaat cagattattc
101 cccagacgcc ttcaggcttc cttccgtgcc accgtaacca tagccgggcg
151 caacacacgg tcggacaggg tataaccctt cttcatcaca ccaaccacgg
201 tattgggttc ctgctcactg gccaccgcct gcacgcctg atggatatcc
251 ggatcgagct tatcgcccgc tttaggattg atttccttga tttgcgtggc
301 atcaaacgcc ttctgcaact cattcaaagt catctgcaca cccattttca
351 gcgcacgaa attaccgctc tgatccaaaa gcgccatttc cagataatcc
401 ttgaccggca acattttcac ggcaaaacttc tgtccggcga acttgtgcgt
451 atcggcaatt tcctgctggt ggcgggcgcg caggttttgc tcgtttgcca
501 aagcgcgcag ttgttcgtct ttcaactgcg cttccagctc ggcaatccgc
551 gcctgcaaat cctcataagc cggctcggcg gcagcctggt cctgtacacc
601 gtccgcattt cctactgtct cgacgggttc caccgcctcc acattttcaa
651 ccgcttcttc actgttttgc tgctgtgtct gttcgtcat atcgatatcc
701 tcaaaacaaa ttggaaatca aaatccggtt attaccgag caagataagg
751 acattttcaa gaaacttcaa gcaaaggcag gaaatttcac atccgccgcc
801 gaatacccta ccgcaaaaac catataaacg gtaa
```

This corresponds to the amino acid sequence <SEQ ID 930; ORF 244.ng>:

```
g244.pep
1 MPPEARPAGS DGIAALLRSV YTQNALQEIN QIIPQTPSGF LPCHRNHSRA
51 QHTVGQGITL LHHTNHGIGF LLTGHRLHRL MDIRIELIAR FRIDFLDLRG
101 IKRLQLIQS HLHTHFORIE ITALIQKRHF QIILDRQHFH GKLLSGELVR
151 IGNFLLVAAA QVLLVCQSAQ LFVFQLRFQL GNPRLQILIS RLGGSLFLYT
201 VRISYCLDGF HRLHIFNRFF TVLLLCFLAH IVSLKTNWKS KSGYYPKIR
251 TFSRNFQQRQ EISHPPNTL PQKPYKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 931>:

```
m244.seq
```

560

```

1  ATGCCGTCTG AAGCCCGACA GCGGGTTCA GACGGCATTG CCGCTTTACT
51  TCGATCGGTT TATACGAAA ACGCGCTTCA GGAAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTTCTGCGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCCTT CTTATCACA CCCACCACGG
201 TATTCGGCTC CTGTTGCTT GCCACCGCCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTAGGGTTG ATTTCTTGA TTTGCGTAGC
301 ATCAAATGCT TTCTGCAACT CGTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA ATTGCCGCTC TGATCCAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCCAC GGCAAATTC TGTCCGGCGA ACTTGTGCGT
451 ATCCGCAATT TyCTGCTGGT GCGGGCGGCG CAGGTTTTC TCGTTTGCCA
501 AAGCGCGCTG CTCGTCTTTC AACTGCGTTT CCAGCTCGGC AATCCGCGCC
551 TGCAAATCCT CATAAGCCGG CTCTGCGGCA GCCTGTTCTT GCACACCGTC
601 CGCATTTTCT ACTGTTTCGA CGGTTTCCAC CGCTCCACA TTTTCAACCG
651 CTTCTTCACT GTTTTGCTGC TGTGTCTGTT CGCTCATATC GTATCCCTTA
701 AAACAAATTG GAAATCAAAA TCCAGTTATT ACCCGCGCAA GATAAGGACA
751 TTTTCAAGAA ACTTCAAKCA AAakCAGAGA ATTTCAAATT CATTTTCAAA
801 TCCCCTACCG AAAAAATAAT ATAGACGGTA A

```

This corresponds to the amino acid sequence <SEQ ID 932; ORF 244>:

m244 . pep

```

1  MPSEARQAGS DGIAALLRSV YTQNALQEIN QIIPQTPSGF LLRHRNHSRA
51  QHAVGQRITL LHHTHHGIRL LFACHRLHRL MDIRIELIAR FRVDFDLRLS
101 IKCFLQLVQS HLHAHFQRIE IAALIQKRHF QIILDRQHFH GKLLSGELVR
151 IRNFLLVAAA QVLLVCQSAL LVFQLRFQLG NPLRLQILIS LCGSLFLHTV
201 RISYCFDGFH RLHIFNRFFT VLLLCLEFAHI VSLKTNWKS SKSYPRKIRT
251 FSRNFXQXQR ISNSFSNPLP KKXYRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 244 shows 86.3% identity over a 277 aa overlap with a predicted ORF (ORF 244.ng) from *N. gonorrhoeae*:

M244/G244

	10	20	30	40	50	60
m244 . pep	MPSEARQAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
g244	MPPEARPAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLPCHRNHSRAQHTVGGGITL					
	10	20	30	40	50	60
m244 . pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRLSIKCFQLVQSHLHAHFQRIE					
g244	LHHTNHGIGFLLTGHRLHRLMDIRIELIARFRIDFLDLRGIKRLLQLIQSHLHTHFQRIE					
	70	80	90	100	110	120
m244 . pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRLSIKCFQLVQSHLHAHFQRIE					
g244	LHHTNHGIGFLLTGHRLHRLMDIRIELIARFRIDFLDLRGIKRLLQLIQSHLHTHFQRIE					
	70	80	90	100	110	120
m244 . pep	IAALIQKRHFQIILDRQHFHKGKLLSGELVRIRNFLLVAAAQVLLVCQSAALLVFQLRFQL					
g244	ITALIQKRHFQIILDRQHFHKGKLLSGELVRIGNFLLVAAAQVLLVCQSAQLFVFQLRFQL					
	130	140	150	160	170	180
m244 . pep	IAALIQKRHFQIILDRQHFHKGKLLSGELVRIRNFLLVAAAQVLLVCQSAALLVFQLRFQL					
g244	ITALIQKRHFQIILDRQHFHKGKLLSGELVRIGNFLLVAAAQVLLVCQSAQLFVFQLRFQL					
	130	140	150	160	170	180
m244 . pep	GNPRLQILISRLCGSLFLHTVIRISYCFDGFHRLHIFNRFFT VLLLCLEFAHIVSLKTNWKS					
g244	GNPRLQILISRLGGSFLYTVIRISYCLDGFHRLHIFNRFFT VLLLCLEFAHIVSLKTNWKS					
	190	200	210	220	230	240
m244 . pep	GNPRLQILISRLCGSLFLHTVIRISYCFDGFHRLHIFNRFFT VLLLCLEFAHIVSLKTNWKS					
g244	GNPRLQILISRLGGSFLYTVIRISYCLDGFHRLHIFNRFFT VLLLCLEFAHIVSLKTNWKS					
	190	200	210	220	230	240
m244 . pep	KSSYYPRKIRTFSRNFXQXQRISNSFSNPLPKKXYRRX					
g244	KSGYYPSKIRTFSRNFKQRQEISHPPNTLPQKPYKRX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 933>:

```
a244.seq
1   ATGCCGTCTG AAGCCCGACA GCGGGGTTCA GACGGCATTG CCGCTTTACT
51  TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTTCTGTGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCCTT CTTTCATCAG CCCACCACGG
201 TATTGGGTTC CTGTTGCTT GCCACCGCCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTTAGGATTG ATTTCTTGA TTTGCGTAGC
301 ATCAAATGCT TTCTGCAACT CGTTCAAAGT CATCTGCACG CCCATTTCAT
351 GCGCATCGAA ATTGCCGCTC TGATCCAAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCAC GGCAAACTTC TGTCCGGCGA ACTTGTGCGT
451 ATCCGCAATT TCCTGCTGGT GGCGGCGGCG CAGGTTTTCG TCGTTTGCCA
501 AAGCGCGCAG CTGCTCGTCT TTCAACTGCG CTTCCAGCTC GGCAATCCGC
551 GCCTGCAAAT CCTCATAAGC CGGCTCTCGC GCAGCCTGTT CCTGCACACC
601 GTCCGCATTT CCTACTGTCT CGACGGTTTC CACCGCCTCC ACATTTTCAA
651 CCGCTTCTTC ACTGTTTTGC TGCTGTGTCT GTTCGTCAT ATCGTATCCC
701 TTAAAACAAA TTGGAAATCA AAATCCAGTT ATTACCCGCG CAAGATAAGG
751 ACATTTTCAA GAAACTTCAA GCAAAGGCAG AGAATTTCAA ATTCATTTTC
801 AAATCCCCTA CCGAAAAAAT AATATAGACG GTAA
```

This corresponds to the amino acid sequence <SEQ ID 934; ORF 244.a>:

```
a244.pep
1   MPSEARQAGS DGIAALLRSV YTQNALQEIN QIIPQTPSGF LLCHRNHSRA
51  QHAVGQRITL LHHAHHGIGF LFACHRLHRL MDIRIELIAR FRIDFLDLRS
101 IKCFLQLVQS HLHAHFQRIE IAALIQKRHF QIILDRQHFH GKLLSGELVR
151 IRNFLVAAA QVLLVCQSAQ LLVFQLRFQL GNPRQLILIS RLCGSFLFHT
201 VRISYCLDGF HRLHIFNRFF TVLLLCFLFAH IVSLKTNWKS KSSYYPRKIR
251 TFSRNFQRQ RISNSFSNPL PKK*YRR*
```

m244/a244 96.8% identity in 277 aa overlap

	10	20	30	40	50	60
m244.pep	MPSEARQAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
a244	MPSEARQAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLLCHRNHSRAQHAVGQRITL					
	10	20	30	40	50	60
m244.pep	70	80	90	100	110	120
	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFLQLVQSHLHAHFQRIE					
a244	LHHAHHGIGFLFACHRLHRLMDIRIELIARFRIDFLDLRSIKCFLQLVQSHLHAHFQRIE					
	70	80	90	100	110	120
m244.pep	130	140	150	160	170	179
	IAALIQKRHFQIILDRQHFHGKLLSGELVRIRNFLVAAAQVLLVCQSA-LLVFQLRFQL					
a244	IAALIQKRHFQIILDRQHFHGKLLSGELVRIRNFLVAAAQVLLVCQSAQLLVFQLRFQL					
	130	140	150	160	170	180
m244.pep	180	190	200	210	220	239
	GNPRQLILISRLCGSLFHTVRISYCFDGFHRLHIFNRFFTVLLLCFLFAHIVSLKTNWKS					
a244	GNPRQLILISRLCGSLFHTVRISYCLDGFHRLHIFNRFFTVLLLCFLFAHIVSLKTNWKS					
	190	200	210	220	230	240
m244.pep	240	250	260	270		
	KSSYYPRKIRTFSRNFXQXQRISNSFSNPLPKKXYRRX					
a244	KSSYYPRKIRTFSRNFKQRQRISNSFSNPLPKKXYRRX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 935>:

```
g244-1.seq
1   atgccgcctg aagcccgggc ggcgggttca gacggcattg cgcgtttact
```

562

```

51  tcgatcgggtt  tatacgcaaa  acgcgcttca  ggaaataaat  cagattattc
101  cccagacgcc   ttcaggcttc  cttccgtgcc  accgtaacca  tagccgggcg
151  caacacacgg   tcggacaggg  tataaccctt  cttcatcaca  ccaaccacgg
201  tattgggttc   ctgctcactg  gccaccgcct  gcacgcctg  atggatatcc
251  ggatcgagct   tatcgcccg  tttaggattg  atttccttga  tttgcgtggc
301  atcaaacgcc   ttctgcaact  cattcaaagt  catctgcaca  cccattttca
351  gcgcatcgaa   attaccgctc  tgatccaaaa  gcgccatttc  cagataatcc
401  ttgaccggca   acatttccac  ggcaaaactt  tgtccggcga  acttgtgctg
451  atcggcaatt   tcctgctggt  ggcgggcgcg  cagggtttgc  tcgtttgcca
501  aagcgcgcag   ttgttcgtct  ttcaactgcg  cttccagctc  ggcaatccgc
551  gcctgcaaat   cctcataagc  cggtcggcg  gcagcctgtt  cctgtacacc
601  gtccgcattt   cctactgtct  cgacggtttc  caccgcctcc  acattttcaa
651  ccgcttcttc   actgttttgc  tgctgtgtct  gttcgtcat  atcgatccc
701  tcaaaacaaa   ttggaatca  aaatccggtt  attaccgcag  caagataagg
751  acattttcaa   gaaacttcaa  gcaaaggcag  gaaattttac  atccgccgcg
801  gaatacccta   ccgcaaaaac  catataaacg  gtaa

```

This corresponds to the amino acid sequence <SEQ ID 936; ORF 244-1.ng>:

g244-1.pep

```

1  MPPEARPAGS  DGIAALLRSV  YTQNALQEIN  QIIPQTPSGF  LPCHRNHSRA
51  QHTVGGQGITL LHHTNHGIGF  LLTGHLRL  MDIRIELIAR  FRIDFLDLRG
101  IKRLQLIQS  HLHTHFQRIE  ITALIQKRHF  QIILDRQHFH  GKLLSGELVR
151  IGNFLLVAAA  QVLLVCQSAQ  LFVFLRFQL  GNPRLQILIS  RLGGSFLYLT
201  VRISYCLDGF  HRLHIFNRFF  TVLLLCFAH  IVSLKTNWKS  KSGYYPKIR
251  TFSRNFKQRQ  EISHPPNTL  PQPKYKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 937>:

m244-1.seq

```

1  ATGCCGTCTG  AAGCCCGACA  GCGGGGTTCA  GACGGCATTG  CCGCTTTACT
51  TCGATCGGTT  TATACGCAAA  ACGCGCTTCA  GGAAATAAAT  CAGATTATTC
101  CCCAGACGCC  TTCAGGCTTC  CTTCTGCGCC  ACCGTAACCA  TAGCCGGGCG
151  CAACACGCGG  TCGGACAGCG  TATAACCCTT  CTTTCATCACA  CCCACCACGG
201  TATTCGGCTC  CTGTTGCTT  GCCACGCCT  GCATCGCCTG  ATGGATATTC
251  GGATCGAGCT  TATCGCCCGC  TTTAGGGTTG  ATTTCTTGA  TTTGCGTAGC
301  ATCAAATGCT  TTCTGCAACT  CGTTCAAAGT  CATCTGCACG  CCCATTTTCA
351  GCGCATCGAA  ATTGCCGCTC  TGATCCAAAA  GCGCCATTTC  CAGATAATCC
401  TTGACCGGCA  GCATTCCAC  GGCAAACCTT  TGTCCGGCGA  ACTTGTGCGT
451  ATCCGCAATT  TyCTGCTGGT  GGCGGCGGCG  CAGGTTTTGC  TCGTTTGCCA
501  AAGCGCGCTG  CTCGTCTTTC  AACTGCGTTT  CCAGCTCGGC  AATCCGCGCC
551  TGCAAATCCT  CATAAGCCGG  CTCTGCGGCA  GCCTGTTCTT  GCACACCGTC
601  CGCATTTCCT  ACTGTTTCGA  CGGTTTCCAC  CGCCTCCACA  TTTTCAACCG
651  CTTCTTCACT  GTTTTGCTGC  TGTGTCTGTT  CGTTCATATC  GTATCCCTTA
701  AAACAATTG  GAAATCAAAA  TCCAGTTATT  ACCCGCGCAA  GATAAGGACA
751  TTTTCAAGAA  ACTTCAAKCA  AAACAGAGA  ATTTCAAATT  CATTTTCAAA
801  TCCCTACCG  AAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 938; ORF 244-1>:

m244-1.pep

```

1  MPSEARQAGS  DGIAALLRSV  YTQNALQEIN  QIIPQTPSGF  LLRHRNHSRA
51  QHAVGQRITL  LHHTNHGIRL  LFACHRLHRL  MDIRIELIAR  FRVDFDLRS
101  IKCFQLVQS  HLHAHFQRIE  IAALIQKRHF  QIILDRQHFH  GKLLSGELVR
151  IRNFLVAAA  QVLLVCQSAL  LVFQLRFQLG  NPRLQILISR  LCGSLFLHTV
201  RISYCFDGFH  RLHIFNRFFT  VLLLCFAHI  VSLKTNWKS  K  SSYYPRKIRT
251  FSRNFXQQR  ISNSFSNPLP  KK*

```

m244-1/G244-1 86.3% identity in 277 aa overlap

	10	20	30	40	50	60
m244-1.pep	MPSEARQAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
g244-1	MPPEARPAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLPCHRNHSRAQHTVGGQGITL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m244-1.pep	LHHTNHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFQLVQSHLHAHFQRIE					
g244-1	LHHTNHGIGFLLTGHLRLHRLMDIRIELIARFRIDFLDLRGIKRLQLIQSHLHTHFQRIE					
	70	80	90	100	110	120

563

	130	140	150	160	170	180
m244-1.pep	IAALIQKRHFQIILDRQHFH GKLLSGELVRIRN FLLVAAQVLLVCQSAALLVFQ LRFQL					
g244-1	ITALIQKRHFQIILDRQHFH GKLLSGELVRIRN FLLVAAQVLLVCQSAQLFVFQ LRFQL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m244-1.pep	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFTVLLLC LFAHIVSLKTNWKS					
g244-1	GNPRLQILISRLGGSFLYTVRISYCLDGFHRLHIFNRFFTVLLLC LFAHIVSLKTNWKS					
	190	200	210	220	230	240
	250	260	270			
m244-1.pep	KSSYYPRKIRTF SRNFXQXQRISNSFSNPLPKKX					
g244-1	KSGYYPSKIRTF SRNFKQRQEISHPPNTLPQKPKYKRX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 939>:

a244-1.seq

```

1  ATGCCGCTCTG AAGCCCGACA GCGGGGTTCA GACGGCATTG CCGCTTTACT
51  TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTTCTGTGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCTT CTTCATCACG CCCACCACGG
201 TATTGGGTTT CTGTTGCTT GCCACCGCTT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTTAGGATTG ATTTCTTGA TTTGCGTAGC
301 ATCAAATGCT TTCTGCAACT CGTTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA ATTGCCGCTC TGATCCAAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTCCAC GGCAACTTC TGTCCGGCGA ACTTGTGCGT
451 ATCCGCAATT TCCTGCTGGT GCGGCGGCG CAGGTTTTCG TCGTTTGCCA
501 AAGCGCGCAG CTGCTCGTCT TTCAACTGCG CTTCCAGCTC GGCAATCCGC
551 GCCTGCAAT CCTCATAAGC CGGCTCTGCG GCAGCCTGTT CCTGCACACC
601 GTCCGCATT CTACTGTCT CGACGGTTTC CACCGCTCC ACATTTTCAA
651 CCGTTCTTC ACTGTTTTC TGCTGTGTCT GTTCGCTCAT ATCGTATCCC
701 TTTAAACAAA TTGAAATCA AAATCCAGTT ATTACCCGCG CAAGATAAGG
751 ACATTTTCAA GAACTTCAA GCAAAGCAG AGAATTCAA ATTCATTTTC
801 AAATCCCTA CCGAAAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 940; ORF 244-1.a>:

a244-1.pep

```

1  MPSEARQAGS DGIAALLRSV YTONALQEI NQIIPQTPSGF LLCHRNHSRA
51  QHAVGQRITL LHHAHHGIGF LFACHRLHRL MDIRIELIAR FRIDFLDLRS
101 IKCFLLVQS HLHAHFQRIE IAALIQKRHF QIILDRQHFH GKLLSGELVR
151 IRN FLLVAAA QVLLVCQSAQ LLVFQ LRFQL GNPRLQILIS RLCGSLFLHT
201 VRISYCLDGF HRLHIFNRFF TVLLLC LFAH IVSLKTNWKS KSSYYPRKIR
251 TFSRNFKQRQ RISNSFSNPL PKK*

```

m244-1/a244-1 96.8% identity in 274 aa overlap

	10	20	30	40	50	60
m244-1.pep	MPSEARQAGSDGIAALLRSVYTONALQEI NQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
a244-1	MPSEARQAGSDGIAALLRSVYTONALQEI NQIIPQTPSGFLLCHRNHSRAQHAVGQRITL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m244-1.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFLLVQSHLHAHFQRIE					
a244-1	LHHAHHGIGFLFACHRLHRLMDIRIELIARFRIDFLDLRSIKCFLLVQSHLHAHFQRIE					
	70	80	90	100	110	120
	130	140	150	160	170	179
m244-1.pep	IAALIQKRHFQIILDRQHFH GKLLSGELVRIRN FLLVAAQVLLVCQSA-LLVFQ LRFQL					
a244-1	IAALIQKRHFQIILDRQHFH GKLLSGELVRIRN FLLVAAQVLLVCQSAQLLVFQ LRFQL					
	130	140	150	160	170	180
	180	190	200	210	220	239
m244-1.pep	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFTVLLLC LFAHIVSLKTNWKS					
a244-1	GNPRLQILISRLCGSLFLHTVRISYCLDGFHRLHIFNRFFTVLLLC LFAHIVSLKTNWKS					
	190	200	210	220	230	240

240 250 260 270
 m244-1.pep KSSYYPRKIRTFSRNFXQQRISNSFSNPLPKXX
 ||||| ||||| ||||| |||||
 a244-1 KSSYYPRKIRTFSRNFKQRQRISNSFSNPLPKXX
 250 260 270

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 941>:

```
g246.seq
1  atgtacgggc ggaacggtag tactcaagcg gccgttgccct tcgttttcga
51  ccagacacag cgtgcccgtt tcggcaacgg cgaagtttac gccgctcaag
101 ccgacatcgg cagtgcctgta aatatcgcgc agggctttgc gggcgaatcc
151 ggtcagttgg tccacgtcgt ctgtaagcgc tgggccgagg ttttcgtgga
201 acagttcgct gcacctgtct ctggttttat ggattgcggg catcacgata
251 tgggtcgggt tttcgccctgc catttggaag ataaactcgc ccaagtcgct
301 ttccaccgcc ttaatgcctt ttgcttcaag ataatggttc agctcgattt
351 cttcgctgac catggatttg cctttgacca tcagcttgcc gtttttggtt
401 gtgatgatgt cgtggataat ttggcaggct tcggcagggg tttccgccca
451 gtgtactttc acgcccgaact tagtcagggt ttcttccaac tgctccagca
501 gcgcgggtaa
```

This corresponds to the amino acid sequence <SEQ ID 942; ORF 246.ng>:

g246.pep

1	MYGRNGSTQA	AVAFVFDQTO	RARFGNGEVY	AAQADIGSAV	NIAQGFGAGES
51	GQLVHVVCKR	CAEVLVEQFA	DLFFGFMDCG	HHDMGRFFAC	HLDDKLAQVA
101	FHRLNAFCFK	IMVQLDDFAF	HGFAFDHQLA	VFGCDDVDVN	LAGFGRGRFP
151	VYFHAQLSQV	FFQLLQQRG*			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 943>:

m246.seq (partial)

1	ATGCACGGGC	GGTACGGTGG	TACTCAAGCG	ACCGTTgCTT	CGTTTTCCAC
51	CAGACACAGC	GTACCTGTTT	CAGCAACGGC	AAAGTTTACG	CCACTCAAAC
101	CGACATCGGC	AGTGCTGTAA	ATATCGCGCA	GTGCTTTACG	GGCGAAGCCG
151	GTCAGTTGGT	CTACATCGTC	TGTCAGCGGC	GTACCGAGGT	TTTGGTGGAA
201	CAGTTCGCTA	ACCTGTTCTT	TGGTTTTGTG	GATAGCAGGC	ATCACGATAT
251	GGGTCCGTTT	TTGCGCTGCC	ATTTGGACGA	TGAACTCGCC	CAAGTCGCTT
301	TCTACCGCTT	TAATGcyTTT	TGCTTCAAGA	TAATGrTTCA	GCTCGATTTC
351	CTCGTGACC	ATCGATTGCG	CTTGACCAT	CAGCTTGC CG	TTTTTGCGTG
401	TGATGATGTC	GTGGATAATT	TGGCAGGCTT	CGGTTCGGGGT	TTCTGCGCG.

This corresponds to the amino acid sequence <SEQ ID 944; ORF 246>:

m246.pep (partial)

1	MHGRYGGTQA	TVAFVFHQIQ	RTCFSGNGKVY	ATQTDIGSAV	NIAQCFTGEA
51	GQLVYIVCQR	RTEVLVEQFA	NLFFGFVDSR	HHDMGRFFAC	HLDDELAQVA
101	FYRFNAFCFK	IMXQLDFLAD	HRFAFDHQLA	VFGCDDVVDN	LAGFGRGFCE...

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 246 shows 80.0% identity over a 150 aa overlap with a predicted ORF (ORF 246.ng) from *N. gonorrhoeae*:

m246/g246

	10	20	30	40	50	60
m246.pep	MHGRYGGTQATVAFVFHQ	TQRTCF	SNGKVYATQ	TDIGSAVNIA	QCFTGEAGQLVYIV	CQR
	:	:	:	:	:	:
g246	MYGRNGSTQAAVAFVFD	Q	TQ	RARFGNGEVYAAQ	ADIGSAVNIA	QGFAGESGQLVHV
	:	:	:	:	:	:
	10	20	30	40	50	60
	70	80	90	100	110	120
m246.pep	RTEVLVEQFANLFFGFVDS	RRHDMGRFF	FACHLDDELAQVAFYR	FN	NAFCFKIMXQLD	FLAD
	:	:	:	:	:	:
g246	CAEVLVEQFADLFFGFMD	CGHDMGRFF	FACHLD	DKLAQVAFHRLNA	FCFKIMVOLDF	FD
	:	:	:	:	:	:

565

	70	80	90	100	110	120
	130	140	150			
m246 . pep	HRFAFDHQLAVFGCDDVVDNLAGFGRGFCP					
g246	HGFADFHDQLAVFGCDDVVDNLAGFGRGFRPVYFHAQLSQVFFQLLQQRGX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 945>:

a246 . seq (partial)

1	ATGCACGGGC	GGAACGGTGG	TACTCAAGCG	ACCGTTGCCT	TCGTTTTCCA
51	CCAGACACAG	CGTACCTGTT	TCAGCAACGG	CGAAGTTCAC	GCCACTCAAA
101	CCGACATCGG	CAGTGCTGTA	AATATCGCGC	AGTGCTTTAC	GGCGGAAGCC
151	GGTCAGTTGG	TCTACGTCGT	CCGTAAACGG	TGTGCCGAGG	TTTTGGTGGA
201	ACAGTTCGCT	AACCTGTTCT	TTGGTTTTAT	GGATTGCGGG	CATCACGATA
251	TGGGTCGGTT	TTTCACCTGC	CATTTGGACG	ATGAACCTCG	CCAAGTCGCT
301	TTCCACCGCT	TTAATGCCTT	TTGCTTCAAG	ATAATGGTTC	AGCTCGATTT
351	CCTCGCTGAC	CATCGATTTG	CCTTTGACCA	TCAGCTTGCC	GTTTTTGGCT
401	GTGATGATGT	CGTGGATGAT	TTCGCAGGCT	TCGGCCGGTG	TTCCGCCCA
451	GTGTACTTTT	ACGCCCAACT	TGGTCAGGTT	TTCTTCCAGC	TGCTCCAGCA
501	G				

This corresponds to the amino acid sequence <SEQ ID 946; ORF 246.a>:

a246 . pep (partial)

1	MHGRNGGTQA	TVAFVFHQQT	RTCFNSNGEVH	ATQTDIGSAV	NIAQCFTGEA
51	GQLVYVVR*R	CAEVLVEQFA	NLFFFGFMDCG	HHDMGRFFTC	HLDELAQVA
101	FHRFNAFCFK	IMVQLDFLAD	HRFAFDHQLA	VFGCDDVDD	FAGFGRCFRP
151	VYFYAQLGQV	FFQLLQQ			

m246/a246 88.0% identity in 150 aa overlap

	10	20	30	40	50	60
m246 . pep	MHGRYGGTQATVAFVFHQQTORTCFNSNGKVYATQTDIGSAVNIAQCFTGEAGQLVYIVCQR					
a246	MHGRNGGTQATVAFVFHQQTORTCFNSNGEVHATQTDIGSAVNIAQCFTGEAGQLVYVVRXR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m246 . pep	RTEVLVEQFANLFFGFVDSRHHDMGRFFACHLDELAQVAFYRFNAFCFKIMXQLDFLAD					
	:					
a246	CAEVLVEQFANLFFGFMDCGHHDMGRFFTCCHLDELAQVAFHRFNAFCFKIMVQLDFLAD					
	70	80	90	100	110	120
	130	140	150			
m246 . pep	HRFAFDHQLAVFGCDDVVDNLAGFGRGFCP					
a246	HRFAFDHQLAVFGCDDVVDVDFAGFGRCFRPVYFYAQLGQVFFQLLQQ					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 947>:

g247 . seq

1	atgaaacgta	aaatgctaaa	cgtaccaaag	ggcgggttatg	atggtatgaa
51	gggttttacc	attgttgaat	ttctggttgc	gggcctgctc	agtataattg
101	tcctgatagc	ggtcgtatcg	agttacttta	catcccgga	attaaatgat
151	gtggcaaacg	agcgtcttgc	cattcaacag	gatttgcgga	atgcggcaac
201	attaattgtc	cgcgatgcaa	gaatggcggg	gagcttcggt	tgtttcaata
251	tgtccgagca	tactaaagac	gatattgttg	attcaagtaa	tcaaaactcaa
301	tctaaccctg	caaaaaccgg	tgccaaacaa	gaaaatcccc	tttttctctt
351	aaaaaggagc	ggcatggata	aacaactgat	tcccgttgct	gaatccatag
401	atattaaata	tccgggtttt	atccagcgcc	ttaacgcatt	ggttttccaa
451	tacggtatcg	atgatcttga	tgcgagtgtc	gagactgttg	tagtcagcag
501	ctgttccaaa	atagcaaaac	cgggtaagaa	aatatctacc	ttgcaagaag
551	caaagagtgc	attacagatt	actaatgatg	ataaacaaaa	tggaaatatc

g247.pcp

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 949>:

m247.seq (partial)

This corresponds to the amino acid sequence <SEQ ID 950; ORF 247>:

m247.pep (partial)

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 247 shows 69.3% identity over a 238 aa overlap with a predicted ORF (ORF 247.ng) from *N. gonorrhoeae*:

m247/g247

	10	20	30	40	50	60
m247.pep	XRRKMLNVXXGSYDGMKGFTTIIIEFLVAGLLSMIVLMAVGSSYFTSRKLNDAA	NERLAAQQ				
	:		:			
g247	MKRKMLNVPKGGYDGMKGFTTIVEFLVAGLLSIIVLIAVVS	SYFTSRKLNDVANERLAIQQ				
	10	20	30	40	50	60
	70	80	90		100	
m247.pep	DLRNAATLIVRDARMAGGFGCFNMSEHPATDVI-----	PDTTQONSPFSLKRN				
				:	:	
g247	DLRNAATLIVRDARMAGSFGCFNMSEHTKODIVDSSNQ	TQSNLAKPGAKQENPLFSLKRS				
	70	80	90	100	110	120
	110	120	130	140	150	160
m247.pep	GIDK-LIP	IAESSNIN	YQNFFQVGSALIFQY	GIDVDVNA	STATTVVSSCAA	ISKPGKQIPT
	:		:		:	

g247 GMDKQLIPVAESIDIKYPGFIQRLNALVFQYGIDDLDAE TVVSSCSKI AKPGKKIST
130 140 150 160 170 180

m247.pep 170 180 190 200 210 220
LEDAKKELKIPDQDKEQNGNIARQRHVVNAYAVGRIAD-EESLFRFQLDDKGKGWNPQL
|::||: |:| ::|| |||||:|:|||||||::: ||||| ||||| ||||| |||||
g247 LQEAKSALQITNDDK-QNGNITRQHVVNAYAVGRFGNNEESLFRFQLDDKGKGWNPQLL
190 200 210 220 230

g247 VKKVKRMDVRYIYVSGCPEDEDAGKEEF RYTNKF DKS KNAVTPAGVEVL LDSGLNAKIA
240 250 260 270 280 290

```
a247.seq
1  ATGAGACGTA  AAATGCTAAA  CGTACCAAAA  GGCAATTATG  ATGGTATGAA
51  GGGTTTTACC  ATTATTGAAT  TTTTGGTTGC  GGGCATGCTC  AGTATGATTG
101 TCCTGATGGC  GGTCCGGATC  AGTTACTTCA  CATCCCGGAA  ATTAATATGAT
151 GCGGCAAAAC  AGCGTCTTTC  GCGCGAACAG  GAGTTGCGGA  ATGCGGCAAC
201 ATTGATTGTC  CGCGATGCAA  GAATGGCAGG  GGGTTCGGT  TGTTTCAATA
251 TGTCCGAGCA  TACTAAAAAT  GATATTATTG  TTGATCCAAG  TAAGCAAAC
301 CAACATGTCC  CTGTAAAACC  CGGTGCCAAA  CAAGAAAATC  CCTTTTTTC
351 TTTAGAGTGG  GCTAATACTA  ATAATACTAA  TAATAATACA  GCTAAATTGA
401 TTCCTATTGC  TGAATCCACA  GATATTAAT  ATCCGGGTTT  TGCCAGGCT
451 CGTCCGGCAT  TGATTTTCCA  ATACGGCATC  GATGATCTTG  ATGCGAGTGC
501 TGAGACTGTT  GTAGTCAGCA  GCTGTTCCAA  AATAGCAAAA  CCGGGTAAGA
551 AAATATCTAC  CTTGCAAGAA  GCAAAGAGTG  CATTACAGAT  TACTAATGAT
601 GATAAACAAA  ATGGAATAT  CACCCGTCAA  AGGCATGTGG  TCAATGCCTA
651 TCGCGTCGGC  AGGATTGCGG  GTGAGGAAG  TTTGTTCCGC  TTCCAATTGG
701 ATGATAAGGG  CAAGTGGGGT  AATCCTCAGT  TGCTCGTGAA  AAGAGTTAGA
751 CATATGAAAG  TGCGGTATAT  CTATGTTTCC  GACTGTCCTG  AAGATGACGA
801 TGCCGGCAAA  GAGGAAAAAT  TCAAATATAC  GGGTACATT  GACAGCTCCA
851 CAAATGCTGT  TACGCCCCGC  GGGGTGGAGG  TTTTATTGAG  TANCGGTACT
901 GATACCAAGA  TTGCCGCTTC  TTCAGACAT  CATATTATG  CTAACCGTAT
951 CGATGCGACA  ATACGCGGGG  GAAATGTATG  CGCAAAACAG  ACTTTTGA
```

a247.pep	1	MRRKMLNVPK	GNYDGMKGFT	IEFLVAGML	SMIVLMAVGS	SYFTSRKLN	D
	51	AANERLSAQQ	DLRNAATLIV	RDARMAGGFG	CFNMSEHTKN	DIIVDPKQT	
	101	QHVNVKPGAK	QENPLFLSEW	ANTNNTNNNT	AKLIPIAEST	DIKYPGFAQ	
	151	RPALIFQYGI	DDLDAEAETV	VVSSCSKIAK	PGKKISTLQE	AKSALQITND	
	201	DKQNGNITRQ	RHVVNAYAVG	RIAGEEGLFR	FQLDDKGGKWG	NPQLLVKKIR	
	251	HKMVRYYIVS	DCPEDDDAGK	EEKFKYTGTG	DSSTNAVTPA	GVEVLLSXGT	
	301	DTKIAASSDN	HIIAYRIDAT	IRGGNVCANR	TL*		

	10	20	30	40	50	60
m247.pep	XRRKMLNVXXGSYDGMKGFTTIEFLVAGLLSMIVLMAVGSSYFTSRKLNDAAANERLAAQQ					
		:				
a247	MRRKMLNVPKGNYDGMKGFTTIEFLVAGMLSMIVLMAVGSSYFTSRKLNDAAANERLSAQQ					
	10	20	30	40	50	60
	70	80	90		100	
m247.pep	DLRNAATLIVRDARMAGGFGCFNMSEHPATDVI-----PDTTQQNSPFSLK-					
a247	DLRNAATLIVRDARMAGGFGCFNMSEHTKNDIIVDPSKQTQHVVPVKPGAKQENPLFSLEW					
	70	80	90	100	110	120
	110	120	130	140	150	160
m247.pep	-----RNGIDKLIPIAESSNINYQNFFQVGSALIFQYGIDDVNASTATTVVSSCAAISK					
	:					
a247	ANTNNTNNNTAKLIPIAESTDIKYPGFAQARPALIFQYGIDDLDAEAETVVVSSCSKIAK					
	130	140	150	160	170	180

568

	170	180	190	200	210	220
m247.pep	PGKQIPTLED	AKKELKIP	DQDKEQNG	NIARQRHV	VNAYAVG	GRIADEES
	:	:	:	:	:	:
a247	PGKKISTL	QEAQSAL	QITNDDK	-QNGNITR	QRHVVN	AYAVGRI
	190	200	210	220	230	

m247.pep	GNPQL
a247	GNPQLLVKKIRHMKVRYIYVSDCPEDDDAGKEEFKYTGTFDSSTNAVTPAGVEVLLSXG
	240 250 260 270 280 290

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 953>:

g247-1.seq (partial) ..

```

1   CCCGGTGCCA AACAAGAAAA TCCCCTTTTT TCCTTAAAAA GGAGCGGCAT
51  GGATAACAA  CTGATTCCCG TTGCTGAATC CATAGATATT AAATATCCGG
101 GTTTTATCCA GCGCCTTAAC GCATTGGTTT TCCAATACGG TATCGATGAT
151 CTTGATGCGA GTGCTGAGAC TGTGTAGTTC AGCAGCTGTT CCAAAATAGC
201 AAAACCGGGT AAGAAAATAT CTACCTTGCA AGAAGCAAAG AGTGCATTAC
251 AGATTACTAA TGATGATAAA CAAAATGGAA ATATCACCCG TCAGAAACAT
301 GTGGTCAATG CCTATGCGGT CGGCAGGTTT GGCAATAATG AGGAAAGTTT
351 GTTCCGCTTC CAATTGGATG ATAAGGGCAA GTGGGGTAAT CCTCAGTTGC
401 TCGTGAAAAA GGTAAACGAT ATGGATGTGC GGTATATTTA TGTTCCTCGG
451 TGTCTGAAG  ATGAAGATGC CGGCAAAGAG GAAAAATTC AATATACGAA
501 TAAATTCGAC AAATCCAAAA ATGCTGTTCG GCCTGCCGGG GTGGAGGTTT
551 TATTGGATAG CGGCCTTAAT GCCAAGATTG CCGCTTCTTC AGACAATAGT
601 ATTTATGCTT ACCGTATCAA TGCGACAATA CGCGGGGAA  ATGTATGCGC
651 AAACAGAACA CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 954; ORF 247-1.ng>:

g247-1.pep (partial) ..

```

1   PGAKQENPLF SLKRSMDKQ  LIPVAESIDI KYPGFIQRLN ALVFQYGIDD
51  LDASAEVTVV SCSKIAKPG  KKISTLQEA SALQITNDDK QNGNITRQKH
101 VVNAYAVGRF  GNNEESLFR FQLDDKGKWN PQLLVKKVKR MDVRYIYVSG
151 CPEDDAGKE  EKFRYTNKF D KSKNAVTPAG VEVLLDSSLN AKIAASSDMS
201 IYAYRINATI RGGNVCANRT L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 955>:

m247-1.seq

```

1   ATGAGACGTA AAATGCTAAA CGTACCAAAA GGCAGTTATG ATGGTATGAA
51  AGGTTTACC  ATTATTGAAT TTTTGTTGTC GGGCCTGCTC AGTATGATTG
101 TCCTGATGGC GGTCCGATCG AGTTACTTCA CATCCCGGAA ATTAATGAT
151 CGCGCAAACG AGCGTCTTGC CGCGCAACAG GATTTGCGGA ATGCGGCAAC
201 ATTGATTGTC CGCGATGCGA GAATGGCAGG CGGCTTCGGT TGTTCATAA
251 TGTCCGAGCA TCCTGCAACT GATGTTATTC CCGATACGAC GCAACAAAAT
301 TCTCCTTTTT CCTTAAAAAG GAACGGTATA GATAAACTTA TTCCCATAGC
351 GGAATCTTCA AATATCAATT ATCAGAATTT TTTCCAGGTT GGTAGCGCAT
401 TGATTTTTCA ATACGGAATC GATGATGTTA ATGCAAGCAC CGCGACTACC
451 GTCGTCAGCA GCTGTGCCGC AATATCGAAA CCGGGCAAGC AAATCCCTAC
501 TTTAGAAGAT GCAAAAAAAG AATTGAAGAT TCCGGATCAG GATAAGGAGC
551 AAAATGGCAA TATAGCGCGT CAAAGGCATG TGGTCAATGC CTATGCGGTC
601 GGCAGGATTG CCGATGAGGA AGGTTTGTTC CGCTTCCAAT TGGATGATAA
651 GGGCAAGTGG GGTAATCCTC AGTTGCTCGT GAAAAAGGTT AGACATATGA
701 AAGTGCGGTA TATCTATGTT TCCGGCTGTC CTGAAGATGA CGATGCCGGC
751 AAAGAGGAAA CATTCAAATA TACGGATAAA TTCGACAGCG CCCAAAATGC
801 TGTTACGCCC GCCGGGTGG  AGGTTTATT GAGTAGCGGT ACTGATACCA
851 AGATTGCCGC TTCTTCAGAC AATCATATTT ATGCTTACCG TATCGATGCG
901 ACAATACGCG GGGGAAATGT ATGCGCAAAC AGAACACTTT GA

```

This corresponds to the amino acid sequence <SEQ ID 956; ORF 247-1>:

m247-1.pep

```

1   MRRKMLNVPK GSYDGMKGFT IIEFLVAGLL SMIVLMAVGS SYFTSRKLND
51  AANERLAAQQ DLRNAATLIV RDARMAGGFG CFNMSEHPAT DVIPDTTQON
101 SPFSLKRNGI DKLPIAESS NINYQNFFQV GSALIFQYGI DDVNASATTT
151 VVSSCAAISK PGKQIPTLED AKKELKIPDQ DKEQNGNIAR QRHVVNAYAV
201 GRIADEEGLF RFQLDDKGKW GNPQLLVKKV RHMKVRYIYV SGCPEDDDAG
251 KEETFKYTDK FDSAQNAVTP AGVEVLLSSG TDTKIAASSD NHIYAYRIDA
301 TIRGGNVCAN RTL*

```


569

m247-1 / g247-1 72.1% identity in 222 aa overlap

```

      70      80      90      100      110      120
m247-1.pep  NAATLIVRDARMAGGFGCFNMSEHPATDVIPDTTQONSPFSLKRNGIDK-LIPIAESSNI
g247-1      | : | : | | | | : | | | | | : |
              PGAKQENPLFSLKRSGMDKQLIPVAESIDI
              10      20      30

      130      140      150      160      170      180
m247-1.pep  NYQNFFQVGSALIFQYGIDDVNASTATTVVSSCAAISKPGKQIPTLEDAKKELKIPDQDK
g247-1      : | : | : | : | | | | : | : | | | : | : | : | : | : | : |
              KYPGFIQRLNALVFQYGIDDLASAETVVVSSCSKIAKPGKKISTLQEAKSALQITNDDK
              40      50      60      70      80      90

      190      200      210      220      230      240
m247-1.pep  EQNGNIARQRHVVNAYAVGRIAD-EEGLFRFQLDDKGKGNPQLLVKKVRHMKVRYIYVS
g247-1      | | | | : | | | | | | | : | | | | | | | | | | | | | | | |
              -QNGNITRQKHVVNAYAVGRFGNNEESLFRFQLDDKGKGNPQLLVKKVRMDVRYIYVS
              100      110      120      130      140

      250      260      270      280      290      300
m247-1.pep  GCPEDDDAGKEETFKYTDKFDSDAQNVAVTPAGVEVLLSSGTDTKIAASSDNHIYAYRIDAT
g247-1      | | | | : | | | : | : | | | | | | | | | | : | | | | | | | |
              GCPEDDAGKEEFKRYTNKFDKSKNAVTPAGVEVLLDSGLNAKIAASSDNSIYAYRINAT
              150      160      170      180      190      200

      310
m247-1.pep  IRGGNVCANRTLX
g247-1      | | | | | | | | | |
              IRGGNVCANRTLX
              210      220

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 957>:

a247-1.seq (partial)

```

1  AATAATACAG CTAAATTGAT TCCTATTGCT GAATCCACAG ATATTAAATA
51  TCCGGGTTTT GCCCAGGCTC GTCCGGCATT GATTTTCCAA TACGGCATCG
101 ATGATCTTGA TGCGAGTGCT GAGACTGTTG TAGTCAGCAG CTGTTCCAAA
151 ATAGCAAAAC CGGGTAAGAA AATATCTACC TTGCAAGAAG CAAAGAGTGC
201 ATTACAGATT ACTAATGATG ATAAACAAAA TGGAAATATC ACCCGTCAAA
251 GGCATGTGGT CAATGCCTAT GCGGTCGGCA GGATTGCCGG TGAGGAAGGT
301 TTGTTCCGCT TCCAATTGGA TGATAAGGGC AAGTGGGGTA ATCCTCAGTT
351 GCTCGTGAAG AAGATTAGAC ATATGAAAGT GCGGTATATC TATGTTCCG
401 ACTGTCTTGA AGATGACGAT GCCGGCAAAG AGGAAAAATT CAAATATACG
451 GGTACATTCG ACAGCTCCAC AAATGCTGTT ACGCCGCCCG GGGTGGAGGT
501 TTTATTGAGT AGCGGTACTG ATACCAAGAT TGCCGCTTCT TCAGACAATC
551 ATATTATGTC TTACCGTATC GATGCGACAA TACGCGGGGG AAATGTATGC
601 GCAAACAGAA CACTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 958; ORF 247-1.a>:

a247-1.pep (partial)...

```

1  NNTAKLIPIA ESTDIKYPGF AQARPALIFQ YGIDDLASA ETVVVSSCSK
51  IAKPGKKIST LQEAKSALQI TNDDKQNGNI TRQRHVVNAY AVGRIAGEEG
101 LFRFQLDDKG KWGNPQLLVK KIRHMKVRYI YVSDCPEDDD AGKEEFKYT
151 GTFDSSTNAV TPAGVEVLLS SGTDTKIAAS SDNHIYAYRI DATIRGGNVC
201 ANRTL*

```

m247-1 / a247-1 80.6% identity in 206 aa overlap

```

      10      20      30
a247-1.pep  NNTAKLIPIAESTDIKYPGFAQARPALIFQ
m247-1      | : | | | | | | : | : | : | | |
              GFGCFNMSEHPATDVIPDTTQONSPFSLKRNGIDKLIPIAESSNINYNQNFFQVGSALIFQ
              80      90      100      110      120      130

      40      50      60      70      80      89
a247-1.pep  YGIDDLASAETVVVSSCSKIAKPGKKISTLQEAKSALQITNDDK-QNGNITRQRHVVN
m247-1      | | | | : | : | : | : | | | : | : | : | : | : | : |
              YGIDDVNASTATTVVSSCAAISKPGKQIPTLEDAKKELKIPDQDKEQNGNIARQRHVVN
              140      150      160      170      180      190

      90      100      110      120      130      140      149
a247-1.pep  YAVGRIAGEEGLFRFQLDDKGKGNPQLLVKKIRHMKVRYIYVSDCPEDDDAGKEEFKY
              | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

570

```

m247-1      YAVGRIADEEGLFRFQLDDKGKGNPQLLVKKVRHMKVRYIYVSGCPEDDDAGKEETFKY
            200      210      220      230      240      250

a247-1.pep  150      160      170      180      190      200
            TGTFDSSSTNAVTPAGVEVLLSSGTDTKIAASSDNHIYAYRIDATIRGGNVCANRTLX
            |   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
m247-1      TDKFDSAQNAVTPAGVEVLLSSGTDTKIAASSDNHIYAYRIDATIRGGNVCANRTLX
            260      270      280      290      300      310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 959>:

```

g248.seq
1   atgcgcaaac agaacacttt gacaggaatc ccgacttctg acggacagag
51  ggggtccgca ctgtttatcg tgctgatggt gatgatagtc gtggcctttt
101 tggttgtaac tgccgcccag tcctacaata ccgaacagag gatcagtgcc
151 aacgaatcag acaggaaatt ggctttgtct ttagccgagg cggctttgcg
201 ggagggcgaa ttccagggtt tggatttggg atatgctgag gacagtaagg
251 ttacgtttag cgaaaactgt gaaaaagggtc tgtgtaccgc agtgaatgtg
301 cggacaaata ataatggtag tgaagagggt tttggcaata tcgtggtgca
351 aggcaagccc gccgttgagg cggtgaaacg ttcttgccct gcaaaagtctg
401 gcaaaaattc taccgacctg tgcatgaca ataaagggat ggaatataat
451 aaaggcgagg caggcgctcag caaatgccg cgctatatta tcgaatattt
501 aggcgtgaag aacggacaaa atgtttatcg gggtactgcc aaggcttggg
551 gtaagaatgc caataccgtg gtcgtccttc aatcttatgt aggcaataat
601 gatgagcaat aa

```

This corresponds to the amino acid sequence <SEQ ID 960; ORF 248.ng>:

```

g248.pep
1   MRKQNTLTGI PTSDGQRGSA LFIVLMVMIV VAFLLVTTAAQ SYNTEQRISA
51  NESDRKLALS LAEAAALREGE FQVLDLEYAA DSKVTFSENC EKGLCTAVNV
101 RTNNNGSEEA FGNIVVQKPK AVEAVKRSCP AKSGKNSTD L CIDNKGMEYN
151 KGAAGVSKMP RYIEYLGVK NGQNVYRVTA KAWGKNANTV VVLQSYVGNN
201 DEQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 961>:

```

m248.seq (partial)
1   ..GGGTTTGCAC TGTTAATCGT GCTGATGGTG ATrATCGTCG TGGCT.Tywt
51  gGwTGTAAct GCCGCGCAGT CTTACAATAC cGAGCAGCGk ATCAGTkCCA
101 ACGAATCAGA CAGGAAATTG GCTwTGCTT TGGCCGAGkC GkCTwTGCgG
151 GAAGGCGAAC TTCAGGTTTT GGATTtGGAA TATGATACGG ACAGTAAGGT
201 TACATTTAGC GAAAACTGTG GAAAAGGTCT GTsTGCCGCA GTGAATGTGC
251 GGACAAATAA TGATAATGAA GAGGCTTTTG ACAATATCGT GGTGCAAGGC
301 AAGCCCACCG TTGAGGCGGT GAAGCGTTCT TGCCCTGCAA ATTCTACCGA
351 CCTGTGCATT GACAAGAAAG GwTGGAATA TAAGAAAGGC ACGAGAAGCG
401 TCAC.AAAAT GCCACGTTAT ATTATCGAAT ATTTGGGCGT GwAGAACGGA
451 GAAATGTTT ATCGGGTTAC TGCCAAGGCT TGGGGAAGA ATGCCAATAC
501 CGTGGTCGTC CTTCAATCTT ATGTAAGCAA TAATGATGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 962; ORF 248>:

```

m248.pep (partial)
1   ..GFALLIVLMV XIVVAFXXVT AAQSYNTEQR ISXNESDRKL AXSLAEXXXXR
51  EGELQVLDLE YDTSKVTFS ENCGKGLXAA VNVRTNNDNE EAFDNIVVQG
101 KPTVEAVKRS CPANSTDLCI DKKGXKEYKKG TRSVTKMPRY IIEYLGvXNG
151 ENVYRVTAKA WGKNANTVVV LQSYVSNNDE *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 248 shows 81.1% identity over a 185 aa overlap with a predicted ORF (ORF 248.ng) from *N. gonorrhoeae*:

m248/g248

```

m248.pep      10      20      30      40
              GFALLIVLMVXIVVAFXXVTAAQSYNTEQRISXNESDRKLAXS
              | | : | | | | | | | | | | | | | | | | | | | |

```

g248		MRKQNTLTGIP	TS	DGQRGSALFIVLMVMIVVAFLVVTTAAQS	YNT	EQRISANESDRKLALS	
		10	20	30	40	50	60
m248.pep		50	60	70	80	90	100
		LAEXXXREGELQVLDLEYD	TDSKVTFSENCGKGLXAAVNVRTNND-NEEAFDNIVVQGKP				
			: :	: :	:		
g248		LAEAALREGEFQVLDLEYAADS	KVTFSENCEKGLCTAVNVRTNNNGSEEA	FGNIVVQGKP			
		70	80	90	100	110	120
m248.pep		110	120	130	140	150	
		TVEAVKRSCPA----	NSTDLCIDKKGXKEYKKGTRSVTKMPRYIIIEYLGVXNGENVYRVTA				
		:	:	: : :	:		
g248		AVEAVKRSCPAPAKSGKNSTDL	CIDNKGM EYNKGAGVSKMPRYIIIEYLGVKNGQN VYRVTA				
		130	140	150	160	170	180
m248.pep		160	170	180			
		KAWGKNANTVVVLQSYVSNNDEX					
			:				
g248		KAWGKNANTVVVLQSYVGNNDEQX					
		190	200				

```
a248.seq
1  ATGCGCAAAC  AGAACACTTT  GACGGGAATC  CCGACTTCTG  ACGGACAGAG
51  GGGGTTTGCA  CTGTTTATCG  TGCTGATGGT  GATGATCGTC  GTGGCTTTTT
101 TGTTGTAACT  TGCCGCGCAG  TCTTACAATA  CCGAGCAGCG  GTCAGTGCC
151 AACGAATCAG  ACAGGAAATT  GGCTTTGTCT  TTGGCCGAGG  CGGCTTTGCG
201 GGAAGGCGAA  CTTCAGGTTT  TGGATTTGGA  ATATGATACG  GACAGTAAGG
251 TTACATTTAG  CGAAAACTGT  GGAAAAGGTC  TGTGTACCCG  AGTGAATGTG
301 CGGACAAATA  ATGATAATGA  AGAGGCTTTT  GACAATATCG  TGGTGCAAGG
351 CAAGCCCACC  GTTGAGGCGG  TGAAGCGTTC  TTGCACTGCA  AAATCTACAG
401 GCCTGTGCAT  TGACAATAAA  GGGATGGAAT  ATAAGAAAGG  CACGCAAAAG
451 GTCAGCAAAA  TGCCACGTTA  TATTATCGAA  TATTTGGGCG  TGAAGAACGG
501 AGAAAATGTT  TATCCGGTTA  TGCCAAAGCG  TTTGGGTAAG  AATGCCAATA
551 CCGTGGTCGT  CCTTCAATCT  TATGTAAGCA  ATAATGATGA  GTAA
```

a248.pap

1	MRKQNTLTGI	PTSDGQGRGFA	<u>LFIVLMVMIV</u>	VAFLVVTTAAQ	SYNTEQRISA
51	NESDRKLALS	LAEAAALREGE	LQVLDLEYDT	DSKVTFSENC	GKGLCTAVNV
101	RTNNDNEEAF	DNIVVQKPT	VEAVKRCTA	KSTGLCLDNK	GMEYKKGTS
151	VSKMPRYIIE	YLGVKGENV	YRVTAKAWGK	NANTVVVLQS	YVSNND*

```

m248.pep      10      20      30      40
               GFALLIVLMVXIVVAFXXVTAAQSYNTEQRISXNESDRKLAXS
               |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
a248          MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFLLVVTAAQSYNTEQRISANESDRKLALS
               10      20      30      40      50      60

               50      60      70      80      90      100
m248.pep      LAEXXXREGELQVLDLEYDTSKVTFSFENCGKGLXAAVNVRTNNDNEEAFDNIVVQ GKPT
               ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
a248          LAEAAALREGELQVLDLEYDTSKVTFSFENCGKGLCTAVNVRTNNDNEEAFDNIVVQ GKPT
               70      80      90      100      110      120

               110      120      130      140      150      160
m248.pep      VEAVKRSCPANSTDLCIDKKGXEYKKGTRSVTKMPRYIIIEYLGXNGENVYRVTA KAWGK
               ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
a248          VEAVKRSTAKSTGLCIDNKGMEYKKGTQSVSKMPRYIIIEYLGVKNGENVYRVTA KAWGK
               130      140      150      160      170      180

               170      180
m248.pep      NANTVVVLQSYVSNNDEX

```

572

|||||
a248 NANTVVVLQSYVSNNDEX
190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 965>:

m248-1.seq

```

1  ATGCGCAAAC AGAACACTTT GACGGGAATC CCGACTTCTG ACGGACAGAG
51  GGGGTTTGCA CTGTTTATCG TGCTGATGGT GATGATCGTC GTGGCTTTT
101 TGGTTGTAAC TGCCGCGCAG TCTTACAATA CCGAGCAGCG GATCAGTGCC
151 AACGAATCAG ACAGGAAATT GGCTTTGTCT TTGGCCGAGG CGGCTTTGCG
201 GGAAGGCGAA CTTCAAGTTT TGGATTGGA ATATGATACG GACAGTAAGG
251 TTACATTTAG CGAAACTGT GGAAAAGGTC TGTGTGCCGC AGTGAATGTG
301 CGGACAAATA ATGATAATGA AGAGGCTTTT GACAATATCG TGGTGAAGG
351 CAAGCCCACC GTTGAGGCGG TGAAGCGTTC TTGCCCTGCA AATTCTACCG
401 ACCTGTGCAT TGACAAGAAA GGGATGGAAT ATAAGAAAGG CACGAGAAGC
451 GTCAGCAAAA TGCCACGTTA TATTATCGAA TATTGGGCGG TGAAGAACGG
501 AGAAATGTT TATCGGGTTA CTGCCAAGGC TTGGGGTAAG AATGCCAATA
551 CCGTGGTCGT CCTTCAATCT TATGTAAGCA ATAATGATGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 966; ORF 248-1>:

m248-1.pep

```

1  MRKQNTLTGI PTSDGQRGFA LFIVLMVMIV VAFLVVTAAQ SYNTEQRISA
51  NESDRKLALS LAEALREGE LQVLDLEYDT DSKVTFSENC GKGLCAAVNV
101 RTNNDNEEAF DNIVVQ GKPT VEA VKRSCPA NSTDL CIDKK GMEYK GTRS
151 VSKMPRYIIE YLGVKNGENV YRV TAKAWGK NANTVVVLQS YVSNNDE*

```

m248-1/g248 89.1% identity in 202 aa overlap

	10	20	30	40	50	60
m248-1.pep	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFLVVTAAQSYNTEQRISANESDRKLALS					
g248	MRKQNTLTGIPTSDGQRGSALFIVLMVMIVVAFLVVTAAQSYNTEQRISANESDRKLALS					
	10	20	30	40	50	60
	70	80	90	100	110	119
m248-1.pep	LAEALREGE LQVLDLEYDTDSKVTFSENC GKGLCAAVNVRTNND-NEEAFDNIVVQ GKPT					
g248	LAEALREGE FQVLDLEYAADSKVTFSENC EKGLCTAVNVRTNNGSEEA FGNIVVQ GKPT					
	70	80	90	100	110	120
	120	130	140	150	160	170
m248-1.pep	TVEAVKRSCPA----NSTDL CIDKKGMEYK GTRSVSKMPRYIIEYLGVKNGENVYRVTA					
g248	AVEAVKRSCPAKSGKNSTDLCIDNKGMEYNKGAAGVSKMPRYIIEYLGVKNGQNVYRVTA					
	130	140	150	160	170	180
	180	190				
m248-1.pep	KAWGKNANTVVVLQSYVSNNDEX					
g248	KAWGKNANTVVVLQSYVGNNDQX					
	190	200				

m248-1/a248 97.0% identity in 197 aa overlap

	10	20	30	40	50	60
m248-1.pep	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFLVVTAAQSYNTEQRISANESDRKLALS					
a248	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFLVVTAAQSYNTEQRISANESDRKLALS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m248-1.pep	LAEALREGE LQVLDLEYDTDSKVTFSENC GKGLCAAVNVRTNNDNEEA FDNIVVQ GKPT					
a248	LAEALREGE LQVLDLEYDTDSKVTFSENC GKGLCTAVNVRTNNDNEEA FDNIVVQ GKPT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m248-1.pep	VEAVKRSCPANSTDLCIDKKGMEYK GTRSVSKMPRYIIEYLGVKNGENVYRV TAKAWGK					
a248	VEAVKRSC TAKSTGLCIDNKGMEYK GTSVSKMPRYIIEYLGVKNGENVYRV TAKAWGK					
	130	140	150	160	170	180

573

```

                190
m248-1.pep  NANTVVVLQSYVSNINDEX
            | | | | | | | | | | | | | | | | | |
a248        NANTVVVLQSYVSNINDEX
                190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 967>:

```

g249.seq
  1  atgaagaata atgattgctt gcgctgaaa aatccccagt ccggtatggc
 51  gttgatagaa gtcttggtcg ctatgctcgt tctgaccatc ggtatatttg
101  cattgctgtc cgtacagttg cggacagtcg cttccgtcag ggaggcggaa
151  acgcaaacca tcgtcagcca aatcacgcaa aacctgatgg aaggaatggt
201  gatgaatccg accattgatt tggacagcaa caagaaaaac tatagtcttt
251  acatgggaaa acagacacta tcagctgtgg atgggtgagt tatgcttgat
301  gccgagaaaa gtaaggcgca gttggcagag gaacaattga agagatttag
351  tcatgagctg aaaaatgcct tgccggatgc ggtagctatt cattacgccg
401  tctgcaagga ttcgtcgggt gacgcgccga cattgtccga cagcgggtgt
451  ttttcttcaa attgcgacaa taaggcaaac ggggatactt tgattaaagt
501  attgtgggta aatgattcgg caggggattc ggatatttcc cgtacgaatc
551  ttgaagtgag cggcgacaat atcgtatata cctatcaggc aagggtcggg
601  ggtcgtgaat ga

```

This corresponds to the amino acid sequence <SEQ ID 968; ORF 249.ng>:

```

g249.pep
  1  MKNNDCRLK NPQSGMALIE VLVAMLVLT I GILALLSVQL RTVASVREAE
 51  TQTIVSQITQ NLMEGMLMNP TIDLSDNKK YSLYMGKQTL SAVDGEFMLD
101  AEKSKAQLAE EQLKRFSHEL KNALPDAVAI HYAVCKDSSG DAPTLSDSGA
151  FSSNCDNKAN GDTLIKVLWV NDSAGDSDIS RTNLEVSGDN IVYTYQARVG
201  GRE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 969>:

```

m249.seq
  1  ATGAAGAATA ATGATTGCTT CCGCCTGAAA GATTCCCAGT CCGGTATGGC
 51  GCTGATAGAA GTCTTGGTTG CTATGCTCGT TCTGACCATC GGTATTTTGG
101  CACTATTGTC TGTACAGTTG CGGACAGTCN NNNNNNNNNN NNNNNNNNNN
151  NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNTTGATGG AGGGAATGTT
201  GATGAATCCG ACCATTGATT CGGACAGCAA CAAGAAAAC TATAATCTTT
251  ACATGGGAAA CCATACACTA TCAGCTGTGG ATGGCGATT TGCATTGAT
301  GCCATGAAAA CTAAGGGGCA ATTGGCAGAG GCACAATTGA AGAGATTTAG
351  TTATGAGCTG AAAAATGCCT TGCCGGATGC GGCAGCCATC CATTACGCCG
401  TCTGCAAGGA TTCGTCGGGT AACCGGCCGA CATTGTCCGG CAATGCTTTT
451  TCTTCAAATT GCGACAATAA GGCAAACGGG GATACTTTAA TTAAAGTATT
501  GTGGGTAAAT GATTCGGCAG GGGATTCGGA TATTCCCCTG ACGAATCTTG
551  AGGTGAGCGG CGACAATATC GTATATACTT ATCAGGCAAG GGTCGGAGGT
601  CCGGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 970; ORF 249>:

```

m249.pep
  1  MKNNDCFRLK DSQSGMALIE VLVAMLVLT I GILALLSVQL RTVXXXXXXXX
 51  XXXXXXXXXXX XLMEGMLMNP TIDSDSNKK YNLYMGNHTL SAVDGDFAID
101  AMKTKGQLAE AQLKRFSYEL KNALPDAAAI HYAVCKDSSG NAPTLGNAF
151  SSNCDNKANG DTLIKVLWVN DSAGDSDISR TNLEVSGDNI VYTYQARVGG
201  RE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 249 shows 81.3% identity over a 203 aa overlap with a predicted ORF (ORF 249.ng) from *N. gonorrhoeae*:

m249/g249

```

                10      20      30      40      50      60
m249.pep  MKNNDCFRLKDSQSGMALIEVLVAMLVLTIGILALLSVQLRTVXXXXXXXXXXXXXXXXXXXX
            | | | | | : | | | | | | | | | | | | | | | | | | | | | : : :

```

574

```

g249      MKNNDCLRLKNPQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAETQTIVSQITQ
           10      20      30      40      50      60

           70      80      90      100     110     120
m249.pep  XLMEGMLMNPTIDSDSNKKNYNLYMGNH-TLSAVDGDFAIDAMKTGQLAEALKRFSYEL
           |||||:|||||:|||||:|||||:|:| |:| ||| |||||:|
g249      NLMEGMLMNPTIDLDSNKKNYSLYMGKQTL SAVDGEFMLDAEKSQAQLAEELKRFSHEL
           70      80      90      100     110     120

           130     140     150     160     170     179
m249.pep  KNALPDAAAIHYAVCKDSSGNAPTLSGN-AFSSNCDNKANGDTLIKVLWVND SAGSDSI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g249      KNALPDAAVAIHYAVCKDSSGDAPTLSDSGAFSSNCDNKANGDTLIKVLWVND SAGSDSI
           130     140     150     160     170     180

           180     190     200
m249.pep  RTNLEVSGDNIVYTYQARVGGREX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||
g249      RTNLEVSGDNIVYTYQARVGGREX
           190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 971>:

```

a249.seq
1   ATGAAGAATA ATGATTGCTT CCGCCTGAAA AACCCCCAGT CCGGTATGGC
51  GCTGATAGAA GTCTTGCTCG CTATGCTCGT TCTGACCATC GGTATTTTGG
101 CACTATTGTC TGTTCACTTG CCGACAGTCG CTTCCGTCAG GGAGGCAGAG
151 ACGCAAACCA TCGTCAGTCA AATCACGCAA AACCTGATGG AAGGAATGTT
201 GATGAATCCG ACCATTGATT CCGACAGCAA CAAGAAAAAC TATAATCTTT
251 ACATGGGAAA CCATCATGCA CTATCAGTTG TGGATGGCGA TTTTCAGGTT
301 GATGCCATAA AAACATAAGAC GCAGTTGGCA GAGGCACAAAT TGAAGAGATT
351 TAGTTATGAG CTGAAAAATG CCTTGCCGGA TCGCGCAGCC ATCCATTACG
401 CCGTCTGCAA GGATTGCTCG GGTGTTGCGC CGACATTGTC CGCCGGCAGT
451 ACTTTTCTT CAAATTGCGA TGGTAGTGCA AATGGGGATA CTTTGATTAA
501 AGTATTGTGG GTAAATGATT CGGCAGGGGA TTCGGATATC GCCCGTACGA
551 ATCTTGAGAC GAACGGCAAC AATATCGTAT ATACCTATCA GGCAAGGGTC
601 GGAGGTCGGG AATGA

```

This corresponds to the amino acid sequence <SEQ ID 972; ORF 249.a>:

```

a249.pep
1   MKNNDCFRLK NPQSGMALIE VLVAMLVLTIGILALLSVQL RTVASVREAE
51  TQTIVSQITQ NLMEGMLMNP TIDSDSNKKN YNLYMGNHHA LSVVDGDFQV
101 DAIKTKTQLA EAQLKRFSYE LKNALPDAAA IHYAVCKDSS GVAPTLSAGS
151 TFSSNCDGSA NGDTLIKVLW VND SAGSDSI ARTNLETNGN NIVYTYQARV
201 GGRE*

```

m249/a249 81.9% identity in 204 aa overlap

```

           10      20      30      40      50      60
m249.pep  MKNNDCFRLKDSQSGMALIEVLVAMLVLTIGILALLSVQLRTVXXXXXXXXXXXXXXXXXXXX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a249      MKNNDCFRLKNPQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAETQTIVSQITQ
           10      20      30      40      50      60

           70      80      90      100     110     119
m249.pep  XLMEGMLMNPTIDSDSNKKNYNLYMGNH-TLSAVDGDFAIDAMKTGQLAEALKRFSYE
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a249      NLMEGMLMNPTIDSDSNKKNYNLYMGNH-HLSVVDGDFQVDAIKTKTQLAEALKRFSYE
           70      80      90      100     110     120

           120     130     140     150     160     170
m249.pep  LKNALPDAAAIHYAVCKDSSGNAPTLS-GNAFSSNCDNKANGDTLIKVLWVND SAGSDSI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a249      LKNALPDAAAIHYAVCKDSSGVAPTLSAGSTFSSNCDGSANGDTLIKVLWVND SAGSDSI
           130     140     150     160     170     180

```

```

      180          190          200
m249.pep    SRTNLEVSGDNIVYTYQARVGGREX
              :|:|||||:|:|||||
a249        ARTNLETNGNNIVYTYQARVGGREX
              190          200

```

m249-1.sec

m249-1.ppt

m249-1/q249 90.1% identity in 203 aa overlap

a249/ L36117

Query: 73 DSDSNKKNYNLYMGNNHALSVVDGDFQVDAIKTKTQLAEA---OLKRFSYELKNALPDAA 129

576

D + M G A + T L +A +L ++ ++KN LP A
 Sbjct: 72 LYDVKDQ-----MATQSDFFKAKGSAFPTAPSSCTPLPDAIKDRLGCWAEQVKNELPGAG 126
 Query: 130 AI---HYAVCKDSSGVAPTLSAGSTFSSNCDGSAANGDTL-IKVLWVNDSDAGSDIARTNL 185
 + Y +C+ S +CDG G L I++ W + A ++
 Sbjct: 127 DLLKSDYYICRSSK-----PGDCDG--KGSML EIRLAWRGKQGACVNAADSSA 172
 Query: 186 ETN 188
 +T+
 Sbjct: 173 DTS 175

m249-1/a249 90.7% identity in 204 aa overlap

	10	20	30	40	50	60
m249-1.pep	MKNND	CFRLKDSQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAETQTIVSQITQ				
a249	MKNND	CFRLKDPQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAETQTIVSQITQ				
	10	20	30	40	50	60
	70	80	90	100	110	119
m249-1.pep	NLM	EGMLMNPTIDSDSNKKNYNLYMGNH-TLSAVDGDFAIDAMKTKGQLAEALKRFSYE				
a249	NLM	EGMLMNPTIDSDSNKKNYNLYMGNHHSVVDGDFQVDAIKTKTQLAEALKRFSYE				
	70	80	90	100	110	120
	120	130	140	150	160	170
m249-1.pep	LKNALPDAAA	IHYAVCKDSSGNAPTLS-GNAFSSNCDNKANGDTLIKVLWVNDSDAGSDSI				
a249	LKNALPDAAA	IHYAVCKDSSGVAPTLSAGSTFSSNCDGSAANGDTLIKVLWVNDSDAGSDSI				
	130	140	150	160	170	180
	180	190	200			
m249-1.pep	SRTNLEVSGDNIVYTYQARVGGREX					
a249	ARTNLETNGNNIVYTYQARVGGREX					
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 975>:

g250.seq

```

1 atgacgcaca cagcctctcc acgtgatgaa ttcatacgcg gcataaaaga
51 aagttcgccc atgctgattg ggcttttgcc ttgggcattg atactcggtg
101 tgcagggcgg gcaaaaaggt atgggcccggc tggaaatgct gctgatgacg
151 gggatgaact ttgccggcgg ctccgaattt gccacggtca acctgtgggc
201 ggaacctctg ccgatactgc ttatcgccac cataaccttt atgattaatt
251 cgcgccatat cctgatgggg ggcgccgctt gccacgcaca tgaaagaaat
301 accgctgaaa aaagccgcgc ccgcgctggt ttttatgtgt ga
  
```

This corresponds to the amino acid sequence <SEQ ID 976; ORF 250.ng>:

g250.pep

```

1 MHTASPRDE FIRGIKESSP MLIGLLPWAL ILGMQGGQKG MGRLEMLLMT
51 GMNFAGGSEF ATVNLWAEPL PILLIATITF MINSRHILMG GGACHAERN
101 TAEKSRARAV FYV*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 977>:

m250.seq

```

1 ATGCACACCT TCCCCGCATA ACGAATTTAT ACGCGGCATC AAAGAAAGTT
51 CGCCTATGCT GATTGGGCTG CTGCCTTGGG CATTAATACT CGGTATGCAG
101 GGCGGACAAA AAGGCATGAG CTGGCTGGAA ATGTTGTTGA TGACCAGTAT
151 GAACTTCGCC GCGGCTCCG AGTTTGCCAC GGTCAACCTG TGGCCsGAAC
201 CTCTGCCGAT ACTGCTTATC GCCACCGTAA CCTTTATGAT TAATTCTCGG
251 CATATCCTGA T.GGGGGCGG CGCTTGCCCC GCACCTGAAA GGAaTACCGC
301 TGAAAAAAGC CGTGCCCACA CTGTTTTTTA TGTGTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 978; ORF 250>:

m250.pep

```

1 MHTPSPHNEF IRGIKESSPM LIGLLPWALI LGMQGGQKGM SWLEMLLMTS
51 MNFAGGSEFA TVNLWAEPLP ILLIATVTFM INSRHILMGG GACPAPERNT
101 AEKSRARTVF YV*
  
```


ORF 250 shows 91.0% identity over a 111 aa overlap with a predicted ORF (ORF 250.ng) from *N. gonorrhoeae*:

		10	20	30	40	50	59
m250.pep		MHTPSPHNEFIRGIKESSPMLIGLLPWALILGMQGGQKGMWLEMLLMTSMNFAGGSEF					
		:: : :					
g250		MHTASPRDEFIRGIKESSPMLIGLLPWALILGMQGGQKGMGRLEMLLMTGMNFAGGSEF					
		10	20	30	40	50	60
	60	70	80	90	100	110	
m250.pep	ATVNLWAEPLPILLIATVTFMINSRHIILMGGGACAPAPERNTAEKSRTAVFYVX						
	: : : : :						
g250	ATVNLWAEPLPILLIATITFMINSRHIILMGGGACHAHERNTAEKSRRARAVFYV						
	70	80	90	100	110		

a250.seq

1	ATGACACACA	TAAGCTCGCC	CCGTAACGAA	TTTATACGCG	GCATCAAAGA
51	AAGTTCGCCC	ATGCTGATCG	GGCTTTTGCC	TTGGGCATTA	ATACTCGGTA
101	TGCAGGGTGG	ACAAAAAGGC	ATGAGCTGGC	TGGAAATGTT	GTTGATGACC
151	GGTATGAACT	TCGCCGCGCG	CTCCGAGTTT	GCCACGGTCA	ACCTGTGGGC
201	GGAACTCTG	CCGATACTGC	TTATCGCCAC	CGTAACCTTT	ATGATTAATT
251	CTCGGCATAT	CCTGATGGGG	G. CGGCAC TT	GCCCCGACC	TGAAAGAAAT
301	ACCGCTGAAA	AAAGCCGTGC	CCGCACTGTT	TTTTATGTGT	GA

a250 . pep

```

1  MTHISSPRNE FIRGIKESS MLIGLLPWAL ILGMQGGQKG MSWLEMLLMT
51  GMNFAGGSEF ATVNLWAEPL PILLIATVTF MINSRHILMG XGTC PAPERN
101 TAEKSARTV FYV*

```

m250/a250 94.6% identity in 111 aa overlap

```

10      20      30      40      50
59
m250.pep
MHTPSPHNEFIRGIKESSPMLIGLLPWALILGMQGGQKGMWLEMLLMTSMNFAGGSEF
      |
||:|||||||||||||||||||||||||||||||||:|||||||
a250
MTHISSPRNEFIRGIKESSPMLIGLLPWALILGMQGGQKGMWLEMLLMTGMNFAGGSEF
      10      20      30      40      50
60

      60      70      80      90      100      110
m250.pep
ATVNLWAEPLPILLIATVTFMINSRHILMGGGACPAPERNTAEKSRARTVFYVX
|||||||||||||||||||||||||||||:|||||||||||||
a250
ATVNLWAEPLPILLIATVTFMINSRHILMGXGTCPAPERNTAEKSRARTVFYVX
      70      80      90      100      110

```

g251.seq

```

seq
1  atgcctgacc caatagggat tcttttcgct gccgtcgggg ttgatttttt
51  tgccgttggt ttgagggggc gttttcaacg aataggcgcg gttggcatgt
101 tqataataat aatcctgatg gcggaggtcg gaaccaaacc ggtcgtaacc

```



```

a251      ADPIGLVLAAGVGGGF----RGRFRRIAGAVGMLIIIIILMAEIRVKAVKTEIHAQVVDVFG
              70              80              90              100             110

              130             140             150             160             170             180
m251.pep  GIEGFFECLQEPVAFPVNHAIGFVIGKRLVGTRAAIFVRTVGRTVRLCLKMIIQTDLAPV
            |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a251      GIEGFFECLQEPVAFPVNHAIGFVVGKRLVGTRAAIFVRTVGRTVRLCLKMIVQTDALPV
              120             130             140             150             160             170

              190             200             210             220             230             240
m251.pep  VREAGIIRPSVFIGIGIDIFQTVAAFGVRLVVKHARTVFRAHQRTVFAVGKQSAVFVVAR
            |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a251      VREAGIIHPSVFIGIGIDIFQTVAAFGVRLVVKHARTVFRAHQRTVFAVGKQTAVFVVAR
              180             190             200             210             220             230

              250             260             270             280             290             300
m251.pep  VFAVTGQTRTLFFICIKNRLGQECRNRIARVESLLRVFEYAADVPLILKTKTRAEQPR
            ||||:|:|:|:|||||:|||||:|||||:|||||:|||||:|||||
a251      VFASVSYRS-VFSIFIKNRLGQECRNRIARVESLLRVFEYAADVPFVFKTKTRAEQPR
              240             250             260             270             280             290

m251.pep  PAFVX
            |||
a251      SAFVX
            300

```

g253.seq

1	atgatcgaca	gggaccgtat	gttgcgggac	acgttggaac	gtgtgcgtgc
51	ggggtcgttc	tggttatggg	tgggtggtggc	atcgatgatg	tttaccgcgc
101	gattttcagg	cacttatctt	ctgatggaca	atcaggggct	gaattttctt
151	ttagcttttg	cgggactggt	gggcataaat	acgctgatgc	tggcagtatg
201	gttggcaacg	ttgttcttgc	gcgtgaaagt	gggacggttt	ttcagcagtc
251	cggcgacgtg	gtttcggggc	aaaggccctg	taaatcaggc	ggtgttgctg
301	ctgtatgcgg	accagtggcg	gcaaccttcg	gtacgatgga	aaataggcgc
351	aacggcgcac	agcttgctgc	tctgcacgct	gctcggaatg	ctggtgtcgg
401	tattgctgct	gcttttgggt	cggcaatata	cgttcaactg	ggaaagcacg
451	ctgttgagca	atgcgccttc	ggtacgcgcg	gtggaaatgt	tggcatggct
501	gccgtcgaaa	ctcggtttcc	ctgtccccga	tgcgcggggc	gtcatcgaa
551	gtcgtctgaa	cggcaatatt	gccgatgcgc	gggctttggt	ggggctgctg
601	gtcggcagta	tgcgtctgcta	cggcatcctg	ccgcgcctct	tggcttgggt
651	agtgtgtaaa	atccttttga	aaacaagcga	aaacggattg	gattttgaaa
701	aaacctatta	tcaggcggtc	atccgcgcgt	ggcagaacaa	aatcaccgat
751	gcggatacgc	ctcgggaaac	cgtgtccgcc	gttttcgccga	aaatcgtctt
801	gaacgatgcg	cgcgaattgg	cgtctatgct	ggagaccgag	tggcaggacg
851	gccaatgggt	cgagggcagg	ctggcgacag	aatggctgga	taaggggcgt
901	gccgccaatc	gggaacagg	tgccgcgctg	gagacagagc	tgaagcagaa
951	accggcgcaa	ctgcttatcg	gcgtacgcgc	ccaaactgtg	ccggaccggg
1001	gcgtgctgcg	gcagatttgt	cggctttcgg	aagcggcgca	gggcggcgcg
1051	gtgggtgcagc	ttttggcgga	acaggggcct	tcagcagcac	tttcggaaaa
1101	gctggaaacat	tggcgtaacg	cgttgaccga	atagcggcgc	gcgtggcctg
1151	agcctgacag	ggtggcgcac	gaaggccgtt	tqaaaqacca	ataa

g253.pep

1	MIDRDRMLRD	TLERVAGSF	WLWVVVASMM	FTAGFSGYTL	LMDNQGLNFF
51	<u>LVLAVGLGMN</u>	<u>TLMLAVWLAT</u>	LFLRVKVGRF	FSSPATWFRG	KGPVNQAVLR
101	<u>LYADQWRQPS</u>	<u>VRWKIGATAH</u>	<u>SLWLCTLLGM</u>	<u>LVSVLLLLLV</u>	RQYTFNWEST
151	LLSNAASVRA	PEMLAWLPSP	LGFPPVDARA	VIEGRNLNGNI	ADARAWNSGLL
201	<u>VGSIVCYGIL</u>	<u>PRLLAWVCK</u>	ILGKTSENGL	DLEKTYQFQV	IRRWNQKITD
251	ADTRRETVSA	VSPKIVLNDA	PKWALMLETE	WODGYYFEGR	LAEWLDKGV

582

	190	200	210	220	230	240
m253 .pep	VIEGRNLNGNIADARAWSGLLVGSIACYGILPRLLAWVVKIILLKTSENGLDLEKPYQAV					
	: : : : :					
g253	VIEGRNLNGNIADARAWSGLLVGSIACYGILPRLLAWVVKIILLKTSENGLDLEKTYQAV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m253 .pep	IRRWQNKITDADTRRETSAVSPKII LNDAPKWAVMLETEWQDGEWFEGRLAQEWLDKGV					
	: : : : :					
g253	IRRWQNKITDADTRRETSAVSPKIVLNDAPKWALMLETEWQDQGWFEGRLAQEWLDKGV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m253 .pep	ATNREQVAALETELKQKPAQLLIGVRAQTVPDRGVLRQIVRLSEAAQGGAVVQLLAEQGL					
	: : : : : :					
g253	AANREQVAALETELKQKPAQLLIGVRAQTVPDRGVLRQIVRLSEAAQGGAVVQLLAEQGL					
	310	320	330	340	350	360
	370	380	390			
m253 .pep	SDDLSEKLEHWRNALAECGAAWLEPDRAAQEGRDKQX					
	: : :					
g253	SDDLSEKLEHWRNALTECGAAWLEPDRVAQEGRLDKQX					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 991>:

a253 .seq	1	ATGATCGACA	GGAACCGTAT	GCTGCGGGAG	ACGTTGGAAC	GTGTGCGTGC
	51	GGGGTCGTTC	TGGTTGTGGG	TGGCGGCGGC	GACGTTTGCG	TTTTTTACCG
	101	GTTTTTCAGT	TACTTATCTT	CTAATGGACA	ATCAGGGTCT	GAATTCTTT
	151	TTGGTTTTGG	CGGCGGTGTT	GGGCATGAAT	ACGCTGATGC	TGGCAGTATG
	201	GTTGGCAATG	TTGTTCTCTG	GCGTGAAAGT	GGGGCGTTTT	TTCAGCAGTC
	251	CGGCGACGTG	GTTTCGGGGC	AAAGACCTTG	TCAATCAGGC	GGTGTTCGGG
	301	CTGTATGCGG	ACGAGTGGCG	GCAACCTTCG	GTACGTTGGA	AAATAGGCGC
	351	AACGTCGCAC	AGCCTGTGGC	TCTGCACGCT	GCTCGGAATG	CTGGTGTCCG
	401	TATTGTTGCT	GCTTTTGGTG	CGGCAATATA	CGTTCAACTG	GGAAAGCACG
	451	CTGTTGGGCG	ATTCGTCTTC	GGTACGGCTG	GTGGAAATGT	TGGCATGGCT
	501	GCCTGCGAAA	CTGGGTTTTT	CCGTGCCTGA	TGCGCGGGCG	GTCATCGAAG
	551	GTCGTCTGAA	CGGCAATATT	GCCGATGCGC	GGGCTTGGTC	GGGGCTGCTG
	601	GTCGGCAGTA	TCGCTGCTA	CGGCATCCTG	CCGCGCTCT	TGGCTTGGGC
	651	GGTATGCAAA	ATCCTTTTGA	AAACAAGCGA	AAACGGCTTG	GATTTGGAAA
	701	AGCCCTATTA	TCAGGCGGTC	ATCCGCCGCT	GGCAGAACAA	AATCACCAGT
	751	CGGATACGC	GTCGGGAAAC	CGTGTCCGCC	GTTTCGCCGA	AAATCGTCTT
	801	GAACGATGCG	CCGAAATGGG	CGGTCATGCT	GGAGACCGAA	TGGCAGGACG
	851	GCGAATGGTT	CGAGGCGAGG	CTGGCGCAGG	AATGGCTGGA	TAAGGGCGTT
	901	GCCGCCAATC	GGGAACAGGT	TGCCGCGCTG	GAGACAGAGC	TGAAGCAGAA
	951	ACCGGCGCAA	CTGCTTATCG	GCGTGCGCGC	CCAACTGTG	CCCGACCGCG
	1001	GCGTGTGCG	GCAGATCGTC	CGACTTTCGG	AAGCGGCGCA	GGGCGGCGCG
	1051	GTGGTGCAGC	TTTGGGCGGA	ACAGGGGCTT	TCAGACGACC	TTTCGGAAAA
	1101	GCTGGAACAT	TGGCGTAACG	CGCTGACCGA	ATGCGGCGCG	GCGTGGCTGG
	1151	AACCCGACAG	AGCGGCGCAG	GAAGGCCGTC	TGAAAACCAA	CGACCGCACT
	1201	TGA				

This corresponds to the amino acid sequence <SEQ ID 992; ORF 253.a>:

a253 .pep	1	MIDRNRMLRE	TLERVAGSF	WLWVAATFA	FFTGFSVTYL	LMDNQGLNFF
	51	LVLAVGLGMN	TLMLAVWLAM	LFLRVKVGFR	FSSPATWFRG	KDPVNQAVLR
	101	LYADEWRQPS	VRWKIGATSH	SLWLCTLLGM	LVSLLLLLV	RQYTFNWEST
	151	LLGDSSSVRL	VEMLAWLPAK	LGFPVPDARA	VIEGRNLNGNI	ADARAWSGLL
	201	VGSIACYGIL	PRLLAWAVCK	ILLKTSENGL	DLEKPYQAV	IRRWQNKITD
	251	ADTRRETSA	VSPKIVLND	PKWAVMLETE	WQDGEWFEGR	LAQEWLDKGV
	301	AANREQVAAL	ETELKQKPAQ	LLIGVRAQTV	PDRGVLRQIV	RLSEAAQGGA
	351	VVQLLAEQGL	SDDLSEKLEH	WRNALTECGA	AWLEPDRAAQ	EGRDKTNDRT
	401	*				

m253/a253 97.2% identity in 395 aa overlap

	10	20	30	40	50	60
m253.pep	MIDRNRMLRETLERVRAGSFWLWVVAATFAFFTGFSVTYLLMDNQGLNFFLVLAGVIGMN					
a253	MIDRNRMLRETLERVRAGSFWLWVVAATFAFFTGFSVTYLLMDNQGLNFFLVLAGVIGMN					
	10	20	30	40	50	60
m253.pep	TLMLAVWLAMLFLRVKVGREFSSPATWFRGKDPVNQAVLRLYADEWRQPSVRWKIGATSH					
a253	TLMLAVWLAMLFLRVKVGREFSSPATWFRGKDPVNQAVLRLYADEWRQPSVRWKIGATSH					
	70	80	90	100	110	120
m253.pep	SLWLCTLLGMLVSVLLLLLVRQYTFNWESTLLSNAASVRAVEMLAWLP SKLGFPVPDARA					
a253	SLWLCTLLGMLVSVLLLLLVRQYTFNWESTLLGDSSSVRLVEMLAWLP AKLGFPVPDARA					
	130	140	150	160	170	180
m253.pep	VIEGRNLNGNIADARAWSGLLVGSIACYGILPRLLAWVVKILLKTSENGLDLEKPYQAV					
a253	VIEGRNLNGNIADARAWSGLLVGSIACYGILPRLLAWAVCKILLKTSENGLDLEKPYQAV					
	190	200	210	220	230	240
m253.pep	IRRWQNKITDADTRRETSAVSPKII LNDAPKWAVMLETEWQDGEWFEGR LAQEWDKGV					
a253	IRRWQNKITDADTRRETSAVSPKIVLNDAPKWAVMLETEWQDGEWFEGR LAQEWDKGV					
	250	260	270	280	290	300
m253.pep	ATNREQVA AE TELKQKPAQLLIGVRAQTVPDRGVL RQIVRLSEAAQGGAVVQLLAEQGL					
a253	AANREQVA AE TELKQKPAQLLIGVRAQTVPDRGVL RQIVRLSEAAQGGAVVQLLAEQGL					
	310	320	330	340	350	360
m253.pep	SDDLSEKLEHWRNALAECGAAWLEPDRAAQEGR LKDQX					
a253	SDDLSEKLEHWRNALTECGAAWLEPDRAAQEGR LKTNDRTX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 993>:

g254.seq

```

1  atgtatgcag gcgaacgctt caatacttac agccatttga gcggtttgat
51  tctggcggcg gcagggttga tgctgatgct gctgaaaacc ataggacacg
101 gggacggata ccgtatcttc agcgtatcgg ttacggcat cagccttctt
151 ctgctctatt tgagtctctc gctgtaccac ggaattgcag ccggaaaact
201 gaaaagcatt ttgaaaaaaa ccgaccactg catgatttat gtgctgattg
251 ccggaagcta cacaccgttt gcaactggtt ctttgagaaa cgggcccggc
301 tggacggtat ttctactgtc ctggctgctg gcggctgcag gaatcgaca
351 agaactcacc atcggacgga aaagcgaaaa acgtctgctg tctattgcga
401 tttatatcgt aatgggctgg atggtcttgg cggtaatgaa atccctgaca
451 gcctcactcc cgccggcagg actggcttgg ctggcggcag gcggtatgct
501 gtacagcgtc ggcatttact ggtttgtaaa cgatgaaaaa atccgacacg
551 ggcacggaat ctggcatctg ttcgtattgg gcggcagcat aaccaattt
601 gtcagcgtgt acggttatgt aatctga

```

This corresponds to the amino acid sequence <SEQ ID 994; ORF 254.ng>:

g254.pep

```

1  MYAGERFNTY SHLSGLILAA AGLMLMLLKT IGHGDGYRIF SVSVYGISLL

```

```
m254.seq      (partial)
1      ..GTATCGGTTT ACGGCATCAG CCTTCTTCTG CTCTATTTGA GTTCCTGGCT
51     GTACCACGGA ATTGCAGCCG GAAAAC TGAA AAGCATTTTG AAAAAAACCG
101    ACCACTGCAT GTATTATGTG CTGATTGCCG GAAGCTACAC ACCGTTTGCA
151    CTGGTTTCTT TAGAGAACGG GCGGGCTGG ACGGTATTTT CACTGTCCTG
201    GCTGCTGGCG GCTGCAGGAA TCGCACAAGA ACTCACCATT CGACGGA AAA
251    GCGAAAAACG TCTGCTGTCT ATTGTGATTT ATGTCGTCAT GGGTTGGATG
301    GTCTTGCGCG TAATGAAATC CCTGACAGCC TACTCCCCT CGGCAGGACT
351    GGCTTGCGTG GCGGCAGGCG GTATGCTGTA CAGTGTCGGC ATTTACTGGT
401    TTGTAAACGA TGA AAAAATC CGACACGGGC ACGGAATCTG GCATCTGTTC
451    GTATTGGGCG GCAGCATCAC CCAATTGTG AGCGTG TACG GTTACGTAAT
501    CTGA
```

```
m254.ppe      (partial)
  1  .VSVYGISLLL LYLSSWLYHG IAAGKLKSIL KKTDHCMIYV LIAGSYTPFA
51  LVSLRNGPGW TVFSLSWLLA AAGIAQELTI GRKSEKRLLS IVIYVVMGWM
101 VLAVMKSSLTA SLPSAGLAWL AAGGMLYSVG IYWFVNDEKI RHGGIWHLF
151 VLGGSITQFV SVHYGYVI*
```

m254 / g254

a254.seq

```
1 ATGTATACAG GCGAACGCTT CAATACTTAC AGCCATTGTA GCGGTTTGAT
51 TCTGGCGGCG GCAGGTTTGG CGCTGATGCT GCTGAAACC ATAGGACACG
101 GGGACGGCTA CCGTATCTTC AGCGTATCGG TTTACGGCAT CAGCCTTCTT
151 CTGCTCTATT TGAGTTCCTC GCTGTACCAC GGAATTGCAG CCGGAAAAC T
201 GAAAAGCATT TTGAAAAAAA CCGACCACGT CATGATTAT GTGCTGATTG
251 CCGGAAGCTA CACACCGTTT GCACTGGTTT CTTTGAGAAA CGGGCCGGGG
```


301	TGGACGGTAT	TTTCACTGTC	CTGGCTGCTG	GCGGCTGCAG	GAATCGCACA
351	AGAACTCACC	ATTGGACGGA	AAAGCGAAAA	ACGACTGCTG	TCTATTGCGA
401	TTTATATCGT	AATGGGCTGG	ATGGTCTTGG	CGTAATGAA	ATCCCTGACA
451	GCCTCACTCC	CGCCGGCAGG	ACTGGCTTGG	CTGGCGGCAG	GCGGTATGCT
501	GTACAGCGTC	GGCATTTACT	GGTTTGTA	CGATGAAAAA	ATCCGACACG
551	GGCAGCGAAT	CTGGCATCTG	TTCTGATTGG	GCGGCAGCAT	CACCCAATTT
601	GTCAGCGTGT	ACGGTTACGT	AATCTGA		

a254 . pep

1	MYTGERFNTY	SHLSGLILAA	AGLALMLLKT	IGHGDGYRIF	SVSVYGISLL
51	LLYLSSSLYH	GIAAGKLKSI	LKKTDHCMYI	VLIAGSYTPF	ALVSLRNGPG
101	WTVFSLSWLL	AAAGIAQELT	IGRKSEKRLL	SIATYIVMGW	MVLAVMKSLT
151	ASLPPAGLAW	LAAGGMLYSV	GIYWFVNDEK	IRHGHIWHL	FVLGGSITQF
201	VSVYGYVI *				

```

30                                     10                                20
m254.pep
VSVYGISLLLLLYLSSWLYHGIAAGKLKSIL
|||||
a254
HLSGLILAAAGLALMLLKTIGHGDGYRIFSVSVYGISLLLLLYLSSSLYHGIAAGKLKSIL
20          30          40          50          60
70
40          50          60          70          80
90
m254.pep
KKTDHCMIIYVLIAGSYTPFALVSLRNGPGWTVFSLSWLLAAAGIAQELTIGRKSEKRLLS
|||||
a254
KKTDHCMIIYVLIAGSYTPFALVSLRNGPGWTVFSLSWLLAAAGIAQELTIGRKSEKRLLS
80          90          100         110         120
130
100         110         120         130         140
150
m254.pep
IVIIYVVMGWMVLAVMKSLTASLPSAGLAWLAAGGMLYSVGIYWVFVNDEKIRHGHGIWHLF
|:|:|
a254
IAIIYVVMGWMVLAVMKSLTASLPPAGLAWLAAGGMLYSVGIYWVFVNDEKIRHGHGIWHLF
140         150         160         170         180
190
160
m254.pep
VLGGSITQFVSVYGYVIX
|
a254
VLGGSITQFVSVYGYVIX
200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 999>:

```
g255.seq
1  atggttggaac aggaagcctt gcggggtcag ttcgtcgccg tgttcgctgc
51  cgcggttcgt tacgtgtca aaacctgcgc cgatttcac gcctttgacg
101 gcggtgatgc ccatcatcgc gtaggcgatt tcggcatcga ggcggtcgaa
151 aacgggttcg cccaaaccga cggggacgtt ggcggtctcg atatgcagtt
201 tcgcgccgac ggaattccaag gatttgcgca caccgtccat atagtgttcc
251 agttcggcga tttggctttg gttggcggca aaaaaaggat tttgggaaat
301 gtgttcgctg ccttcaaacc ggattttttt ttcgccgact tgggtaacgt
351 aggcggtgat ttccgtgccg aatttttctt tcagccattt tttggcaacg
401 gctccggcgg caacgcgggc tcgggttttcg cgggcggaac tcctgccgcc
451 gccccggtag tcgcgcgtac cgtatttgtg ccaataggtg tagtcggcgt
501 gtccggggcg gaaggcggtg gcgatgtcgc cgtagtcttc gctgcgctgg
551 tcggtgttgc ggattag
```

g255.pep

1	<u>MVGQEALRGQ</u>	<u>FVAVFAAALR</u>	YAVKTCADFH	AFDGVDAHHR	VGDFGIEAVE
51	NGFAQTDGDV	GGFDLMQFRAD	GIOGFAHTVH	IVFQFGDLAL	VGGKKRILGN
101	VFAAFKPDFF	FADLGNVGGD	FGAEFFQPF	FGNGSGGNAG	CGFAGGTPAA
151	APVVARTVfV	PIGIVGVSGA	EGGGDVAVVF	AALVGVAD*	

```
m255.seq
1      GTGGTTGGAC  AGGAAGCCTT  GCGGGGTCAG  TTCGTCGCCG  TGTTCGCTGC
51     CGCGTTGCGT  TACGCTGTCA  AAACCTTGC  CGATTTCAC  GCCTTTGACG
101    GCGTTGATGC   CCATCATCGC  GTAGGCGATT  TCGGCATCGA  GCGGGTCAA
151    AACAGGTTTCG  CCAAGCCGA  CAGGGACATT  GGCTGCTTCG  ATATGCAGCT
201    TCGCGCCGCA  GGAATCCAA  GATTTGCGCA  CGCTGTCCAT  ATAGTTTTCC
251    AGCTCGGCCAA  TTTGGCTATG  GTTGGCGGCA  AAAAAAGGAT  TTTGGGAAAT
301    GTGTTTCGAG  CTTTCAAACC  GGATTTCCTT  TTCGCCGACT  TGGGTAAACG
351    AGGCGGTGAT  TTCCGTGCCG  AATTTTTCTT  TCAACCATTT  TTTGGCAACG
401    GCTCCGCGAG  CAACGCGGG  GCGGTTTCA  CGGGCGGAGC  TCTGCGGCC
451    GCCGCGGTAG  TCGCGCTGC  CGTATTTGTG  CCAATAGGTA  TAGTCGGCGT
501    GGCCGGGCG  GAAGCTGGT  GCGATGTTGC  CGTAGTCTTT  GCTGCGCTGG
551    TCGGTATTGC  GGATTA
```

```
m255.pep
1  VVGQEALRGQ FVAVFAAALR YAVKTCADFH AFDGVDAAHR VGDFGIEAVK
51  NRFAQADRFI GCDLMQLRAD GIQGFHAVHV IVFQLGNLAM VGGKKRILGN
101 VFAAFKPDFF FAFDLNVGGD FRAEFFFFQP FGNSGSNAG GGFTGGAPAA
151 AAVVARAVFV PIGIVGVAGA EAGGDVAVVF AALVGIAD*
```

ORF 255 shows 88.8% identity over a 188 aa overlap with a predicted ORF (ORF 255.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m255.pep	VVGQEALRGQFVAVFAAALRYAVKTCADFHAFDGVDAHHRVVGDFGIEAVKNRFAQADRI					
	:					
g255	MVGQEALRGQFVAVFAAALRYAVKTCADFHAFDGVDAHHRVVGDFGIEAVENGFAQTDGDV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m255.pep	GCFDMQLRADGIQGFHAVHIVFQLGNLAMVGGKKRILGNVFAAFKPDPFFADLGNVGGD					
g255	GGFDMQFRADGIQGFHAHTVHIVFQFDLALVGGKKRILGNVFAAFKPDPFFADLGNVGGD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m255.pep	FRAEFFFQPFNGSGSNAGGGFTGGAPAAAAVVARAVFVPIGIVGVAGAEAGGDVAVVF					
	:					
g255	FRAEFFFQPFNGSGGNAGCGFAGGTAAAAPVVARTVFVPIGIVGVSGAEGGGDVAVVF					

587

		130	140	150	160	170	180
	189						
m255 . pep	AALVGIADX						
	:						
g255	AALVGVADX						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1003>:

```

a255 . seq
1   GTGGTTGGAC AGGAAGCCTT GCGGGGTGAG TTCGTCGCCG TGTTGCTGCTGC
51  CGCGTTGCGT TACGCTGTCA AAACCTGCGC CGATTTCCAC GCCTTTGACG
101 GCGTTGATGC CCATCATGGC GTAGGCGATT TCGGCATCGA GGCGGTGCGAA
151 TACGGGTTCG CCCAAGCCGA CGGGGACGTT GGCGGCTTCA ATATGCAGCT
201 TCGCGCCGAC GGAATCCAAG GATTGCGCA CGCTGTCCAT ATAGTTTCC
251 AGCTCGGCAA TTTGGCTATG GTTGGCGGCA AAAAAAGGAT TTTGGGAAAT
301 GTGTCGCAG CCTTCAAACC GGATTTCTTT TTCGCCGACT TGGGTAACGT
351 AGGCGGTGAT TTCCGTGCCG AATTTTCTTT TCAACCATT TTTGGCAACG
401 GCTCCGGCGG CAACGCGGGC GCGGTTTCG CGGGCGGAAC TCCTGCCGCC
451 GCCCGGCTAG TCGCGCGTGC CGTATTTGTG CCAATAGGTA TAGTCGGCGT
501 GGCCGGGGCG GAAGCTGGTG GCGATGTTGC CGTAGTCTTT GCTGCGCTGG
551 TCGGTATTGC GGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1004; ORF 255.a>:

```

a255 . pep
1   VVGQALRGE FVAVFAAALR YAVKTCADFH AFDGVDAHHG VGDFGIEAVE
51  YGFAQADGDV GGFNMQLRAD GIQGFAHAVH IVFQLGNLAM VGGKKRILGN
101 VFAAFKPDFF FADLGNVGGD FRAEFFFQPF FGNGSGGNAG GGFAGGTPAA
151 APVVARAVFV PIGIVGVAGA EAGGDVAVVF AALVGIAD*

```

m255/a255 93.1% identity in 188 aa overlap

	10	20	30	40	50	60
m255 . pep	VVGQ ALRGE FVAVFAAALRYAVKTCADFHAFDGVDAHHRVGD	FDGIEAVKNRFAQAD	RDI			
	:					
a255	VVGQ ALRGE FVAVFAAALRYAVKTCADFHAFDGVDAHHRVGD	FDGIEAVEYGF	AQADGDV			
	10	20	30	40	50	60
	70	80	90	100	110	120
m255 . pep	GCFDMQLRADGIQGF AHAVH IVFQLGNLAMVGGKKRILGNVFAAFKPDF	FFADLGNVGGD				
	:					
a255	GGFNMQLRADGIQGF AHAVH IVFQLGNLAMVGGKKRILGNVFAAFKPDF	FFADLGNVGGD				
	70	80	90	100	110	120
	130	140	150	160	170	180
m255 . pep	FRAE FFFQPF FGNGSGSNAGGGFTGGAPAAA	AVVARAVFVPIGIVGVAGAEAGGDVAVVF				
	:					
a255	FRAE FFFQPF FGNGSGSNAGGGFTGGAPAAA	AVVARAVFVPIGIVGVAGAEAGGDVAVVF				
	130	140	150	160	170	180
	189					
m255 . pep	AALVGIADX					
a255	AALVGIADX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1005>:

```

g256 . seq
1   atgctcgcgg tacgcaatcg gggttggcac ggcgcgatcg tccatttcg
51  cagctcgggc ggcgtagcga acaccgcccc ggtgttctac cacttgggtg
101 ataccgccga aatcgctttt gctttggaca cgctcaccgc gcgttaccgt
151 gaaatatacg ccgtcggcgt atcgctgggc ggcaacgcgc cggcaaaata
201 tttgggcgaa cagggcaaaa aggcattgcc gcacgcctcg gccgccgtat
251 ccgcccccg tcatgcagag gcggcaggca gccgcttcga cagcggcatc
301 acgcggtgc tctacacgcg ctacttcctc cgcacactga taccctaaagc

```

588

```

351  acgttcgctc caaggttttc agacggcatt tgccgcaggg tgcaaaacac
401  tgggcgagtt tgacgaccgt ttcaccgcac cgctgcacgg ctttgccgac
451  cggcacgact actaccgcca aacttcctgc aaaccgctgc tcaaacacgt
501  tgccaaaccg ctgctcctgc tcaatgccgc caacgacccc ttcctgccgc
551  ccgaagccct gccccgtgca gacgaagcgt ccgaagccgt taccctgttc
601  caacctgcac acggcgggca cgccggcttt gtcagcagca ccggcggcag
651  gctgcacctg caatggctgc cgcagaccgt cctgtcctat tttgacagct
701  tccgcacaaa caggcgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1006; ORF 256.ng>:

```

g256.pep
  1  MLAVRNRGWH GAVVHFRSCG GVANTAPVIFY HLGDTAEIAF ALDTLTARYR
 51  EIYAVGVSLG GNAPAKYLGE QGKKALPHAS AAVSAPVDAE AAGSRFDSGI
101  TRLLYTRYFL RTLIPKARSL QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD
151  RHDYYRQTSC KPLLKHVAKP LLLLNAANDP FLPPEALPRA DEASEAVTLF
201  QPAHGGHAGF VSSTGGRHLH QWLPQTVLSY FDSFRNRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1007>:

```

m256.seq
  1  ATGCTTGCGG TACGCGATCG GGGTTGGCAC GCGTAGTCG TCCATTTCCG
 51  CAGCTGCGGC GGCATTGCCA ACACCGCTCC GGTGTTCTAC CA.CTtGGCG
101  ATACCGCCGA AATCGCCTTT ACTTTGGACA CGTTCGCCGC GCGTTACCGT
151  GAAAtATACG CCGTCGGCGT ATCGCTGGGC GGCAACGCGC TGGCAAAATA
201  TTTGGGCGAA CAGGGCAAAA AGGCATTGCC GCAAGCCGCT GCCGTCATCT
251  CCGCCCCCGT CGATGCAGAG GCGGCAGGCA GACGCTTCGA CAGCGGCATC
301  ACGCGGCTGC TCTACACGCG TACTTCTCTC CGCACCCTGA TACCCAAAGC
351  AAAATCGCTC CAAGGTTTTC AGACGGCATT TGCCGCAGGG TGCAAAACAC
401  TGGGCGAGTT TGACGACCGC TTCACCGCAC CGCTGCACGG CTTTGCCGAC
451  CGGCACGACT ACTACGCCA AACTTCTCTG AAACCGCTGC TCAAACACGT
501  TGCCAAACCG CTGCTCCTGC TCAATGCCGT CAACGACCCC TTCCTGCCGC
551  CCGAAGCCCT GCCCGCGCA GACGAAGTAT CCGAAGCCGT TACCCTGTTT
601  CAGCCGGCAT ATGGTGGTCA TGTCGGCTTT GTCAGCAGCA CCGGCGGCAG
651  GCTGCACCTG CAATGGCTGC CGCAGACCGT CCTGTCCTAT TTCGACAGCT
701  TCCGCACAAA CAGGCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1008; ORF 256>:

```

m256.pep
  1  MLAVRDRGWH GVVVHFRSCG GIANTAPVIFY XLGDTAEIAF TLDTF AARYR
 51  EIYAVGVSLG GNALAKYLGE QGKKALPQAA AVISAPVDAE AAGRFRDSGI
101  TRLLYTRYFL RTLIPKAKSL QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD
151  RHDYYRQTSC KPLLKHVAKP LLLNNAVNDP FLPPEALPRA DEVSEAVTLF
201  QPAYGGHVG FVSSTGGRHLH QWLPQTVLSY FDSFRNRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 256 shows 92.9% identity over a 239 aa overlap with a predicted ORF (ORF 256.ng) from *N. gonorrhoeae*:

```

m256/g256
      10      20      30      40      50      60
m256.pep  MLAVRDRGWHGVVHFRSCGGIANTAPVIFYHLGDTAEIAFTLDTF AARYREIYAVGVSLG
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g256       MLAVRNRGWHGAVVHFRSCGGVANTAPVIFYHLGDTAEIAFALDTLTARYREIYAVGVSLG
          10      20      30      40      50      60

      70      80      90      100     110     120
m256.pep  GNALAKYLGEQGKKALPQAAVISAPVDAE AAGRFRDSGITRLLYTRYFLRTLIPKAKSL
          ||| |||||:|||||:|:|:| ||||| ||||| ||||| ||||| |||||:|
g256       GNAPAKYLGEQGKKALPHASAAVSAPVDAE AAGSRFDSGITRLLYTRYFLRTLIPKARSL
          70      80      90      100     110     120

      130     140     150     160     170     180
m256.pep  QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHDYYRQTSC KPLLKHVAKP LLLLNAVNDP
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g256       QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHDYYRQTSC KPLLKHVAKP LLLLNAANDP

```

589

	130	140	150	160	170	180
	190	200	210	220	230	240
m256.pep	FLPPEALPRADEVSEAVTLFQPAYGGHVGVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	: : : : :					
g256	FLPPEALPRADEASEAVTLFQPAHGGHAGFVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1009>:

```

a256.seq
1  ATGCTCGCGG TACGCGATCG GGGTTGGAAC GCGTAGTCG TCCATTTCCG
51  CAGCTGCGGC GCGTAGCGA ACACGCCCC GGTGTTCTAC CACTTGGGCG
101 ATACGCCGA AATTGCCTTT ACTTTGGACA CGCTCGCCG GCGTTACCGT
151 GAAATATACG CCGTCGGCGT ATCGCTGGGC GGCAACGCGC TGGCAAAATA
201 TTTGGGCGAA CAGGGCGAAA ACGCGCTGCC GCAAGCCGCC GCCGTCATCT
251 CCGCACCCGT CGATGCAGAG GCGGCAGGCA ACCGCTTCGA CAGCGGCATC
301 ACACGGCTGC TCTACACGCG CTACTTCCTC CGCACACTGA TACCCAAAGC
351 ACGGTCGCTC CAAGGTTTTT AGACGGCATT TGCCGCAGGG TGCAAAACAC
401 TGGGCGAGTT TGACGACCGT TTCACCGCAC CGCTGCACGG CTTTGCCGAT
451 CGGCACGACT ACTACCGCCA AACTTCCTGC AAACCGCTGC TCAAACACGT
501 TGCCAAACCG CTGCTCCTGC TCAATGCCGT CAACGACCCC TTCCTGCCGC
551 CCGAAGCGCT GCCCGCGCA GACGAAGTGT CCGAAGCCGT TACCTGTTC
601 CAGCCGACAC ACGGTGGTCA TGTCCGCTTT GTCGGCAGCA CCGGCGGACG
651 GCTGCACCTG CAATGGTTGC CGCAGACCGT CCTGTCTAT TCGACAGCT
701 TCCGCACAAA CAGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1010; ORF 256.a>:

```

a256.pep
1  MLAVRDRGWN GVVVHFRSCG GVANTAPVFY HLGDTAEIAF TLDTLAARYR
51  EIIYAVGSLG GNALAKYLGE QGENALPQAA AVISAPVDAE AAGNRFDSCI
101 TRLLYTRYFL RTLIPKARSL QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD
151 RHDYYRQTSC KPLLKHVAKP LLLNNAVNDP FLPPEALPRA DEVSEAVTLF
201 QPTHGGHVG FVSTGGRLHL QWLPQTVLSY FDSFRTNRR*

```

m256/a256 95.4% identity in 239 aa overlap

	10	20	30	40	50	60
m256.pep	MLAVRDRGWHGVVVHFRSCGGIANTAPVIFYXLGDTAEIAFTLDTFAARYREIYAVGVSLG					
	: : : : :					
a256	MLAVRDRGWNQVVVHFRSCGGVANTAPVIFYHLGDTAEIAFTLDTLAARYREIYAVGVSLG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m256.pep	GNALAKYLGEQGGKALPQAAVISAPVDAEAGRRFDSGITRLLYTRYFLRTLIPKAKSL					
	: : : : :					
a256	GNALAKYLGEQGENALPQAAVISAPVDAEAGNRFDSGITRLLYTRYFLRTLIPKARSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m256.pep	QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHYYRQTSCKPLLKHVAKPLLLLNAVNDP					
	: : : : :					
a256	QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHYYRQTSCKPLLKHVAKPLLLLNAVNDP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m256.pep	FLPPEALPRADEVSEAVTLFQPAYGGHVGVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	: : : : :					
a256	FLPPEALPRADEVSEAVTLFQPTHGGHVGVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1011>:

```

g256-1.seq
1  ATGATTTTGA CACCGCCGGA CACGCCCTT TTCCTCCGCA ACGGCAATGC
51  CGACACGATT GCCGCCAAAT TCCTGCAACA CCGGCACCC GCATACCGCC

```

590

```

101 GCGAGATGCT TCCCGACAGC ACGGGTAAAA CCAAACCCGC CTACGACTTT
151 TCAGCAGGCG GCATTTTCGCC CGATGCGCCG CTGGTCGTGC TGTTCACGG
201 TTTGGAAGGA AGCAGCCGCA GCCATTACGC GGTCGAAGTG ATGCTCGCGG
251 TACGCAATCG GGGTTGGCAC GGCGCAGTCG TCCATTTCCG CAGCTCGGGC
301 GGCCTAGCGA ACACCGCCCC GGTGTTCTAC CACTTGGGTG ATACCGCCGA
351 AATCGCCTTT GCTTTGGACA CGCTCACC GC GTTACC GT GAAATATACG
401 CCGTCGGCGT ATCGCTGGGC GGCAACGCGC CGGCAAAATA TTTGGGCGAA
451 CAGGGCAAAA AGGCATTGCC GCACGCCTCG GCCGCCGTAT CCGCCCCCGT
501 TGATGCAGAG GCGGCAGGCA GCCGCTTCGA CAGCGGCATC ACGCGGCTGC
551 TCTACACGCG CTAATTCCTC CGCACACTGA TACCCAAAGC ACGTTGCTC
601 CAAGGTTTTT AGACGGCATT TGCCGCAGGG TGCAAAACAC TGGGCGAGTT
651 TGACGACCGT TTCACCGCAC CGCTGCACGG CTTTGCCGAC CGGCACGACT
701 ACTACCGCCA AACTTCCTGC AAACCGCTGC TCAAACACGT TGCCAAACCG
751 CTGCTCCTGC TCAATGCCGC CAACGACCCC TTCCTGCCGC CCGAAGCCCT
801 GCCCCGTGCA GACGAAGCGT CCGAAGCCGT TACCCTGTTC CAACCTGCAC
851 ACGGCGGGCA CGCCGGCTTT GTCAGCAGCA CCGGCGGCAG GCTGCACCTG
901 CAATGGCTGC CGCAGACCGT CCTGTCTAT TTTGACAGCT TCCGCACAAA
951 CAGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1012; ORF 256-1.ng>:

g256-1.pep

```

1 MILTPPDTPF FLRNGNADTI AAKFLQHPAP AYRREMLPDS TGKTKTAYDF
51 SAGGISPDAP LVVLFHGLEG SSRSHYAVEL MLAVRNRGWH GAVVHFRSCG
101 GVANTAPVVFY HLGDTAEIAF ALDTLTARYR EIYAVGVSLG GNAPAKYLG
151 QGKKALPHAS AAVSAPVDAE AAGSRFDSGI TRLLYTRYFL RTLIPKARSL
201 QGFQTAFAAG KTLGEFDDDR FTAPLHGFAF RHDYRQTSC KPLLKHVAKP
251 LLLLNAANDP FLPEALPRA DEASEAVTLF QPAHGHHAGF VSSTGGRLLH
301 QWLPQTVLSY FDSFRTNRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1013>:

m256-1.seq

```

1 ATGATTTTAA CACCGCCGGA CACGCCCTTT TTCCTCCGCA ACGGCAATGC
51 CGACACGATT GCCGCCAAAT TCCTGCAACG CCCC GCGCCC GCATACCGCC
101 GAGAGCTGCT TCCCGACAGC ACGGGTAAAA CCAAAGTCGC CTACGACTTT
151 TCAGACGGCA TTTCGCCCGA TGCGCCGCTG GTCGTGCTGT TTCACGGTTT
201 GGAAGGAAGC AGCCGCAGCC ATTACGCGGT CGAACTGATG CTTGCGGTAC
251 GCGATCGGGG TTGGCACGGC GTAGTCGTCC ATTTCCGCAG CTGCGGCGGC
301 ATTGCCAACA CCGCTCCGGT GTTCTACCAC TTGGGCGATA CCGCCGAAAT
351 CGCCTTTACT TTGGACACGT TCGCCGCGCG TTACCGTGAA ATATACGCCG
401 TCGGCGTATC GCTGGGCGGC AACCGCTGG CAAAATATTT GGGCGAACAG
451 GGC AAAAGG CATTGCCGCA AGCCGCTGCC GTCATCTCCG CCCCCTCGA
501 TGCAGAGGCG GCAGGCAGAC GCTTCGACAG CGGCATCAG CGGCTGCTCT
551 ACACGCGCTA CTTCTCCGC ACCCTGATAC CCAAAGCAAA ATCGCTCCAA
601 GGT TTTT CAGA CGGCATTTGC CGCAGGGTGC AAAACACTGG GCGAGTTTGA
651 CGACCGCTTC ACCGCACCGC TGCACGGCTT TGCCGACCGG CACGACTACT
701 ACCGCCAAAC TTCCTGCAAA CCGCTGCTCA AACACGTTGC CAAACCGCTG
751 CTCCTGTCTA ATGCCGTCAA CGACCCCTTC CTGCCGCCCC AAGCCCTGCC
801 CCGCGCAGAC GAAGTATCCG AAGCCGTTAC CCTGTTCAG CCGGCATATG
851 GTGGTCATGT CGGCTTTGTC AGCAGCACCG GCGGCAAGGCT GCACCTGCAA
901 TGGCTGCCCG AGACCGTCTT GTCCTATTTT GACAGCTTCC GCACAAACAG
951 GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1014; ORF 256-1>:

m256-1.pep

```

1 MILTPPDTPF FLRNGNADTI AAKFLQRPAP AYRRELLPDS TGKTKVAYDF
51 SDGISPDAPL VVLFHGLEGS SRSHYAVELM LAVRDRGWHG VVVHFRSCGG
101 IANTAPVVFYH LGDTAEIAFT LDTFAARYRE IYAVGVSLGG NALAKYLGEQ
151 GKKALPQAAA VISAPVDAEA AGRRFDSGIT RLLYTRYFLR TLI PKAKSLQ
201 GFQTAFAAGC KTLGEFDDRF TAPLHGFAFR HDYRQTSC K PLLKHVAKPL
251 LLLNAVNDPF LPPEALPRAD EVSEAVTLFQ PAYGGHVGFV SSTGGRLLHLQ
301 WLPQTVLSYF DSFRTNRR*

```

m256-1/g256-1 93.1% identity in 319 aa overlap

```

          10      20      30      40      50      59
m256-1.pep MILTPPDTPFFLRNGNADTIAAKFLQRPAPAYRRELLPDSTGKTKVAYDFS-DGISPDAP
          |||||:|||||:|||||:|||||:|||||:|||||
g256-1      MILTPPDTPFFLRNGNADTIAAKFLQHPAPAYRREMLPDSTGKTKTAYDFSAGGISPDAP
          10      20      30      40      50      60

          60      70      80      90     100     110     119
m256-1.pep LVVLFHGLEGSSSRSHYAVELMLAVRDRGWHGVVVHFRSCGGIANTAPVVFYHLGDTAEIAF

```

591

```

|||||:|||||:|||||:|||||:|||||
g256-1  LVVLFHGLEGSSRSHYAVELMLAVNRGWHGAVVHFRSCGGVANTAPVFYHLGDTAEIAF
              70      80      90      100     110     120

      120      130      140      150      160      170      179
m256-1.pep  TLDTF AARYREIYAVGVSLGGNALAKYLGEQKKALPQAAAVISAPVDAEAAAGRRFDSGI
|||||:|||||:|||||:|||||:|||||:|||||
g256-1  ALDTLTARYREIYAVGVSLGGNAPAKYLGEQKKALPHASAAVSAPVDAEAAAGSRFDSGI
              130      140      150      160      170      180

      180      190      200      210      220      230      239
m256-1.pep  TRLLYTRYFLRTLIPKAKSLQGFQTAF AAGCKTLGEFDDRFTAPLHGFADRHDYYRQTSC
|||||:|||||:|||||:|||||:|||||:|||||
g256-1  TRLLYTRYFLRTLIPKARSLQGFQTAF AAGCKTLGEFDDRFTAPLHGFADRHDYYRQTSC
              190      200      210      220      230      240

      240      250      260      270      280      290      299
m256-1.pep  KPLLKHVAKPLLLNNAVNDPFLPPEALPRADEVSEAVTLFQPAYGGHGVFVSSTGGRHLH
|||||:|||||:|||||:|||||:|||||:|||||
g256-1  KPLLKHVAKPLLLNNAANDPFLPPEALPRADEASEAVTLFQPAHGGHAGFVSSTGGRHLH
              250      260      270      280      290      300

      300      310      319
m256-1.pep  QWLPQTVLSYFDSFRTNRRX
|||||:|||||:|||||
g256-1  QWLPQTVLSYFDSFRTNRRX
              310      320

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1015>:

```

a256-1.seq
1  ATGATTTTGA CACCGCCGGA CACACCCTTT TTCCTCCGCA ACGGCAATGC
51  CGACACGATT GCCGCCAAAT TCCTGCAACG CTCCGCACCT GCATACCGCC
101 GCGAGCTGCT TCCCGACAGC ACGGGTAAAA CCAAAACCGC CTACGACTTT
151 TCAGACGGCA TTTCGCCCGA TCGCCGCTG GTCGTGCTGT TTCACGGTTT
201 GGAGGGCGGC AGTGGCAGCC ATTACGCGGT CGAACTGATG CTCGCGGTAC
251 GCGATCGGGG TTGGAACGGC GTAGTCGTCC ATTTCCGCAG CTGCGGCGGC
301 GTAGCGAACA CCGCCCGGTT GTTCTACCAC TTGGGCGATA CCGCCGAAAT
351 TGCCTTTACT TTGGACACGC TCGCCGCGCG TTACCGTGAA ATATACGCCG
401 TCGGCGTATC GCTGGGCGGC AACGCGCTGG CAAAATATTT GGGCGAACAG
451 GCGGAAAACG CGCTGCCGCA AGCCGCGGCC GTCATCTCCG CACCCGTCGA
501 TGCAGAGGCG GCAGGCAACC GCTTCGACAG CGGCATCACA CGGCTGCTCT
551 ACACGCGCTA CTTCTCCCGC AACTGATAC CCAAAGCAGC GTCGCTCCAA
601 GGTTTTTCAGA CCGCATTTGC CGCAGGGTGC AAAACACTGG GCGAGTTTGA
651 CGACCGTTTC ACCGCACCGC TGCACGGCTT TGCCGATCGG CACGACTACT
701 ACCGCCAAAC TTCCTGCAAA CCGCTGCTCA AACACGTTGC CAAACCGCTG
751 CTCCTGCTCA ATGCCGTCAG CGACCCCTTC CTGCCGCCCC AAGCGCTGCC
801 CCGCGCAGAC GAAGTGTCCG AAGCCGTTAC CCTGTTCCAG CCGACACACG
851 GTGGTCATGT CGGCTTTGTC GGCAGCACCG GCGGCAGGCT GCACCTGCAA
901 TGGTTGCCCG AGACCGTCCT GTCCTATTTC GACAGCTTCC GCACAAACAG
951 GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1016; ORF 256-1.a>:

```

a256-1.pep
1  MILTPPDTPF FLRNGNADTI AAKFLQRSAP AYRRELLPDS TGKTKTAYDF
51  SDGISPDAPL VVLFHGLEGG SGSHYAVELM LAVRDRGWNG VVHFRSCGG
101 VANTAPVFYH LGDTAEIAFT LDTLAARYRE IYAVGVSLGG NALAKYLGEQ
151 GENALPQAAA VISAPVDAEA AGNRFDSGIT RLLYTRYFLR TLIPKARSLQ
201 GFQTAF AAGC KTLGEFDDR FTAPLHGFADR HDYYRQTSCK PLLKHVAKPL
251 LLLNAVNDPF LPPEALPRAD EVSEAVTLFQ PTHGGHGVFV GSTGGRHLHQ
301 WLPQTVLSYF DSFRTNRR*

```

a256-1/m256-1 95.6% identity in 318 aa overlap

```

      10      20      30      40      50      60
a256-1.pep  MILTPPDTPFLLRNGNADTIAAKFLQRSAPAYRRELLPDSTGKTKTAYDFSDGISPDAPL
|||||:|||||:|||||:|||||:|||||:|||||
m256-1  MILTPPDTPFLLRNGNADTIAAKFLQRPAPAYRRELLPDSTGKTKVAYDFSDGISPDAPL
      10      20      30      40      50      60

      70      80      90      100     110     120
a256-1.pep  VVLFHGLEGGSGSHYAVELMLAVRDRGWNGVVHFRSCGGVANTAPVFYHLGDTAEIAFT
|||||:|||||:|||||:|||||:|||||:|||||
m256-1  VVLFHGLEGSSRSHYAVELMLAVRDRGWNGVVHFRSCGGIANTAPVFYHLGDTAEIAFT

```

592

	70	80	90	100	110	120
a256-1.pep	130	140	150	160	170	180
	LDTLAARYREIYAVGVSLGGNALAKYLGEQGENALPQAAAVISAPVDAEAAGNRFDSGIT					
m256-1	130	140	150	160	170	180
	LDTF AARYREIYAVGVSLGGNALAKYLGEQGKKALPQAAAVISAPVDAEAAGRRFDSGIT					
a256-1.pep	190	200	210	220	230	240
	RLLYTRYFLRTLIPKARSLQGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHDYRQTSCK					
m256-1	190	200	210	220	230	240
	RLLYTRYFLRTLIPKARSLQGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHDYRQTSCK					
a256-1.pep	250	260	270	280	290	300
	PLLKHVAKPLLLNNAVNDPFLPPEALPRADEVSEAVTLFQPTHGGHVGFGVSTGGRLHLQ					
m256-1	250	260	270	280	290	300
	PLLKHVAKPLLLNNAVNDPFLPPEALPRADEVSEAVTLFQPAYGGHVGFGVSTGGRLHLQ					
a256-1.pep	310	319				
	WLPQTVLSYFDSFRTNRRX					
m256-1	310					
	WLPQTVLSYFDSFRTNRRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1017>:

g257.seq

```

1  atgggcaggc atttcgggcg cagacgtttt ctgacggctg ccgccgttgc
51  tgtggccggt gcggcggttt cttttttgcc gaatcctttt gccgccggcg
101 gcgaaaaacg caacatggat aaaaaacgag atgaaaatgt gtttttctgg
151 aaaggtgtcg cgctgggttc cggcgcgag ctgcgctgt tcggcggtga
201 cgacagacag gcggcggtt tggtaataa ggttttggcg gaagtggcg
251 gtttggaaaa aatgttcagc cttaccgtg aagacagcct gatcagccgt
301 ctgaaccgag acggttatct gacttcgctt ccggcggtt ttttggaa
351 gttgagcctg gccgcgatat tcacgcgctg a

```

This corresponds to the amino acid sequence <SEQ ID 1018; ORF 257.ng>:

g257.pep

```

1  MGRHFGRRRF LTAAAVAVAG AAVSFLPNPF AAGGEKRNMD KKRDENVFFW
51  KGVALGSGAE LRLFGVDDRQ AADLVNKLVA EVARLEKMFS LYREDSLIR
101 LNRDGYLTSP PADFLELLSL AAIFFTR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1019>:

m257.seq

```

1  ATGGGCAGGC ATTCGGGCG .CAGCGTTT CTGACGGTTG CCGCCGTTGC
51  GGCGGGGAC . GCGGCGGTTT CTTTCCTGCC GAATCCTTTT GCCGCCGATG
101 ATGAAAAACG CAACGGGGAT GAAAAACGCA ATGAAAATGT GTTTTCTGG
151 AAAGGTGTCT CACTGGGTTC CGGTGCGGa . CTCCGTCTGT TCGGTGTGGA
201 CGACAGGCGT GCGGCGGATT TGGTCAACAA GGTTTTGGCG GAAGTGGCGC
251 GTTTGGAATA ATTGTTCAGC CTTTACCGTG AAGACAGCCT GATCAGCCGC
301 CTGAACAGGG ACGGTTATCT GACTTCGCGG TCGGCGGATT TTTTGGAACT
351 GkTGAGCCTG GCCGCGATAT TCACGCKCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1020; ORF 257>:

m257.pep

```

1  MGRHFGXQRF LTVAAVAAGX AAVSFLPNPF AADDEKRNMD EKRDENVFFW
51  KGVALGSGAX LRLFGVDDR AADLVNKLVA EVARLEKLFS LYREDSLIR
101 LNRDGYLTSP SADFLELXSL AAIFFTX*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 257 shows 88.0% identity over a 125 aa overlap with a predicted ORF (ORF 257.ng) from *N. gonorrhoeae*:

m257/g257

593

```

m257.pep      MGRHFGRQRFLTVAAVAAGTAAVSFLPNPFAADDEKRNKGDEKRNENVFFWKGVALGSGAD
               |||||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:
g257          MGRHFGRRRRFLTAAAVAVAGAAVSFLPNPFAAGGEKRNMDKKRDENVFFWKGVALGSGAE
               10      20      30      40      50      60

               70      80      90      100     110     120
m257.pep      LRLFGVDDRRRAADLVNKKVLAEEVARLEKLFSLYREDSLISRLNRDGYLTSPSADFLLELXSL
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g257          LRLFGVDDRQAADLVNKKVLAEEVARLEKMFSLYREDSLISRLNRDGYLTSPPADFLELLSL
               70      80      90      100     110     120

m257.pep      AAIFTXX
               |||||
g257          AAIFTRX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1021>:

```

a257.seq
1  ATGGGCAGGC  ATTTCTGGGCG  CAGGCGTTTT  TTGACAGTTG  CCGCCGTTCG
51 GGCGGCGGGC  GCGGCGGTTT  CTTTCCTGCC  GAATCCTTTT  GCCGCCGATG
101 ATGAAAAACG  CAATAAAGAT  GAAAAACGCA  ATGAAAATGT  GTTTTCTGCG
151 AAAGGTGTCG  CACTGGGTTC  CGGTGCGGAG  CTCCGTCTGT  TCGGTGTGGA
201 CGACAGGCGT  GCGGCGGATT  TGGTCAACAA  GGTTTGGCG  GAAGTGGCGC
251 GTTTGGAAAA  AATGTTTCAGC  CTTTACCGTG  AAGACAGCCT  GATCAGCCGT
301 CTGAACCGTG  ACGGTTATTT  GACTTCGCCG  CCGGCGGATT  TTTTGAAGT
351 GTTGAGCCTG  GCCGTGATAT  TCACGCGCTG  A

```

This corresponds to the amino acid sequence <SEQ ID 1022; ORF 257.a>:

```

a257.pep
1  MGRHFGRRRF  LTVAAVAAAG  AAVSFLPNPF  AADDEKRNKD  EKRNENVFFW
51 KGVALGSGAE  LRLFGVDDRR  AADLVNKKVLA  EVARLEKMFS  LYREDSLISR
101 LNRDGYLTSP  PADFLELLSL  AVIFTR*

```

m257/a257 92.0% identity in 125 aa overlap

```

               10      20      30      40      50
60
m257.pep      MGRHFGXQRFLTVAAVAAGXAAVSFLPNPFAADDEKRNKGDEKRNENVFFWKGVALGSGAX
               |||||:|||||:|||||:|||||:|||||:
a257          MGRHFGRRRRFLTVAAVAAGAAVSFLPNPFAADDEKRNKDEKRNENVFFWKGVALGSGAE
               10      20      30      40      50
60
               70      80      90      100     110
120
m257.pep      LRLFGVDDRRRAADLVNKKVLAEEVARLEKLFSLYREDSLISRLNRDGYLTSPSADFLLELXSL
               |||||:|||||:|||||:|||||:|||||:|||||:
a257          LRLFGVDDRRRAADLVNKKVLAEEVARLEKMFSLYREDSLISRLNRDGYLTSPPADFLELLSL
               70      80      90      100     110
120

m257.pep      AAIFTXX
               |||||
a257          AVIFTRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1023>:

```

g258.seq
1  atgcgccgct tcctaccgat cgcagccata tgcgccgtcg tcctgctgta
51  cggattgacg gcgggcgaccg gcagcaccag ttcgctggcg gattatttct
101 ggtggatagt ctcgttcagc gcaatgctgc tgctggtggt gtccgccgtt
151 ttggcacgtt atgtcatatt gctgttgaaa gacaggcgca acggcgtggt
201 cggttcgcag attgccaaac gcctttccgg gatgttcacg ctggtcgccg
251 tactgcccgg cttgttcctg ttcggcattt ccgcgcagtt tatcaacggc
301 acgattaatt cgtggttcgg caacgacacc cacgaagccc tcgaacgcag
351 ccttaatttg agcaagtccg cactggattt ggccgcagac aatgccgtca
401 gcaacgccgt tcccgtacag atagacctca tcggcaccgc ctccctgtcg
451 ggcaatatgg gcagtgtgct ggaacactac gccggcagcg gttttgccca
501 gcttgccctg tacaatgccg caagcgggaa aatcgaaaaa agcatcaatc
551 cgcaccaatt cgaccagccg cttcccgaca aagaacattg ggaacagatt
601 cagcagaccg gttcggttcg gagtttgtaa agcataggcg gcgtattgta
651 cgcgcagggg tggttgctcg caggtagcga caacgggcgc gattacgcgc
701 tgttcttccg ccagccgatt cccgaaaatg tggcacagga tgccgttctg
751 attgaaaagg cgcgggcgaa atatgccgaa ttgagttaca gcaaaaaagg
801 tttgcagacc ttttttctgg taaccctgct gattgcctcg ctgctgtcga
851 ttttcttgc gctggtaatg gcactgtatt ttgcccgccg tttcgtcgaa
901 cccattctgt cgcttgccga gggcgcaaag gcggtggcgc aggggtgattt
951 cagccagacg cgcccgtat tgcgcaacga cgagttcgga cgtttgacca
1001 agctgttcaa ccatatgacc gagcagcttt ccatcgccaa agaagcagac
1051 gaacgcaacc gccggcgcgga ggaagccgcc cgctactacc tcgagtgcggt
1101 gttgatggg ttgactaccg gtgtggtggt ctctacccc ctctctgtt
1151 gccgtaccgc ggtgttttcc acttgtcatt cctccctct tcttatttc
1201 taa

```

This corresponds to the amino acid sequence <SEQ ID 1024; ORF 258.ng>:

```

g258.pep
1  MRRELPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVSFS AMLLLVLSAV
51  LARYVILLLK DRRNGVFGSQ IAKRLSGMFT LVAVLPGLFL FGISAQFING
101 TINSWFGNDT HEALERSLNL SKSALDLAAD NAVSNAVPVQ IDLIGTASLS
151 GNMGSVLEHY AGSGFAQLAL YNAASGKIEK SINPHQFDQP LPDKEHWEQI
201 QQTGSVRSLE SIGGVLYAQG WLSAGTHNGR DYALFFRQPI PENVAQDAVL
251 IEKARAKYAE LSYSKKGLOT FFLVTLIAS LLSIFLALVM ALYFARRFVE
301 PILSLAEGAK AVAQGDFSQT RPVLRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVDLG LTTGVVVSYP LSCCRTAVFS TCHSSPLSYF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1025>:

```

m258.seq
1  ATGCGCCGTT TTCTACCGAT CGCAGCCATA TGCGCCGTCT TCCTGTTGTA
51  CGGACTGACG GCGGCAACCG GCAGCACCAG TTCGCTGGCG GATTATTCTT
101 GGTGGATTGT TCGTTCAGC GCAATGCTGC TGCTGGTGTT GTCCGCCGTT
151 TTGGCACGTT ATGTCATATT GCTGTTGAAA GACAGGCGCG ACGGCGTATT
201 CGGTTCGCAG ATTGCCAAAC GCCTTTCTGG GATGTTTACG CTGGTTGCCG
251 TACTGCCCCG CGTGTTCCTG TTCGCGGTTT CCGCACAGTT CATCAACGGC
301 ACGATTAATT CGTGGTTCGG CAACGATACC CACGAGGCGC TTGAACGCAG
351 CCTCAATTG AGCAAGTCCG CATTGAATTT GGCGGCAGAC AACGCCCTCG
401 GCAACGCCGT CCCGTGCAG ATAGACCTCA TCGGCGCGGC TTCCCTGCCC
451 GGGGATATGG GCAGGGTGCT GGAACATTAC GCCGCGAGCG GTTTTGCCCA
501 GCTTGCCCTG TACAATGCCG CAAGCGGCAA AATCGAAAAA AGCATCAACC
551 CGCACAAGCT CGATCAGCCG TTTCCAGGTA AGGCGCGTTG GGAAAAAATC
601 CAACGGGCGG GTTCGGTCAG GGATTGGAA AGCATAGGCG GCGTATTGTA
651 CGCGCAGGGC TGGCTGTCGG CGGGTACGCA CAACGGGCGC GATTACGCCT
701 TGTTTTTCCG TCAGCCGGTT CCCAAAGGCG TGGCAGAGGA TGCCGTCTTA
751 ATCGAAAAGG CAAGGGCGAA ATATGCTGAG TGAGTTACA GCAAAAAGG
801 TTTGCAGACC TTTTCTCTGG CAACCCTGCT GATTGCCTCG CTGCTGTCGA
851 TTTTCTTGC ACTGGTCATG GCACTGTATT TCGCCGCGCG TTTCTGTCGA
901 CCCGTCCTAT CGCTTGCCGA GGGGGCGAAG GCGGTGGCGC AAGGCGATTT
951 CAGCCAGACG CGCCCCGTGT TGCGCAACGA CGAGTTCGGA CGCTTGACCA

```

595

```

1001 AGTTGTTCAA CCACATGACC GAGCAGCTTT CCATCGCCAA AGAAGCAGAC
1051 GAGCGCAACC GCCGGCGCGA GGAAGCCGCC AGGCATTATC TTGAATGCGT
1101 GTTGGAGGGG CTGACCACGG GCGTGGTGGT GTTTGACGAA CAAGGCTGTC
1151 TGAAACsTT CAACAAAGCG GCGGAACAGA TTyTGGGGAT GCCGCTTACC
1201 CCCcTGTGGG GCAGCAGCCG GCACGGTTGG CACGGCGTTT CGGCGCAGCA
1251 GTCCCTGCTT GCCGAAGTGT TTGCCGCCAT CGGCGCGGCG GCAGGTACGG
1301 ACAAACCGGT CCATGTGAAA TATGCCGCGC CGGACGATGC CAAAATCCTG
1351 CTGGGCAAGG CAACCGTCCT GCCCGAAGAC AACGGCAACg GCGTGGTAAT
1401 GGTGATTGAC GACATCACCG TTTTGATACA CGCGCAAAAA GAAGCCGCGT
1451 GGGGCGAaGT GGCgaAgCGG CTGGCACACG AAATCCGCAA TCCGCTCACG
1501 CCCATCCAGC TTTCCGCCGA ACgGsTGGCG TkGAAATTGG GCGGGAAGCT
1551 GGATGAGCAG GATGCGCAA TCCTGACGCG TTCGACCGAC ACCATCGTCA
1601 AACAGGTGGC GGCATTGAAG GAAATGGTCG AAGCATTCCG CAATTATGCG
1651 CGTTCCCTT CGCTCAAATT GGAAAATCAG GATTTGAACG CCTTAATCGG
1701 CGATGTGTTG GCATGTATG AAGCCGGTCC GTGCCGGTTT GCGGCGGACT
1751 TGCCGGCGAA CCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1026; ORF 258>:

```

m258.pep
  1 MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVAFS AMLLLVLSAV
 51 LARYVILLLK DRRDGVFGSQ IAKRLSGMFT LVAVLPGVFL FGVSAQFING
101 TINSWFGNDT HEALERSLNL SKSALNLAAD NALGNAVVPQ IDLIGAASLP
151 GDMGRVLEHY AGSGFAQLAL YNAASGKIEK SINPHKLDQP FPGKARWEKI
201 QRAGSVRDLE SIGGVLYAQG WLSAGTHNGR DYALFFRQPV PKGVAEDAVL
251 IEKARAKYAE LSYSKKGLQT FFLATLLIAS LLSIFLALVM ALYFARRFVE
301 PVLSLAEGAK AVAQGDFSQT RPVLRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVLEG LTGVVVVFDE QGCLKTFNKA AEQILGMPLT
401 PLWGSSRHGW HGVSAAQSSL AEFVFAAIGAA AGTDKPVHVK YAAPDDAKIL
451 LGKATVLPED NGNGVVMVID DITVLIHAQK EAAWGEVAKR LAHEIRNPLT
501 PIQLSAERXA XKLGGKLEDEQ DAQILTRSTD TIVKQVAALK EMVEAFRNYA
551 RSPSLKLENQ DLNALIGDVL ALYEAGPCR F AADLPANR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 258 shows 90.9% identity over a 386 aa overlap with a predicted ORF (ORF 258.ng) from *N. gonorrhoeae*:

```

m258/g258
      10      20      30      40      50      60
m258.pep MRRFLPIAAICAVVLLYGLTAATGSTSSLA DYFWWIVAFS AMLLLVLSAVLARYVILLLK
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g258      MRRFLPIAAICAVVLLYGLTAATGSTSSLA DYFWWIVSFS AMLLLVLSAVLARYVILLLK
          10      20      30      40      50      60

      70      80      90      100     110     120
m258.pep DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSLNL
          ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g258      DRRNGVFGSQIAKRLSGMFTLVAVLPGFLFLFGISAQFINGTINSWFGNDTHEALERSLNL
          70      80      90      100     110     120

      130     140     150     160     170     180
m258.pep SKSALNLAADNALGNAVVPQIDLIGAASLP GDMGRVLEHYAGSGFAQLALYNAASGKIEK
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g258      SKSALDLAADNAVSNVAVPQIDLIGTASLSGNMGSVLEHYAGSGFAQLALYNAASGKIEK
          130     140     150     160     170     180

      190     200     210     220     230     240
m258.pep SINPHKLDQPFPGKARWEKIQRAGSVRDLESIGGVLYAQGWLSAGTHNGRDYALFFRQPV
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g258      SINPHQFDQPLPDKEHWEIQQTGSVRSLESIGGVLYAQGWLSAGTHNGRDYALFFRQPI
          190     200     210     220     230     240

```

	250	260	270	280	290	300
m258.pep	PKGVAEDAVLIEKARAKYAELSYSKKGLQTFFLATLLIASLLSIFLALVMALYFARRFVE					
	:: : :					
g258	PENVAQDAVLIEKARAKYAELSYSKKGLQTFFLVTLLIASLLSIFLALVMALYFARRFVE					
	250	260	270	280	290	300
	310	320	330	340	350	360
m258.pep	PVLSLAEGAKAVAQGDFSQTRPVLRNDEFGRLTKLFNHMTQLSIAKEADERNRRREEAA					
	: :					
g258	PILSLAEGAKAVAQGDFSQTRPVLRNDEFGRLTKLFNHMTQLSIAKEADERNRRREEAA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m258.pep	RHYLECVLEGLTTGVVVVFDEQGCLKTFNKAAEQILGMPLTPLWGSSRHGWHGVSAQQSLL					
	: : :					
g258	RHYLECVLDGLTTGVVVSYPLSCCRTAVFSTCHSSPLSYFX					
	370	380	390	400		

```

a258.seq
1 ATGCGCCGTT TTCTACCGAT CGCAGCCATA TGCGCCGTCG TCCTGTTGTA
51 CGGACTGACG GCGGCAACCG GCAGCACCAG TTCGCTGGCG GATTATTTCT
101 GGTGGATTGT TGCCTTTCAGC GCAATGCTGC TGCTGGTGTT GTCCGCCGTT
151 TTGGCACGTT ATGTTCATATT GCTGTTGAAA GACAGGCGCG ACGGCGTATT
201 CGGTTTCGCAG ATTGCCAAAC GCCTTTCCGG GATGTTTACG CTGGTTGCCG
251 TACTGCCCGG CGTGTTCCTG TTCGGCGTTT CCGCACAGTT TATCAACGGC
301 ACGATTAATT CGTGGTTCGG CAACGATACC CACGAGGCGC TTGAACGCAG
351 CCTCAATTGT AGCAAGTCCG CATTGAATCT GGCGCAGAC AACCGCCTTG
401 GCAACGCCAT CCCCCTGCGC ATAGACATCT TCGCGCGCGC TTCCTGCCCC
451 GGGGATATGG GCAGGGTGCT GGAACATTAC CGCGGCAGCG GTTTTGCCCA
501 GCTTGCCCTG TACAATGCCG CAAGCGGCAA AATCGAAAAA AGCATCAACC
551 CGCACAAAGT CGATCAGCCG TTTCCAGGTA AGGCGCGTTG GGAAAAAATC
601 CAACAGGCGG GTTCGGTCAG GGATTGGGAA AGCATAGGCG GCGTATTGTA
651 CCGCGAGGGC TGGCTTCCGG CAGGTACGCA CAACGGGCGC GATTACGCCT
701 TGTTTTTCCG TCAGCCGGTT CCCAAAGGCG TGGCAGAGGA TGCCGCTCTTA
751 ATCGAAAAGG CAAGGGCGAA ATATGCTGAG TTGAGTTACA GCAAAAAGG
801 TTGCGAGACC TTTTTCCTGG CAACCCTGCT GATTGCCTCG CTGCTGTCTGA
851 TTTTCTTTCG ACTGGTCATG GCACTGTATT TCGCCCGGCT TTTTCGTCGAA
901 CCGCTCTAT CGCTTGCCGA GCGGGCGAAG CGCGTGCCGC AAGCGGATTT
951 CAGCCAGACG CGCCCCGTGT TGCGCAACGA CGAGTTCGGA CGCTTGACCA
1001 AGTTGTTCAA CCACATGACC GAGCAGCTTT CCATCGCCAA AGAAGCAGAC
1051 GAGCGCAACC GCCGCGCGCA GGAAGCCGCC AGACATTATC TCGAATGCGT
1101 GTTGGAGGGG CTGACCACGG GCGTGGTGGT GTTTGACGAA CAAGGCTGTC
1151 TGAAAACCTT GCAAAAGCG CGGAAACAGA TTTTGGGGAT CGCGCTTACC
1201 CCCCTGTGGG GCAGCAGCCG GCACGGTTGG CACGGCGTTT CGGCGCAGCA
1251 GTCCCTGCTT GCCGAAGTGT TTGCCGCCAT CGGCGCGGCG GCAGGTACGG
1301 ACAAAACGGT CCATGTGAAA TATGCCGCGC CGGACGATGC CAAAATCCTG
1351 CTGGGCAAGG CAACCTCCT GCCGAAGAC AACGCGCAAC GCGTGGTAAT
1401 GGTGATTGAC GACATCACCG TTTTGATACA CGCGCAAAA GGAAGCCGCT
1451 GGGGCGAAGT GGCAAAACGG CTGGCACACG AAATCCGCAA TCCGCTCACG
1501 CCCATCCAGC TTTCTGCCGA ACGGCTGGCG TGGAAATTGG GCGGGAAGCT
1551 GGACGAGCAG GACGCGCAAA TCCTGACACG TTCGACCGAC ACCATCATCA
1601 AACAAAGTGG GCATTAATAA GAAATGGTCG AGGCATTCCG CAATTACCGC
1651 CGTTCCCCTT CGCTCAAATT GAAAATCAG GATTGAAAG CTTAATCCGG
1701 CGATGTGTTG GCATTGTACG AAGCTGGTCC GTGCCGTTT GCGGCGGAAC
1751 TTGCCGGCGA ACCGCTGATG ATGGCGGCGG ATACGACCGC CATGCGGCAG
1801 GTGCTGCACA ATATTTTCAA AAATGCCGCG GAAGCGGCGG AAGAAGCCGA
1851 TGTGCCCGAA GTCAGGGTAA AATCGGAAGC GGGCGAGGAG GGACGGATTG
1901 TCCTGACAGT TTGCGACAAC GGCAAGGGGT TCGCGCAGGA AATGCTGCAC
1951 AATGCCTTCG AGCCGTATGT AACGGACAAA CCGGCTGGAA CGGGATTGGG
2001 ACTGCCCGTG GTGAAAAAAA TCATTGAAGA ACACGGCGGC CGCATCAGCC
2051 TGAGCAATCA GGATGCGGGC GCGCGGTGTG TCAGAATCAT CTTGCCAAAA
2101 ACGGTAGAAA CTTATGCGTA G

```

This corresponds to the amino acid sequence <SEQ ID 1028; ORF 258.a>:

```

a258.pep
1  MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVAFS AMLLLVLSAV
51  LARYVILLLK DRRDGVFGSQ IAKRLSGMFT LVAVLPGVFL FGVSAQFING
101 TINSWFGNDT HEALERSLNL SKSALNLAAD NALGNAIPVQ IDLIGAASLP
151 GDMGRVLEHY AGSGFAQLAL YNAASGKIEK SINPHKLDQP FPGKARWEKI
201 QQAGSVRDLE SIGGVLYAQQ WLSAGTHNGR DYALFFRQPV PKGVAEDAVL
251 IEKARAKYAE LSYSKKGLOT FFLATLLIAS LLSIFLALVM ALYFARRFVE
301 PVLSLAEGAK AVAQGDFSQT RPVLRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEEA RHYLECVLEG LTTGVVVFDE QGCLKTFENKA AEQILGMPLT
401 PLWGSSRHGW HGVSAQQSLL AEVFAAIGAA AGTDKPVHVK YAAPDDAKIL
451 LGKATVLPED NGNGVVMVID DITVLIHAQK EAAWGEVAKR LAHEIRNPLT
501 PIQLSAERLA WKLGGKLDEQ DAQILTRSTD TTIKQVAALK EMVEAFRNYA
551 RSPSLKLENQ DLNALIGDVL ALYEAGPCRF AAELAGEPLM MAADTTAMRQ
601 VLHNIKFNAE EAAEEADVPE VRVKSEAGQD GRIVLTVCDN GKGFGREMLH
651 NAFEPYVTDK PAGTGLGLPV VKKIIEEHGG RISLSNQDAG GACVRIILPK
701 TVETYA*

```

m258/a258 99.0% identity in 584 aa overlap

	10	20	30	40	50	60
m258.pep	MRRFLPIAAICAVVLLYGLTAATGSTSSLDYFWWIVAFSAMLVVLSAVLARYVILLK					
a258	MRRFLPIAAICAVVLLYGLTAATGSTSSLDYFWWIVAFSAMLVVLSAVLARYVILLK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m258.pep	DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSLNL					
a258	DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSLNL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m258.pep	SKSALNLAADNALGNAVQIDLIGAASLPDGMGRVLEHYAGSGFAQLALYNAASGKIEK					
a258	SKSALNLAADNALGNAIPVQIDLIGAASLPDGMGRVLEHYAGSGFAQLALYNAASGKIEK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m258.pep	SINPHKLDQFPFGKARWEKIQRAGSVRDLESIGGVLYAQQWLSAGTHNGRDYALFFRQPV					
a258	SINPHKLDQFPFGKARWEKIQQAGSVRDLESIGGVLYAQQWLSAGTHNGRDYALFFRQPV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m258.pep	PKGVAEDAVLIEKARAKYAEISYSKKGLOTFFLATLLIASLLSIFLALVMALYFARRFVE					
a258	PKGVAEDAVLIEKARAKYAEISYSKKGLOTFFLATLLIASLLSIFLALVMALYFARRFVE					
	250	260	270	280	290	300
	310	320	330	340	350	360
m258.pep	PVLSLAEGAKAVAQGDFSQTRPVLRNDEFGRLTKLFNHMTQEQLSIAKEADERNRRREEEA					
a258	PVLSLAEGAKAVAQGDFSQTRPVLRNDEFGRLTKLFNHMTQEQLSIAKEADERNRRREEEA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m258.pep	RHYLECVLEGLTTGVVVFDEQGCLKTFENKAAEQILGMPLTPLWGSSRHGW HGVSAQQSLL					
a258	RHYLECVLEGLTTGVVVFDEQGCLKTFENKAAEQILGMPLTPLWGSSRHGW HGVSAQQSLL					
	370	380	390	400	410	420
	430	440	450	460	470	480
m258.pep	AEVFAAIGAAAGTDKPVHVKYAAPDDAKILLGKATVLPEDNGNGVVMVIDDITVLIHAQK					
a258	AEVFAAIGAAAGTDKPVHVKYAAPDDAKILLGKATVLPEDNGNGVVMVIDDITVLIHAQK					

598

	430	440	450	460	470	480
	490	500	510	520	530	540
m258.pep	EAAWGEVAKRLAHEIRNPLTPIQLSAERXAXKLGGKLDEQDAQILTRSTDTIVKQVAALK					
a258	EAAWGEVAKRLAHEIRNPLTPIQLSAERLAWKLGGKLDEQDAQILTRSTDTIIKQVAALK					
	490	500	510	520	530	540
	550	560	570	580	589	
m258.pep	EMVEAFRNYARSPSLKLENQDLNALIGDVLALYEAGPCRFAADLPANRX					
a258	EMVEAFRNYARSPSLKLENQDLNALIGDVLALYEAGPCRFAELAGEPLMMAADTTAMRQ					
	550	560	570	580	590	600
a258	VLHNIFKNAAEAAEEADVPEVRVKSEAGQDGRIVLTVCDNGKGFGREMLHNAFEPYVTDK					
	610	620	630	640	650	660

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1029>:

g259.seq

```

1   atgatgatgc acgcttctgt ccaaagtcgt ttcgcaccga tactttatgt
51  tttgattttc tttgccggtt ttttgaccgc gcaaatctgg ttcaatcaga
101 aagcctatac tgaagagctg cctccgcttc tgtccgcatt gtccgccgtc
151 gcgctggtgt ggctggcgtg ggcgttcgtg tcggtgcgtt caaaggctaa
201 ggcagaaaag ttctaccgcg aaaaaatgat acagaacgaa agcatacacc
251 ccgtcctgca cgcttctttg caacacttgg aacacaagcc gcaaatgtct
301 gccctgctgg tcaaaaacca cggcaaaggc atggcggaac aggtcaggtt
351 caaggcggaa gtgctgcccg acgacgaaga cgcgcgacg attgccgccg
401 agttggcaaa aatggatatg ttcgcattgg ggacggacgc ggtcgccctc
451 ggcgaaacct atgggcgcgt gttcgccgat attttcgagt tgcggcgccg
501 tttggaaagg cgcgcttca aagggatact gaaactgacg gcggaatata
551 aaaaacatct tcggcgatgc ctgccgttcg gaaacggcgt tggatttggg
601 cgcgctcaat caggcggtga gggaaatctc gaaaacgccg gaaaagccta
651 a

```

This corresponds to the amino acid sequence <SEQ ID 1030; ORF 259.ng>:

g259.pep

```

1   MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SVRSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHGKG MAEQVRFAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALER RAFKGILKLT AEYKKHLRRC LPFGNGVGFG
201 RAQSGVEGNL ENAGKA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1031>:

m259.seq (partial)

```

1   ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GGC GTTCGTG TCGGCGCGTT CAAAGGCCAA
201 GCGGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCsTGCA CGCCTCTTTG CAACACTTGG AACACAAGCC GCAAATACTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCACG ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACKGACGC GGTGCGCTCG
451 GGCgAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTGCGmGGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AA.AACATCT TCGGmGATGC CTGCCGTTTC GAAACGGCGT TGGAGTTGGG
601 CGCACTCAAT CAGGCGTTC AGGAGATTTC AAAACATCC GG..

```

This corresponds to the amino acid sequence <SEQ ID 1032; ORF 259>:

m259.pep (partial)

```

1   MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVXHASL QHLEHKPQIL
101 ALLVKNHGKG MAEQVRFAE VLPDDEDART IAAELAKMDM FALGTDAVAS

```

599

151 GETYGRVFAD IFELSXALEG RAFKGMLKLT AEYKXHLRRC LPFGNGVGVG
201 RTQSGVAGDF KNIR..

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 259 shows 94.3% identity over a 212 aa overlap with a predicted ORF (ORF 259.ng) from *N. gonorrhoeae*:

m259/g259

	10	20	30	40	50	60
m259.pep	MMMHASVQSRFAPILYVLIFFAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV					
g259	MMMHASVQSRFAPILYVLIFFAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m259.pep	SARSKAKAEKFYREKMIQNESIHPVXHASLQHLEHKPQILALLVKNHGKGMAEQVRFKAE					
	:					
g259	SVRSKAKAEKFYREKMIQNESIHPVLHASLQHLEHKPQMLALLVKNHGKGMAEQVRFKAE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m259.pep	VLPDDEDARTIAAELAKMDMFALGTDAVASGETYGRVFADIFELSXALEGRAFKGMLKLT					
g259	VLPDDEDARTIAAELAKMDMFALGTDAVASGETYGRVFADI FELSAALERRAFKGILKLT					
	130	140	150	160	170	180
	190	200	210			
m259.pep	AEYKKHLRRLPFGNGVGVGRTQSGVAGDFKNIR					
g259	AEYKKHLRRLPFGNGVGFGRAQSGVEGNLENAGKAX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1033>:

a259.seq (partial)

1	ATGATGATGC	ACGCTTCTGT	CCAAAGCCGT	TTCGCACCGA	TACTTTATGT
51	TTTGATTTTC	TTTGCCGGTT	TTTGACCGC	GCAAATCTGG	TTCAATCAGA
101	AAGCCTATAC	TGAAGAGCTG	CCTCCGCTTC	TGTCCGCATT	GTCCGCCGTC
151	GCGCTGGTGT	GGCTGGCGTG	GGCGTTCGTG	TCGGCGCGTT	CAAAGGCTAA
201	GGCGGAAAAG	TTCTACCGCG	AAAAAATGAT	ACAGAACGAA	AGCATACACC
251	CCGTCCTGCA	CGCTTCTTTG	CAACACTTGG	AACACAAGCC	GCAAATGCTC
301	GCCCTGCTGG	TCAAAAACCA	CGGCAAAGGG	ATGGCGGAAC	AGGTCAGGTT
351	CAAGGCGGAA	GTGCTGCCCG	ACGACGAAGA	CGCGCGCACG	ATTGCCGCCG
401	AGTTGGCAAA	AATGGATATG	TTTGCATTGG	GGACGGACGC	GGTCGCCTCG
451	GGCGAAACCT	ATGGACGCGT	GTTCCGCGAT	ATTTTCGAGT	TGTCGGCGGC
501	TTTGGAGGGG	CGCGCGTTCA	AAGGAATGTT	GAAACTGACG	GCGGAATATA
551	AAAA.CATCT	TCGGCGATGC	CTGCCGTTTC	GAAACGGCGT	TGGAGTTGGG
601	CGCGCTCAAT	CAGGCGTTGC	AGGAGATTTC	AAAAACATCG	GAAAAGTCCA
651	A				

This corresponds to the amino acid sequence <SEQ ID 1034; ORF 259.a>:

a259.pep (partial)

1	MMMHASVQSR	FAPILYVLIF	FAGFLTAQIW	FNQKAYTEEL	PPLLSALSAV
51	ALVWLAWAFV	SARSKAKAEK	FYREKMIQNE	SIHPVLHASL	QHLEHKPQML
101	ALLVKNHGKG	MAEQVRFKAE	VLPDDEDART	IAAELAKMDM	FALGTDAVAS
151	GETYGRVFAD	IFELSXALEG	RAFKGMLKLT	AEYKXHLRRC	LPFGNGVGVG
201	RAQSGVAGDF	KNIGKVQ			

m259/a259 98.1% identity in 213 aa overlap

	10	20	30	40	50	60
m259.pep	MMMHASVQSRFAPILYVLIFFAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV					
a259	MMMHASVQSRFAPILYVLIFFAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV					

600

	10	20	30	40	50	60
	70	80	90	100	110	120
m259.pep	SARSKAKAEKFYREKMIQNESIHPVXHASLQHLEHKPQILALLVKNHKGKMAEQVRFKAE					
a259	:					
	70	80	90	100	110	120
	130	140	150	160	170	180
m259.pep	VLPDDEDARTIAAELAKMDMFALGTDAVASGETYGRVFADIFELSALEGRAFGMLKLT					
a259	:					
	130	140	150	160	170	180
	190	200	210			
m259.pep	AEYKXHLRRCLPFGNGVGVGRTQSGVAGDFKNIR					
a259	:					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1035>:

g259-1.seq

```

1  ATGATGATGC ACGCTTCTGT CCAAAGTCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGGTTCTGT TCGGTGCGTT CAAAGGCTAA
201 GGCAGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCTCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAAATGCTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGC ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCAGC ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACGGACGC GGTCCGCTCG
451 GGCGAAACCT ATGGGCGCGT GTTCGCCGAT ATTTTCGAGT TGTCGGCGGC
501 TTTGGAA

```

This corresponds to the amino acid sequence <SEQ ID 1036; ORF 259-1.ng>:

g259-1.pep

```

1  MMHVASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SVRSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHKGK MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALE

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1037>:

m259-1.seq

```

1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGGTTCTGT TCGGCGCGTT CAAAGGCCAA
201 GCGGAAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCTCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAAATACTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCAGC ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACGGACGC GGTCCGCTCG
451 GGCGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTCGGCGGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AAAACATCTT CGGCGATGCC TGCCGTTCGG AAACGCGGTT GGAGTTGGGC
601 GCACTCAATC AGGCGTTGCA GGAGATTTCA AAAACATCGG AAAAGTCCAA
651 ACGGATATTT TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1038; ORF 259-1>:

m259-1.pep

```

1  MMHVASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQIL
101 ALLVKNHKGK MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALEG RAFKGMLKLT AEYKNIFGDA CRSETALELG
201 ALNQLQEIS KTSEKSRIF_Y*

```

g259-1/m259-1 98.8% identity in 169 aa overlap

601

	10	20	30	40	50	60
g259-1.pep	MMMHASVQSRFAPILYVLIF	FAGFLTAQIWFNQKAYTEEL	PPLLSALS	SAVALVWLAWAFV		
m259-1	MMMHASVQSRFAPILYVLIF	FAGFLTAQIWFNQKAYTEEL	PPLLSALS	SAVALVWLAWAFV		
	10	20	30	40	50	60
	70	80	90	100	110	120
g259-1.pep	SVRSKAKAEK	FYREKMIQNESIHPVLHASL	QHLEHKPQMLALLVKNHGK	MAEQVRFKAE		
m259-1	SARSKAKAEK	FYREKMIQNESIHPVLHASL	QHLEHKPQILALLVKNHGK	MAEQVRFKAE		
	70	80	90	100	110	120
	130	140	150	160	169	
g259-1.pep	VLPDDEDARTIAAELAKMDM	FALGTD	DAVASGETYGRVFADIFEL	SAALE		
m259-1	VLPDDEDARTIAAELAKMDM	FALGTD	DAVASGETYGRVFADIFEL	SAALEGRAFGMLKLT		
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1039>:

a259-1.seq

```

1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCGGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGGTTCTGT TCGCGCGGTT CAAAGGCTAA
201 GCGCGAAAGG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCTCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAAATGCTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAAGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCAGC ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTGCATTGG GGACGGACGC GGTCGCCTCG
451 GCGGAAACCT ATGGACGCGT GTTCGCGGAT ATTTTCGAGT TGTCGGCGGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AAAACATCTT CGGCGATGCC TGCCGTTTCG AAACGGCGTT GGAGTTGGGC
601 GCGCTCAATC AGGCGTTGCA GGAGATTTC AAAACATCGG AAAAGTCCAA
651 ACGGATATTT TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1040; ORF 259-1.a>:

a259-1.pep

```

1  MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHGKG MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDASV
151 GETYGRVFAD IFELSAALEG RAFKGMLKLT AEYKNIFGDA CRSETALELG
201 ALNQALQEIS KTSEKSKRIF Y*

```

a259-1/m259-1 99.5% identity in 221 aa overlap

	10	20	30	40	50	60
a259-1.pep	MMMHASVQSRFAPILYVLIF	FAGFLTAQIWFNQKAYTEEL	PPLLSALS	SAVALVWLAWAFV		
m259-1	MMMHASVQSRFAPILYVLIF	FAGFLTAQIWFNQKAYTEEL	PPLLSALS	SAVALVWLAWAFV		
	10	20	30	40	50	60
	70	80	90	100	110	120
a259-1.pep	SARSKAKAEK	FYREKMIQNESIHPVLHASL	QHLEHKPQMLALLVKNHGK	MAEQVRFKAE		
m259-1	SARSKAKAEK	FYREKMIQNESIHPVLHASL	QHLEHKPQILALLVKNHGK	MAEQVRFKAE		
	70	80	90	100	110	120
	130	140	150	160	170	180
a259-1.pep	VLPDDEDARTIAAELAKMDM	FALGTD	DAVASGETYGRVFADIFEL	SAALEGRAFGMLKLT		
m259-1	VLPDDEDARTIAAELAKMDM	FALGTD	DAVASGETYGRVFADIFEL	SAALEGRAFGMLKLT		
	130	140	150	160	170	180
	190	200	210	220		
a259-1.pep	AEYKNIFGDACRSETALEL	GALNQALQEISK	TSEKSKRIFYX			
m259-1	AEYKNIFGDACRSETALEL	GALNQALQEISK	TSEKSKRIFYX			
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1041>:

g260.seq

602

```

1  atgggtgctg  gtgtagtatt  cgttgctctt  cagccgttct  tcagcctgtt
51  tcgagcggtt  ttcgagggcg  gtagtcggtat  agtcgagggg  gcgcacgatg
101  ccgctgaatg  cgacttcctt  tccgaggaat  ttacccgtat  ccggatcggg
151  gatgttttta  ttgattcggg  aggtcagata  acggcccggg  tctttcaggc
201  ctttggtgta  aaccctggcg  cctttggtgt  acagcagcct  gccttcgggg
251  cccgagagca  ggcgcggcgc  ggcagcgggt  tctttgcggg  aaacgatttg
301  cgggtgctgc  ataaagacgc  ggtagaagtt  gacatcgatg  gcgggaatac
351  cgtatccgga  cacttcctta  tccggactga  ttttgacgac  ggggatgccg
401  tctgtctgtt  ccaagccgag  gcgcgggtcg  ccgccaacgt  agcgcaacac
451  caatacctgg  cccggataaa  tcaggtcggg  attgtggatt  tgatcccggt
501  tcgcgcccc  cagggggggg  ccattgccac  gggctgtaca  ggtatttgcc
551  cgaaataccc  cacaggggtg  cgccctgttt  ga

```

This corresponds to the amino acid sequence <SEQ ID 1042; ORF 260.ng>:

g260.pep

```

1  MGAGVVFVVF QPFFSLFRAL FEGGVGIVEG AHDAECDLFL SEEFTRIRIG
51  DVFIDSVGQI TARFFQAFGV NPGAQGVQQP AFRAREQARR GSGFFAGNDL
101  RVLHKDAVEV DIDGGNTVSG HFLIRTDFFD GDAVCLFQAE ARFAANVAQH
151  QYLARINQVG IVDLIPVRAP QGGTIATGCT GICPKYPTGC RPV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1043>:

m260.seq

```

1  ATGGGTGCGG GTATGGTATT CGTTGTCTTT CGGCCGTTCT CCAGCCTGTT
51  TCGAGCGTTG TTCGAGGACA GAGTCGGTAT AGTCGAGGGA GCGCACGATG
101  CCGCTGAATG CGACTTCCTG CCGGAGGAAT TTACCCGTAT CCGGATCGGT
151  GATGTTTTTA TTGATTCGGT AGGTCAGGTA GCGGCCCGGC TCTTTCAGGC
201  CTTTGGTGTA AACCTGGTG CCTTGGTGT ACAGCAGCCT GCCTCCGGG
251  CCGAGwCA sGCGCGGyGC GGCAGCGGTT TCTTTCGGG AAACGATTG
301  CGGATGCCGC ATAAAGATGC GGTAGAAGTT GACATCGATG GCGGGAATAC
351  CGTATCCGGA CACTTCCTTA TCCGGACTCA TTTTGACGAC GGGGATGCCG
401  TCTGTCTGTT CCAAGCCGAG GCGCGGTTTC CCGTCAACGT GGCGCAACAC
451  CAATACCTGG TCCGGATAAA TCAGGTCGGG ATTGTGGATT TGATCCCGGT
501  TCGCGTyCCA CAG

```

This corresponds to the amino acid sequence <SEQ ID 1044; ORF 260>:

m260.pep

```

1  MGAGMVVFVF RPFSSLFRAL FEDRVGIVEG AHDAECDLFL PEEFTRIRIG
51  DVFIDSVGQV AARLFQAFGV NPGAQGVQQP AFRARXXARX GSGFFAGNDL
101  RMPHKDAVEV DIDGGNTVSG HFLIRTHFDD GDAVCLFQAE ARFAVNVAQH
151  QYLVIRINQVG IVDLIPVRVP Q

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 260 shows 89.5% identity over a 171 aa overlap with a predicted ORF (ORF 260.ng) from *N. gonorrhoeae*:

m260/g260

	10	20	30	40	50	60
m260.pep	MGAGMVVFVFRPFFSSLFRALFEDRVGIVEGAHDAECDLFLPEEFTRIRIGDVFIDSVGQV					
g260	MGAGVVFVVFQPFSSLFRALFEGGVGIVEGAHDAECDLFLSEEFTRIRIGDVFIDSVGQI					
	10	20	30	40	50	60
m260.pep	AARLFQAFGVNPGAQGVQPAFRARXXARXGSGFFAGNDLRMPHKDAVEVDIDGGNTVSG					
g260	TARFFQAFGVNPGAQGVQQPFRAREQARRGSGFFAGNDLRVLHKDAVEVDIDGGNTVSG					
	70	80	90	100	110	120
m260.pep	HFLIRTHFDDGDAVCLFQAEARFAVNVAQHQYLVIRINQVGIVDLIPVRVPQ					
g260	HFLIRTDFFDDGDAVCLFQAEARFAANVAQHQYLARINQVGIVDLIPVRAPQGGTIATGCT					
	130	140	150	160	170	180

603

g260 GICPKYPTGCRPV
190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1045>:

a260.seq
1 ATGGGTGCGG GTATGGTATT CGTTGTCTTT CGGCCGTTCT CCAGCCTGTT
51 TCGAGCGTTG TTCGAGGACA GAGTCGGTAT AGTCGAGGGA GCGCACGATG
101 CCGCTGAATG CGACTTCCTG CCCGAGGAAT TTACCCGTAT CCGGATCGGT
151 GATGTTTTTA TTGATTCGGT AGGTCAGGTA GCGGCCCGGC TCTTTCAGGC
201 CTTTGGTGTA AACCTGGTG CCTTTGGTGT ACAGCAGCCT GCCTTCCGGG
251 CCCGAGAGCA GCGCGGCGC GGCAGCGGT TCTTTGCGGG AAACGATTTG
301 CGGGTGCCGC ATAAAGATGC GGTAGAAGTT GACATCGATG GCGGGAATAC
351 CGTATCCGGA CACTTCCTTA TCCGGACTCA TTTTGACGAC GGGGATGCCG
401 TCTGTCTGTT CCAAGCCGAG GCGCGGTTTC CCGTCAACGT GGCGCAACAC
451 CAATACCTGG TCCAGATAAA TCAGGTCGGG ATTGTGGATT TGATCCCGGT
501 TCGCGTCCCA CAGGCGGCC CCATTGCCAC GGGCTGTACA GGTATTTGCC
551 CGAAATGCCC CACAGGGTGT CGCCCTGTTT GA

This corresponds to the amino acid sequence <SEQ ID 1046; ORF 260.a>:

a260.pep
1 MGAGMVVFVF RPFSSLFRAL FEDRVGIVEG AHDAECDFL PEEFTRIRIG
51 DVFIDSVGQV AARLFQAFGV NPGAQVQGP AFRAREQARR GSGFAGNDL
101 RVPKDAVEV DIDGGNTVSG HFLIRTHFDD GDAVCLFQAE ARFAVNVAQH
151 QYLVQINQVG IVDLIPVRVP QAAXIATGCT GICPKCPTGC RPV*

m260/a260 97.1% identity in 171 aa overlap

	10	20	30	40	50	60
m260.pep	MGAGMVVFVFRPFSSLFRALFEDRVGIVEGAHDAECDFLPEEFTRIRIGDVFIDSVGQV					
a260	MGAGMVVFVFRPFSSLFRALFEDRVGIVEGAHDAECDFLPEEFTRIRIGDVFIDSVGQV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m260.pep	AARLFQAFGVNPGAQVQGPFRARXXARXGSGFFAGNDLRMPHKDAVEVDIDGGNTVSG					
a260	AARLFQAFGVNPGAQVQGPFRAREQARRGSGFFAGNDLRVPHKDAVEVDIDGGNTVSG					
	70	80	90	100	110	120
	130	140	150	160	170	
m260.pep	HFLIRTHFDDGDAVCLFQAEARFAVNVAQHQYLVQRINQVGIVDLIPVRVPQ					
a260	HFLIRTHFDDGDAVCLFQAEARFAVNVAQHQYLVQINQVGIVDLIPVRVPAAXIATGCT					
	130	140	150	160	170	180
a260	GICPKCPTGCRPVX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1047>:

g261.seq
1 atggagcttg ggcataatcgt attccttctg ctttgcgcg gttcagacgg
51 cctttttact ttccagacat tccgccagcc cgcgttcgcy caagatacac
101 ctccggcatt cgcggcagcc gccgacgata cccttgtagc aggtgtgggt
151 ctgttcgcyg atgtagtcca acacgccccat ttcgtccgcy aacgccccacg
201 tttgcyctt ggtcaggtac atcagcgcyg tgtggatttg aaaatcgtag
251 tccatcgcca gattaagggt aacgttcctg gatttgacga acacgccccg
301 gcagtcggga tagcccgaaa aatcggtttc gcacacgccc gcgatgatgt
351 gccggatacc ctgccccttg gcaaaaatgg cggcgtaaag caggaaaagc
401 gcgttacgcc cgtccacaaa ggtattggga acgcccgtgt cggcggtttc
451 gatggcgcyg gtttcgatgg cggcggtttc gtccatcagg gcgttggtgcg
501 taatctgccg catcaggctc aaatcgagta cggtttgact gacacccaaa
551 tcctgcgcga tccactctgc gcgttcacgc tcgacggcat ggcgttgccc
601 gtatcggaag gtgatggctt ggacgttttc gcgccgtag gtttgattg

604

651 cctgaatcag gcaggtggtc gaatcctgac cgcccagaaa gatgaccaag
 701 gctttttggt ttga

This corresponds to the amino acid sequence <SEQ ID 1048; ORF 261.ng>:

g261.pep

1 MELGHIVFLV LCARSDGLFT FQTFRQPAFA QDTARAFAAA ADDTLVAGVG
 51 LFADVQHAH FVRQRPRLRL GQVHQRRVDL KIVVHRQIKG NVHGFDEHAA
 101 AVGIARKIGF AHARDDVPDT LPFGKNGGVK QEKRVTPVHK GIGNAVVGGF
 151 DGGGFDGGGF VHQGVVRNLP HQAQIEYGLT DTQILRDPLC AFQLDGMALP
 201 VSEGDLDFV APVGLDCLNQ AGGRILTARE DDQGLV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1049>:

m261.seq

1 ATGGAGCTTG GGCATATCGT ATTCCTTATG GTTTGCGCGT GTTCAGACGG
 51 CCTTTTACT TTCCAGATAT TCCGCCAGCC cGcGTTCCGCG CAAGATACAG
 101 CTCGGGCATT CGCGgCAGCC GCCGACGATG CCGTTATAGC AGGTGTGGGT
 151 TTGCTCGCGG ATATAGTCCA GCACGCCCAT TTCGTCCGCC AACGCCACG
 201 TTTGCGCCTT GGTCAGATAC ATCAGCGGCG TGTGGATTG AAAATCATAG
 251 TCCATCGCCA AATTAAGGGT AACGTTTCATC GATTGACAA ACACGTCGCG
 301 GCAGTCGGGA TAGCCGGAGA AGTCGGTTTC GCACACGCCC GCGATGATGT
 351 GCCGTATCCC CTGCCCTTTG GCGTAAATCG CGGCATAGAG CAGGAAAAGC
 401 gCGTTGCGGC CGTCTACAAA GGTATTCGGA ACGCCGTTTT CGGCAGTTTC
 451 GATGGCGGCG GTGTCGTCCA TCAGGGCATT GTGCGTAATC TGCCGCATCA
 501 GgCTcAAGTC GAGTACGGTT TGTGTGACGC CCAAATCCTG CGCAATCCAG
 551 CGGGCACGTT CCAGCTCGAC GGCATGGCGT TGCCCGTATT GGAAAGTAAT
 601 GGCTTGACG TTTTCGCGCC CGTAGGTTTG GATTGCCTGA ATCAGGCAGG
 651 TGGTCGAATC CTGACCGCCC GAAAAGATGA CCAAGGCTTG TTGGTTTGA

This corresponds to the amino acid sequence <SEQ ID 1050; ORF 261>:

m261.pep

1 MELGHIVFLM VCACSDGLFT FQIFRQPAFA QDTARAFAAA ADDAVIAGVG
 51 LLADIVQHAH FVRQRPRLRL GQIHQRRVDL KIIVHRQIKG NVHRFDKHVA
 101 AVGIAGEVGF AHARDDVPYP LPFGVNRGIE QEKRVAAVYK GIRNAVFGSF
 151 DGGGVVHQGI VRNLPHQAV EYGLFDAQIL RNPAGTFQLD GMALPVLESN
 201 GLDVFAFVGL DCLNQAGGRI LTARKDDQGL LV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 261 shows 79.7% identity over a 237 aa overlap with a predicted ORF (ORF 261.ng) from *N. gonorrhoeae*:

m261/g261

	10	20	30	40	50	60
m261.pep	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVGLLADIVQHAH					
	:::					
g261	MELGHIVFLVLCARSDGLFTFQTFRQPAFAQDTARAFAAAADDTLVAGVGLFADVQHAH					
	10	20	30	40	50	60
	70	80	90	100	110	120
m261.pep	FVRQRPRLRLGQIHQRRVDLKIIVHRQIKGNVHRFDKHVA AVGIAGEVGF AHARDDVPYP					
	: :					
g261	FVRQRPRLRLGQVHQRRVDLKIVVHRQIKGNVHGFDEHAA AVGIARKIGFAHARDDVPDT					
	70	80	90	100	110	120
	130	140	150	160	170	
m261.pep	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGV-----VHQGIVRNLPHQAVEYGLF					
	: :					
g261	LPFGKNGGVKQEKRVTPVHKGIGNAVVGGFDGGGFDGGGFVHQGVVRNLPHQAQIEYGLT					
	130	140	150	160	170	180
	180	190	200	210	220	230
m261.pep	DAQILRNPAFTFQLDGMALPVLESNGLDVFAFVGLDCLNQAGGRILTARKDDQGLLVX					
	: :					
g261	DTQILRDPLCAFQLDGMALPVSEGDLDFVFAFVGLDCLNQAGGRILTAREDDQGLVX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1051>:

```
a261.seq
1  ATGGAGCTTG GGCATATCGT ATTCCTTATG GTTTGCGCGT GTTCAGACGG
51  CCTTTTTACT TTCCAGATAT TCCGCCAGCC CGCGTTCGCG CAAGATACAG
101 CTCGGGCATT CGCGGCAGCC GCCGACGATG CCGTTATAGC AGGTGTGGGT
151 TTGCTCGCGG ATATAGTCCA GCGCGCCCAT TTCGTCCGCC AACGCCAAG
201 TTTGCGCCTT GGTCAAGATC ATCAGCGGCG TGTGGATTG AAAATCATAG
251 TCCATCGCCA GATTAAGGGT AACGTTTCATG GATTTGACAA ACACGTCACG
301 GCAGTCGGGA TAGCCGGAGA AGTCGGTTTC GCACACGCCC GCGATGATGT
351 GCCGTATCCC CTGCCCTTTG GCGTAAATCG CGGCATAGAG CAGGAAAAGC
401 GCGTTGCGGC CGTCTACAAA GGTATTCGGA ACGCCGTTTT CGGCAGTTTC
451 GATGGCGGCG GTGTCGTCCA TCAGGGCATT GTGCGTAATC TGCCGCATCA
501 GGCTCAAGTC GAGTACGGTT TGTTTGACGC CCAAATCCTG CGCAATCCAG
551 CGGGCACGTT CCAGCTCGAC GGCATGGCGT TGCCCGTATT GGAAAGTAAT
601 GGCTTGGACG TTTTCGCGCC CGTAGGTTTG GATTGCCTGA ATCAGGCAGG
651 TGGTCGAATC CTGACCGCCC GAAAAGATGA CCAAGGCTTT TTGGTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1052; ORF 261.a>:

```
a261.pep
1  MELGHIVFLM VCACSDGLFT FOIFRQPAFA QDTARAFAAA ADDAVIAGVG
51  LLADIVQRAH FVRQRPSLRL GQIHQRRVDL KIIVHRQIKG NVHGFDPKHVT
101 AVGIAGEVGF AHARDDVPYP LPFGVNRGIE QEKRVAAVYK GIRNAVFGSF
151 DGGGVVHQGI VRNLPHQAV EYGLFDAQIL RNPAGTFQLD GMALPVLESN
201 GLDVFAFVGL DCLNQAGGRI LTARKDDQGF LV*
```

m261/a261 97.8% identity in 232 aa overlap

	10	20	30	40	50	60
m261.pep	MELGHIVFLMVCACSDGLFTFOIFRQPAFAQDTARAFAAAADDAVIAGVG	LLADIVQRAH				
a261	MELGHIVFLMVCACSDGLFTFOIFRQPAFAQDTARAFAAAADDAVIAGVG	LLADIVQRAH				
	70	80	90	100	110	120
m261.pep	FVRQRPSLRLGQIHQRRVDLKIIVHRQIKGNVHREFDKHVA	AVGIAGEVGF	AHARDDVPYP			
a261	FVRQRPSLRLGQIHQRRVDLKIIVHRQIKGNVHREFDKHVT	AVGIAGEVGF	AHARDDVPYP			
	130	140	150	160	170	180
m261.pep	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGIVRNLPHQAV	EYGLFDAQIL				
a261	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGIVRNLPHQAV	EYGLFDAQIL				
	190	200	210	220	230	
m261.pep	RNPAGTFQLDGMALPVLESNGLDVFAFVGLDCLNQAGGRILTARKDDQGLLVX					
a261	RNPAGTFQLDGMALPVLESNGLDVFAFVGLDCLNQAGGRILTARKDDQGLLVX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1053>:

```
g263.seq
1  atggcacggt taaccgtaca caccctcgaa accgccccg aagccgccaa
51  accgcgcgta gagggcgtag ccaaaaacaa cggctttatc ccaacctca
101 tcggcggtatt ggcaaacgcc cccgaagctt tggcgtttta ccaagaagtc
151 ggcaagctca acgcccgaac cagcctgacc gccggcgaag tcgaagtgat
201 ccgatcatc gccgtccgca ccaaccaatg cagctctctg gtggcagggc
251 acaccaaaact cgcaaccctg aaaaaactcc tgtccgagca atccctcaat
301 gccgcccgcg ctttgggcgc aggtaaatct gacgatgcca aactcggcgc
351 gcttgccgcc ttcacccaag ccgtaatggc gaaaaaaggc gcagtatccg
401 acgacgaact caacgccttc ctccaagcgg gctacaaccg gcagcaggca
```

g263.pcp

m263.seq (partial)

m263.pep (partial)

m263/g263

a263.seq

a263.pep

```

1 MARLTVHTLE TAPEAAKARV EAVLQNNGFI PNLIGVLSNA PEALAFYQEV
51 GKLNAANSLT AGEVEVIQII AARTNQCGFC VAGHTKLATL KLLSEQSVK
101 AARALAAGEF DDAKLGALAA FTQAVMAKKG AVSDEELKAF FDAGYNQQQA
151 VEVVMGVALA TLCNYVNNLG QTEINPELQA YA*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1059>:

This corresponds to the amino acid sequence <SEQ ID 1060; ORF 264.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1061>:

This corresponds to the amino acid sequence <SEQ ID 1062; ORF 264>:

m264.pep

1	<u>LTLTRKTLFL</u>	<u>LTAAFGTHSL</u>	QTASADAVVK	AEKLHASANR	SYKVAGKRYT
51	PKNQVAEFTQ	TGNASWYGGF	FHGRKTSNGE	RYDMNAFTAA	HKTLPIPSYV
101	RVTNTKNGKS	VIVRVNDRGP	FHGNRIIDVS	KAAAQKLGFF	NQGTAVHKIE
151	QIVPGQSAPV	AENKDFIDL	KSFGTEHAQ	AYLNQAAQNF	AVSSSGTNLS
201	VEKRRYEYVV	KMGPFSTQER	AAEAQAQARG	MVRAVLTAG*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 264 shows 91.6% identity over a 239 aa overlap with a predicted ORF (ORF 264.ng) from *N. gonorrhoeae*:

m264/g264

	10	20	30	40	50	60
m264 . pep	LTLTRKTLFLLTAAFGTHSLQTASADAVVKA EKLHASANRSYKVAGKRYTPKNQVAEFTQ					
g264	LTLTRKTLFLLTAAFGTHSLQTASADAVVKPEKLHASANRSYKVA-----EFTQ					
	10	20	30	40		
	70	80	90	100	110	120
m264 . pep	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
g264	TGNASWYGGRFHGRKTSGGDRYDMNAFTA AHKTLPIPSHVRVTNTKNGKSVIVRVNDRGP					
	50	60	70	80	90	100
	130	140	150	160	170	180
m264 . pep	FHGNRIIDVSKAAQKLG FVNQGT AHVKIEQIVPGQSAPVAENKDIFIDLKSFSGTEHEAQ					
g264	FHGNRIIDVSKAAQKLG FVSQGT AHVKIEQIVPGQSAPVAENKDIFIDLKSFSGTEHEAQ					
	110	120	130	140	150	160
	190	200	210	220	230	240
m264 . pep	AYLNQAAQNFAVSSSGTNLSVEKRRYEYVVKMGPF TSQERAAEAEAQARGMVR AVLTAGX					
g264	AYLNQAAQNFAASSSPNLSVEKRRYEYVVKMGPF ASQERAAEAEAQARGMVR AVLTSGX					
	170	180	190	200	210	220

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1063>:

a264 . seq

1	TTGACTTTAA	CCCGAAAAAC	CCTTTTCCTC	CTCACC GCCG	CATT CGGCAT
51	ACATTCCTTT	CAGACGGCAT	CCGCCGACGC	AGTGGTCAGG	GCAGAAAAAC
101	TGCACGCCTC	CGCCAACCGC	AGCTACAAAG	TCGCCGGAAA	ACGCTACACG
151	CCGAAAAACC	AAGTCGCCGA	ATTACGCAA	ACCGGCAACG	CCTCGTGGTA
201	CGCGCGCAGG	TTTCACGGGC	GCAAACTTC	CGCGGAGAA	CGATACGATA
251	TGAACGCCTT	TACCGCCGCC	CACAAAACCC	TGCCCATCCC	CAGCTATGTG
301	CGCGTAACCA	ATACCAAAAA	CGGCAAAAGC	GTCATCGTCC	GCGTCAACGA
351	CCGCGGCCCC	TTCCACGGCA	ACCGCATCAT	CGACGTATCC	AAAGCCGCGC
401	CGCAAAATT	GGGCTTTGTC	AACCAAGGGA	CGGCGCACGT	CAAAATCGAA
451	CAAATCGTCC	CGGCGCAATC	CGCACC GGTT	GCCGAAAACA	AAGACATCTT
501	CATCGACTTG	AAATCTTTTCG	GTACGGAACA	CGAAGCACAA	GCCTATCTGA
551	ACCAAGCCGC	CCAAAACCTG	GCTTCATCGG	CATCAAACCC	GAACCTCTCG
601	GTTGAAAAAC	GCCGTTACGA	ATACGTCGTC	AAAATGGGAC	CGTTTGCCCTC
651	GCAGGAACGC	GCCGCCGAGG	CCGAAGCTCA	GGCGCGCGGT	ATGGTTCGGG
701	CGGTATTAAC	CGCCGGTTGA			

This corresponds to the amino acid sequence <SEQ ID 1064; ORF 264.a>:

a264 . pep

1	LTLTRKTLFL	LTAAFGIHSF	QTASADAVVR	AEKLHASANR	SYKVAGKRYT
51	PKNQVAEFTQ	TGNASWYGGR	FHGRKTS GGE	RYDMNAFTA	AHKLPIPSYV
101	RVTNTKNGKS	VIVRVNDRGP	FHGNRIIDVS	KAAAQKLG FV	NQGT AHVKIE
151	QIVPGQSAPV	AENKDIFIDL	KSFSGTEHEAQ	AYLNQAAQNL	ASSASNPNLS
201	VEKRRYEYV	KMGPFASQER	AAEAEAQARG	MVR AVLTAG*	

m264/a264 96.2% identity in 239 aa overlap

	10	20	30	40	50	60
m264 . pep	LTLTRKTLFLLTAAFGTHSLQTASADAVVKA EKLHASANRSYKVAGKRYTPKNQVAEFTQ					
a264	LTLTRKTLFLLTAAFGIHSFQTASADAVVRAEKLHASANRSYKVAGKRYTPKNQVAEFTQ					
	10	20	30	40	50	60

609

	70	80	90	100	110	120
m264 . pep	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
a264	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m264 . pep	FHGNRIIDVSKAAQKLG FVNQGT AHVKIEQIVPGQSAPVAENKDIFIDLKSFGEHEAQ					
a264	FHGNRIIDVSKAAQKLG FVNQGT AHVKIEQIVPGQSAPVAENKDIFIDLKSFGEHEAQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m264 . pep	AYLNQAAQNFAVSSSGTNLSVEKRRYEYVVKMGPFQSQERAAEAEQAQARGMVRVLTAGX					
a264	AYLNQAAQNFAVSSSGTNLSVEKRRYEYVVKMGPFQSQERAAEAEQAQARGMVRVLTAGX					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1065>:

```

m265 . seq
  1  ATGTCGGTGA TTTTGCCGCC GACACGCGCC AACGCTGCTT TTTTCGGCTTG
 51  GCGCGCGCTG ATGATTTTGT CTTGTTTGTG GTGTTGGTGT GCGGCGTGTC
101  CGTGGTCGTC ATCGCCGTGT CCGTCGTGGT GGGCGAGCGC GGGGGCGGAA
151  ATGCTCAGCA GTGCGGTTGC GCGCGAGGTC AAGAGAAGGT GTTTGATGTT
201  CATAT.TTTT GCCTTTGTAA ATCGTGGGTT GGAAAATGTG GATATTAATA
251  AGGTATCAAA TAACCGTCAG CCGGCGGTCA ATACCGCCCG AACCATACCG
301  CGCGCCTGAG CTTCGGCTTC GCGGCGCGCT TCCTGCGAGG TAAACGGTCC
351  CATTTTGACG ACGTATTCGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1066; ORF 265>:

```

m265 . pep
  1  MSVILPPTRA NAAFSAWARL MILSCLLCWC AACPWSSSPC PSWWASAGAE
 51  MLSSAVAAEV KRRCLMFI XF AFVNRGLENV DINKVSNRQ PAVNTARTIP
101  RAXASASAAR SCEVNGPILT TYS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 265 shows 88.6% identity over a 123 aa overlap with a predicted ORF (ORF 265.ng) from *N. gonorrhoeae*:

m265/g265	10	20	30	40	50	60
m265 . pep	MSVILPPTRANA AFSAWARLMILSCLLCWCAACPWSSSPCPSWWASAGAEMLSSAVAAEV					
g265	MSVILPPTRAQA AFSAWARLMILSCLPCWCAACPWSSSPCPSWWASAGAEMPNSAVAAAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m265 . pep	KRRCLMFI XFAFVNRGLENV DINKVSNRQPAVNTARTIPRAXASASAARSCEVNGPILT					
g265	KRRCLMFI -FALVNQGLKNGDINKVSNRQPEVSTARTIPRACASASAARSCEANGPILT					
	70	80	90	100	110	
m265 . pep	TYSX					
g265	TYSX					
	120					

610

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1067>:

```
a265.seq
1   ATGTCGGTGA TTTTGCCGCC GACACGCGCC AACGCTGCTT TTTCGGCTTG
51  GCGCGGGCTG ATGATTTTGT CTTGTTTGCT GTGTTGGTGT GCGGCGTGTC
101 CGTGGTCGTC ATCGCCGTGT CCGTCGTGGT GGGCGAGTGC GGGGGCGGAA
151 ATGCCCATCA GTGCGGTTGC GCGGCGGGTC AAGAGAAGGC GTTTGAAGTT
201 CATTTTGTCT CCTGCGAAGT ATCTGGT... . . . . GGTGT TTGAAGGACG
251 TAAAGGCGGG ACATCAACCG GCGGTTAATA CCGCCCGAAC CATACCGCGC
301 GCCTGAGCTT CGGCCTCGGC GCGCGGTTCC TCGAGGCAA ACGGTCCCAT
351 TTTGACGACG TATTCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1068; ORF 265.a>:

```
a265.pep
1   MSVILPPTRA NAAFSAWARL MILSCLLCWC AACPWSSSPC PSWWASAGAE
51  MPISAVAAAV KRRRLKFIFA PAKYLX..XC LKDVKAGHQP AVNTARTIPR
101 A*ASASAARS CEANGPILTT YS*
```

m265/a265 79.7% identity in 123 aa overlap

	10	20	30	40	50	60
m265.pep	MSVILPPTRANA	AFSAWARLMIL	SCLLCWCAAC	PWSSSPCPS	WWASAGAEM	LSSAVAAEV
a265	MSVILPPTRANA	AFSAWARLMIL	SCLLCWCAAC	PWSSSPCPS	WWASAGAEM	PISAVAAAV
	10	20	30	40	50	60
	70	80	90	100	110	120
m265.pep	KRRCLMFI	FAFVNRGLE	NDINKVSN	RQPAVNTA	RIPRAXASA	SAAARSCEV
a265	KRRRLKFI	---FAPAKY	LXXCLKDV	KAGHQPAV	NTARTIPR	AXASAARS
	70	80	90	100	110	
m265.pep	TYSX					
a265	TYSX					
	120					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1069>:

```
g266.seq
1   agttcagacg gcatcgccgc cgacaatgcc caaacagaaa gcccatcatg
51  accgcatcca tgtacatcct tttggtcttg gcactcatct ttgccaacgc
101 ccccttcctc acgaccagac tgctcgcgct ggccgcgctc aagcgcaaac
151 atttcggaca ccacctgate gagctggcgg cagggtttcgc gctgaccgcc
201 tctcttgccct acatcctcga atcccgtgcg ggagcggtag acaatcaggg
251 ttgggagttt tacgccaccg tcgtctgcct gtacctcatt ttcgccttcc
301 cgtggttcgt gcggcgggat tttgggcaca cgcgcaacag ggaataaa
```

This corresponds to the amino acid sequence <SEQ ID 1070; ORF 266.ng>:

```
g266.pep
1   MQFRRHRRRQ CPNRKPIMTA SMYILLVLAL IFANAPFLT TRLFVAAALKR
51  KHFGHHLIEL AAGFALTASL AYILESRAGA VHNQWGFYA TVVCLYLIFA
101 FPCFVRRYFW HTRNRE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1071>:

```
m266.seq
1   ATGCCGTTCC GCAACGCGtT cAGACGGCAT CGCCGCCGAC AACGCCTAAA
51  CAGAAAGCCC ACCATGACCG CATCCATGTA CATCCTTTTG GTCTTGACAC
101 TCATCTTTGC CAACGCCCCC TTCCTCACGA CCAGACTGTT CGGCGTGCC
151 rCACTCAAGC GCAAACATTT CGGACACCAC ATGATCGAGC TGGCGGCAGG
201 TTTGCGGCTG ACCGCCGTTT TTGCCTACAT CCTsGAATCC CGTGACAGGAT
251 CGGTACACGA TCAGGGTTGG GAGTTTATG CCACAGTCGT CTGCTGTAC
301 CTGATTTTGT CGTTTCCATG TTTTGTGTGG CGGTATTTTT GGCACACGCG
351 CAACAGGGAA TAG
```

This corresponds to the amino acid sequence <SEQ ID 1072; ORF 266>:

```
m266.pep
  1  MPFRNAFRRH RRRQRLNRKP TMTASMYILL VLALIFANAP FLTTRLFGVA
 51  XLKRKHFGHH MIELAAGFAL TAVLAYILES RAGSVHDQGW EFYATVVCLY
101  LIFAFPCFVW RYFWHTRNRE *
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 266 shows 92.1% identity over a 114 aa overlap with a predicted ORF (ORF 266.ng) from *N. gonorrhoeae*:

```
m266/g266

      10      20      30      40      50      60
m266.pep  MPFRNAFRRHRRRQRLNRKPTMTASMYILLVLALIFANAPFLTTRLFGVAXLKRKHFGHH
          |||||  |||||  |||||  |||||  |||||  |||||
g266      MQFRRHRRRQCPNRKPIMTASMYILLVLALIFANAPFLTTRLFGVAALKRKHFGHH
          10      20      30      40      50

      70      80      90      100     110     120
m266.pep  MIELAAGFALTAVLAYILES RAGSVHDQGW EFYATVVCLYLI FAFPCFVWRYFWHTRNREX
          :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
g266      LIELAAGFALTASLAYILES RAGAVHNQGW EFYATVVCLYLI FAFPCFVWRYFWHTRNREX
          60      70      80      90      100     110
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1073>:

```
a266.seq
  1  ATGCCGTTCC GCAATGCGTT CAGACGGCAT CGCCGCCGAC AATGCCCAAA
 51  CAGAAAGCCC GCCATGACCG CATCCATGTA CATCCTTTTG CTGCTTGCCT
101  TGATTTTTCG CAACGCCCCC TTCCTCACGA CCAAGCTGTT CGGCATCGTA
151  CCGCTCAAGC GCAAACATTT CGGACACCAC CTGATCGAGC TGGCGGCAGG
201  TTTCGCGCTG ACCGCCGTTT TTGCCTACAT CCTCGAATCC CGTGCGGGAG
251  CGGTACACGA TCAGGGTTGG GAGTTTTACG CCACCGTCGT CTGCCTGTAC
301  CTGATTTTTC CGTTTCCCTG TTTCGTGTGG CGGTATTTT GGCACACGCG
351  CAACAGGGAA TAG
```

This corresponds to the amino acid sequence <SEQ ID 1074; ORF 266.a>:

```
a266.pep
  1  MPFRNAFRRH RRRQCPNRKP AMTASMYILL LLALIFANAP FLTTKLFGIV
 51  PLKRKHFGHH LIELAAGFAL TAVLAYILES RAGAVHDQGW EFYATVVCLY
101  LIFAFPCFVW RYFWHTRNRE *
```

m266/a266 91.7% identity in 120 aa overlap

```
      10      20      30      40      50      60
m266.pep  MPFRNAFRRHRRRQRLNRKPTMTASMYILLVLALIFANAPFLTTRLFGVAXLKRKHFGHH
          |||||  |||||  |||||  |||||  |||||  |||||
a266      MPFRNAFRRHRRRQCPNRKPAMTASMYILLLLALIFANAPFLTTLKLFIVPLKRKHFGHH
          10      20      30      40      50      60

      70      80      90      100     110     120
m266.pep  MIELAAGFALTAVLAYILES RAGSVHDQGW EFYATVVCLYLI FAFPCFVWRYFWHTRNRE
          :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
a266      LIELAAGFALTAVLAYILES RAGAVHDQGW EFYATVVCLYLI FAFPCFVWRYFWHTRNRE
          70      80      90      100     110     120

m266.pep  X
          |
a266      X
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1075>:

```
g267.seq
```

```

1   atgcaagtcg ccttttttct cgccgtggta ttcaaaaata tgggtttcca
51  caatcgcata ggtcgggcag gcctcttcgc agaaaccgca gaagatgcac
101 ttggtcaggt cgatgtcgta acgcttggtg cggcgggtgc cgtcttcgcg
151 ttcttcgat  tcgatgtga tcgccattgc cggacacacc gcctcgcaca
201 atttacacgc gatgcagcgt tcctctccgt tcggaaaacg gcgttgcgcg
251 ttcgagaccgc ggaacgcac ggattgcggc gttttctctt cgggaaaata
301 aattgtgtct ttgcgggcaa aaaagttttt gagcgttacg cccatgcctt
351 tgaccagttc qccaagcaqa aaqqttttta ctaa

```

This corresponds to the amino acid sequence <SEQ ID 1076; ORF 267.ng>:

q267.pep

1 MQVAFFLAVV FKNMGFHNRI GRAGLFAETA EDALGQVDVV TLGAAGAVFA
51 FFRFDVDRHC RTHRLAQFTR DAAFLSVRKT ALRVQTAETH GLRRFLPGKI
101 NCVFAGKKVF ERYAHAFDOF AKOKGEY*

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1077>:

m267.seq

1	GTGCAAGTCG	CCTTTTTTCT	CGCCGTGGTA	TTCAAAAATA	TGGGTTTCCA
51	CAATCGCATC	AGTCGGGCAT	GCCTCTTCGC	AGAAACCGCA	GAAGATGCAC
101	TTGGTCAGGT	CGATGTCGTA	ACGCTTGGTG	CGGCGCGTAC	CGTCTTCACG
151	TTCTTCCGAT	TCGATGTAA	TCGCCATTGC	CGGACACACT	GCCTCACACA
201	ACTTACACGC	GATACACCGC	TCTTCGCCGT	TCGGATACCG	CcGCTGCGCG
251	TGCAGACCGC	GGAAACGCAC	GGATTTCGGC	GTTTTCTCTT	CGGGGAAATA
301	AATTGTGTCT	TTGCGGGCGA	AAAAGTTTTT	GAGCGTTACG	CCCATACCTT
351	TTACCAATTC	GCCAAGCAGA	AAGGTTTTTA	CTAA	

This corresponds to the amino acid sequence <SEQ ID 1078; ORF 267>:

m267.pep

1 VQVAFFLAVV FKNMGFHNRI SRACLFAETA EDALGQVDVV TLGAARTVFT
51 FFRFDVNRHC RTHCLTQLTR DTPLFAVRIP PLRVQTAETH GLRRFLFGEI
101 NCVEAGEKVF ERYAHTFYOF AKOKGEFY*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 267 shows 82.7% identity over a 127 aa overlap with a predicted ORF (ORF 267.ng) from *N. gonorrhoeae*:

m267/q267

		10	20	30	40	50	60
m267.pep		VQVAFFLAVVFKNMGFHNRI	SRACLFAETAEDALGQVDV	VTLGAARTVFTFFRFDVNRHC			
		:					
g267		MQVAFFLAVVFKNMGFHNRI	GRAGLFAETAEDALGQVDV	VTLGAAGAVFAFFRFDVDRHC			
		:					
		10	20	30	40	50	60
		70	80	90	100	110	120
m267.pep		RTHCLTQLTRDTPLFAVRIP	PLRVQTAETHGLRRFLFGEI	NCVFAGEKVFERYAHTFYQF			
			: : : :	: : :			
g267		RTHRLAQFTRDAAPLSVRKT	ALRVQTAETHGLRRFLFGKI	NCVFAGKKVFERYAHAFDQF			
			: : : :	: : :			
		70	80	90	100	110	120
m267.pep		AKQKGFIYX					
g267		AKQKGFIYX					

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1079>:

a267.seq

1	GTGCAAGTCG	CCTTTTTTCT	CGCCGTGGTA	TTCAAAAATA	TGGGTTTCCA
51	CAATCGCATC	GGTCGGGAG	GCTTCTTCGC	AGAAACCGCA	GAAGATGCAC
101	TGGTCAGGT	CGATGTCGTA	ACGCTTGGTG	CGCGCGCTGC	CGTCTTCGCG
151	TTCTTCCGAT	TCGATGTTGA	TCGCCATTGC	GGGGCAAACG	GCTTCACACA
201	ATTTACACGC	GATGCAGCGT	TCCTCGCCGT	TTGGATAACG	CGGTTGCGCG
251	TGCACACCGC	GGAAACGCAC	GGATTGCGGC	GTTTCTCTCT	CGGGAAAATA
301	AATCGTGTCT	TTGCGGGCAA	AAAAGTTTTT	GAGCGTTACG	CCCATACCTT
351	TTACCAATTTC	GCCAAAGCAGA	AAGGTTTTTA	CTAA	

This corresponds to the amino acid sequence <SEQ ID 1080; ORF 267.a>:

```
a267.pep
  1  VQVAFFLAVV FKNMGFHNRI GRAGFFAETA EDALGQVDVV TLGAARAVFA
 51  FFRFDVDRHC GANGFTQFTR DAAFLAVWIT ALRVQTAETH GLRRFLFGKI
101  NRVFAGKKVF ERYAHTFYQF AKQKGFY*
```

m267/a267 82.7% identity in 127 aa overlap

	10	20	30	40	50	60
m267.pep	VQVAFFLAVVFKNMGFHNRI	SRACLFAETAEDALGQVDVV	TLGAARTVETFFRFDVNRHC			
a267	VQVAFFLAVVFKNMGFHNRI	GRAGFFAETAEDALGQVDVV	TLGAARAVFAFFRFDVDRHC			
	10	20	30	40	50	60
	70	80	90	100	110	120
m267.pep	RTHCLTQLTRDTPLFAVRIP	PLRVQTAETHGLRRFLFGE	INCVFAGEKVFERYAHTFYQF			
	:::	:::				
a267	GANGFTQFTRDAAFLAVWIT	ALRVQTAETHGLRRFLFGK	INRVFAGKKVFERYAHTFYQF			
	70	80	90	100	110	120
m267.pep	AKQKGFYX					
a267	AKQKGFYX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1081>:

```
G268.seq
  1  atgaaaaaaaa atttaccgc actggcattg gcaagtatgc tgattttgtc
 51  gggctgcgac cgtttgggaa taggcaacc gttttccgga aaggaaattt
101  cctgcggaag cgaagagact aaagagattt tggcctaaact ggtccgcgac
151  aatgtcgaag gtgaaaccgt caaaactttt gacgacgacg cattcaaaga
201  ccaagcattt gccgatatcg gcatatcgca tatccgcaga atggtcgaac
251  gtttgggcat aaccgtcgat gaagtccgaa ctaccgagaa aaccgacacg
301  tccagcaaac tcaaatgtga agccgcgtta aaactggacg tgcccagcga
351  tgtgtcgat tatgccgtcg ccgccaacca atctataggc aacagccata
401  agaaaacgcc cgactttttt gaaccctact accgcaaaga aggcgcgtat
451  tatgtcaaaa ctattttctta cagcgtccag ccgacagacg acaaaagcaa
501  aatctttgcc gaactcagtc aggcacacga tatcatccat ccgctcagcg
551  agctggtgtc tatggcactg attaaagagc cgttggacaa agcgaaacaa
601  aggaacgaaa aacttgaagc ggcagaagcc accgcgcagg aagcgaggga
651  ggcagaagaa gcggcggcgc aggaggcatt gggtcgggag caggaagccg
701  cccgcgtatc cgaatgggaa gaacgctaca agctgtcgcg cagcgagttc
751  gagcagtttt ggaaaggatt gcctcaaact gtacagaata agctgcaagc
801  ctgcagaaaa acatggaaaa gcggtatgga caagatctgt gccacaatg
851  cgaaagccga aggtgaaacg ccaaaccgca taaaagtcag tgagttggcg
901  tgtaaaacgg cagaaaccga agcacgcttg gaagagctgc acaaccgtaa
951  aaaagccctt atcgacgaaa tggtcaggga agaggacaag aaagaactgc
1001 caaagcggct ctga
```

This corresponds to the amino acid sequence <SEQ ID 1082; ORF 268.ng>:

```
m268.pep
  1  MKKNLPALAL ASMLILSGCD RLGIGNPFSG KEISCGSEET KEILVKLVRD
 51  NVEGETVKTF DDDAFKDQAF ADIGISHIRR MVERLGITVD EVRTTEKTD
101  SSKLKCEAAL KLDVPDDVDV YAVAAQSIG NSHKKTPDFF EPYYRKEGAY
151  YVKTISYSVQ PTDDKSKIFA ELSQAHDIIH PLSELVSMAL IKEPLDKAKQ
201  RNEKLEAAEA TAQEAREAE AAQAEALGRE QEAARVSEWE ERYKLSRSEF
251  EQFWKGLPQT VQNKLQASQK TWKSGMDKIC ANNAKAEGET PNGIKVSELA
301  CKTAETEAREL EELHNRKKAL IDEMVREEDK KELPKRL*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1083>:

```
m268.seq (partial)
  1  ..ATGGCACTGA TTAAAGAGCC GTTGACAAA GTGAAACAAA GGAACGAAGA
```

614

```

51   ACTTGAAGCG GCAGAAGAAG CGGCGGCGCA GGAGGCATTG GGTCGGGAGC
101  AGGAAGCCGC CCGCGTATCC GAATGGGAAG AACGCTACAA GCTGTCGCGC
151  AG.CAGTTCG AGCAGTTCTG GAAAGGATTG CCTCAAACCG TACAGAATAA
201  GCTGCAACCn TCACAGAAAA CATGGAAAAG CGGGATGGAT AAAATCTGTG
251  CCAACAATGC GAAAGCTGAA GGTAAAACGC CAAACGGCAT AAAATTCAGC
301  GAACTGGCAT GCAAAACGGC GAAAACCGAA GCACGCTTGG AAGAGCTGCA
351  CAACCGTAAA AAAGCCCTTA TCGACGAAAT GGyCAGGGAA GCGGACAmGA
401  AAGAACTGTC AAAGCGGCTs TGA

```

This corresponds to the amino acid sequence <SEQ ID 1084; ORF 268>:

```

m268.pep (partial)
1   .MALIKEPLDK VKQRNEELEA AEEAAAQEAL GREQEAAARVS EWEERYKLSR
51  XQFEQFWKGL PQTQVQNKLP SQKTWKSMD KICANNAKAE GKTPNGIKFS
101 ELACKTAKTE ARLEELHNRK KALIDEMXRE ADXKELSKRL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 268 shows 86.0% identity over a 150 aa overlap with a predicted ORF (ORF 268.ng) from *N. gonorrhoeae*:

m268/g268

```

                                10      20
m268.pep                      MALIKEPLDKVKQRNEELEAAE-----
                                |||:|||:|||:|||:|||:|||:|||
g268      SVQPTDDKSKIFAELSQAHDIIHPLSELVSMALIKEPLDKAKQRNEKLEAAEATAQEARE
          160      170      180      190      200      210

                                30      40      50      60      70      80
m268.pep  - -EAAAQEALGREQEAAARVSEWEERYKLSRSQFEQFWKGLPQTQVQNKLP SQKTWKSMD
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g268      AEEAAAQEALGREQEAAARVSEWEERYKLSRSEFEQFWKGLPQTQVQNKLPQASQKTWKSMD
          220      230      240      250      260      270

                                90      100     110     120     130     140
m268.pep  KICANNAKAE GKTPNGIKFSELACKTAKTEARLEELHNRKKALIDEMXREADXKELSKRLX
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g268      KICANNAKAEGETPNGIKVSELACKTAETEARLEELHNRKKALIDEMVREEDKKELPKRLX
          280      290      300      310      320      330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1085>:

```

a268.seq
1   ATGGCACTGA TTAAAGAGCC GTTGGACAAA GCGAAACAAA GGAACGAAGA
51  ACTTGAAGCG GCAGAAGAAG CGGCGGCGCA GGAGGCATTG GGTCGGGAGC
101 AGGAAGTCGA CCGCGTATCC GAATGGGAAG AACGCTACAA GCTGTCGCGC
151 AGCGAGTTCG AGCAGTTCTG GAAAGGATTG CCTCAAACCG TACAGAATAA
201 GCTGCAAGCC TCACAGAAAA CATGGAAAAG CGGGATGGAT AAAATCTGTG
251 CCAACAATGC GAAAGCTGAA GGTGAAACGC CAAACGGCAT AAAATTCAGC
301 GAACTGGCAT GCAAAACGGC GGAAACCGAA GCACGCTTGG AAGAGCTGCA
351 CAACCGTAAA AAAGCCCTTC TCGACGAAAT GGCCAGGGAA GCGGACAAGA
401 AAGAACTGCC AAAGCGGCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1086; ORF 268.a>:

```

a268.pep
1   MALIKEPLDK AKQRNEELEA AEEAAAQEAL GREQEVDRVS EWEERYKLSR
51  SEFEQFWKGL PQTQVQNKLP SQKTWKSMD KICANNAKAE GETPNGIKFS
101 ELACKTAETE ARLEELHNRK KALLDEMARE ADKKELPKRL *

```

m268/a268 91.4% identity in 140 aa overlap

```

                                10      20      30      40      50      60
m268.pep  MALIKEPLDKVKQRNEELEAAEAAAQEALGREQEAAARVSEWEERYKLSRXQFEQFWKGL
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a268      MALIKEPLDKAKQRNEELEAAEAAAQEALGREQEVDRVSEWEERYKLSRSEFEQFWKGL

```

615

	10	20	30	40	50	60
	70	80	90	100	110	120
m268.pep	PQTVQNKLPQSQKTWKSMDKICANNAKAEGKTPNGIKFSELACKTAKTEARLEELHNRK					
	: : : : : : : : : : : : : : : :					
a268	PQTVQNKLPQASQKTWKSMDKICANNAKAEGETPNGIKFSELACKTAETEARLEELHNRK					
	70	80	90	100	110	120
	130	140				
m268.pep	KALIDEMXREADXKELSKRLX					
	:					
a268	KALLDEMAREADKKELPKRLX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1087>:

m268-1.seq

```

1  GTGCAATCCC GATATGATGG TTTGCATAAA TTAAACATA TATGTTCCGC
51  AGCTATGGCA CTGATTAAAG AGCCGTGGA CAAAGTGAAA CAAAGGAACG
101 AAGAACTTGA AGCGGCAGAA GAAGCGGCGG CGCAGGAGGC ATTGGGTCGG
151 GAGCAGGAAG CCGCCCGCGT ATCCGAATGG GAAGAACGCT ACAAGCTGTC
201 GCGCAGCGAG TTCGAGCAGT TCTGGAAAGG ATTGCCTCAA ACCGTACAGA
251 ATAAGCTGCA AGCCTCACAG AAAACATGGA AAAGCGGGAT GGATAAAATC
301 TGTGCCAACA ATGCGAAAGC TGAAGGTAAA ACGCCAAACG GCATAAAATT
351 CAGCGAACTG GCATGCAAAA CGGCGAAAAC CGAAGCACGC TTGGAAGAGC
401 TGCACAACCG TAAAAAAGCC CTTATCGACG AAATGGCCAG GGAAGCGGAC
451 AAGAAAGAAC TGTCAAAGCG GCTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1088; ORF 268-1>:

m268-1.pep

```

1  VQSRDGLHK FKHICSAAMA LIKEPLDKVK QRNEELEAAE EAAAEALGR
51  EQEAAARVSEW EERYKLSRSE FEQFWKGLPQ TVQNKLPASQ KTWKSGMDKI
101 CANNAKAEGK TPNGIKFSEL ACKTAKTEAR LEELHNRKKA LIDEMAREAD
151 KKELSKRL*

```

m268-1/g268 82.3% identity in 164 aa overlap

		10	20	30
m268-1.pep		VQSRDGLHKFKHICSAAMALIKEPLDKVKQRNE		
		: : : : : : : : : :		
g268	KEGAYYVKTISYSVQPTDDKSKIFAELSQAHDIIHPLSELVS--MALIKEPLDKAKQRNE			
	150 160 170 180 190 200			
	40 50 60 70 80			
m268-1.pep	ELEAAE-----EAAAEALGREQEAARVSEWEERYKLSRSEFEQFWKGLPQTVQN			
	: : : : : : : : : :			
g268	KLEAAEATAQEAREAEAAAEALGREQEAARVSEWEERYKLSRSEFEQFWKGLPQTVQN			
	210 220 230 240 250 260			
	90 100 110 120 130 140			
m268-1.pep	KLQASQKTWKSMDKICANNAKAEGKTPNGIKFSELACKTAKTEARLEELHNRKKALIDE			
	: : : : : : : : : : : : : : :			
g268	KLQASQKTWKSMDKICANNAKAEGETPNGIKVSELACKTAETEARLEELHNRKKALIDE			
	270 280 290 300 310 320			
	150 159			
m268-1.pep	MAREADKKELSKRLX			
	: : : :			
g268	MVREEDKKELPKRLX			
	330			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1089>:

a268-1.seq

```

1  GTGCAATCCC GATATGATGG TTTGCATAAA TTAAACATA TATGTTCCGC
51  AGCTATGGCA CTGATTAAAG AGCCGTGGA CAAAGCGAAA CAAAGGAACG
101 AAGAACTTGA AGCGGCAGAA GAAGCGGCGG CGCAGGAGGC ATTGGGTCGG
151 GAGCAGGAAG TCGACCGCGT ATCCGAATGG GAAGAACGCT ACAAGCTGTC
201 GCGCAGCGAG TTCGAGCAGT TCTGGAAAGG ATTGCCTCAA ACCGTACAGA
251 ATAAGCTGCA AGCCTCACAG AAAACATGGA AAAGCGGGAT GGATAAAATC
301 TGTGCCAACA ATGCGAAAGC TGAAGGTGAA ACGCCAAACG GCATAAAATT
351 CAGCGAACTG GCATGCAAAA CGGCGGAAAC CGAAGCACGC TTGGAAGAGC

```

616

401 TGCACAACCG TAAAAAGCC CTTCTCGACG AAATGGCCAG GGAAGCGGAC
 451 AAGAAAGAAC TGCCAAAGCG GCTCTGA

This corresponds to the amino acid sequence <SEQ ID 1090; ORF 268-1.a>:

a268-1.pep

1 VQSRDGLHK FKHICSAAMA LIKEPLDKAK QRNEELEAAE EAAAEALGR
 51 EQEVDVSEW EERYKLSRSE FEQFWKGLPQ TVQNKLASQ KTWKSGMDKI
 101 CANNKAEGE TPNGIKFSEL ACKTAETEAR LEELHNRKKA LDEMAREAD
 151 KKELPKRL*

a268-1/m268-1 95.6% identity in 158 aa overlap

	10	20	30	40	50	60
a268-1.pep	VQSRDGLHKFKHICSAAMALIKEPLDKAKQRNEELEAAE	EAEEAAAEALGREQEVDRVSEW				
m268-1	VQSRDGLHKFKHICSAAMALIKEPLDKVQRNEELEAAE	EAEEAAAEALGREQEAARVSEW				
	10	20	30	40	50	60
	70	80	90	100	110	120
a268-1.pep	EERYKLSRSEFEQFWKGLPQTVQNKLASQKTWKS	GMDKICANNAKAEGETPNGIKFSEL				
m268-1	EERYKLSRSEFEQFWKGLPQTVQNKLASQKTWKS	GMDKICANNAKAEGKTPNGIKFSEL				
	70	80	90	100	110	120
	130	140	150	159		
a268-1.pep	ACKTAETEARLEELHNRKKALDEMAREADKKELPKRLX					
m268-1	ACKTAKTEARLEELHNRKKALIDEMAREADKKELSKRLX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1091>:

g269.seq

1 atggtttggc gtgtgaattg cgcggcaacg gcggcgctga ttttttcgtc
 51 cagcccttgg atttgggcgg tgggtggtggt gtggtcgcgg tcggcttttt
 101 cctgcaaac ttgcgccagc cttgacgcgt ccagtgcgcc ggcgttggcg
 151 gtttcgccgt gggactttat ccggaacacg gcttcgccca aggtgtcggc
 201 ggctttgatg cacagtttta aaaccagggc tttggggcgg ttttctgcgc
 251 cggccgttgc cattttgctg tccaatcgcg gggttaaaaa accgttgctg
 301 ttttaagtcgc cgtccgtcca agtcgatacg agcgcgcttc tttgcctttc
 351 attgcggtct tcgtaa

This corresponds to the amino acid sequence <SEQ ID 1092; ORF 269.ng>:

g269.pep

1 MVWRVNCAAT AALIFSSSPW IWAVVWWSR SAFSCKPCAS LDASSAPALA
 51 VSPWDFIRNT ASPKVSALM HSFKTRALGR FSAPPVAILL SNRGVKKPLS
 101 FKSPSVQVDT SALLCLSLRS S*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1093>:

m269.seq

1 ATGGTTTGGC GTGTGAATTG CGCGGCAACG GCGGTGCTGA TTTTTCGTC
 51 CAGCCCTTGG ATTTGGGCGG CGGTGTGGGT GTGCTCTCGG TCGGCTTTGT
 101 CTTGCAAACC TTGCGCCaCG TGCCGCGTC CAGCGCCTGC GTTGATGGTT
 151 TCGCCGTGGG ACTTTATCCA AAACACGGCT TCGCCAAGG TGTCGGCGGC
 201 TTTGATGCAC AGTTTAAAA CCAGGGCTTT GGGGCGGTTT TCGTCGCCGC
 251 CTGTCGCCAT TTTGCTGTCC GAGCGCGGGG TAAAAAGCC GTTGTCGTTT
 301 AAATTTTCGT CCGTCCAAGT CGATACGAGC GCGCTTCTCT GCCTTTCGTT
 351 GCGGTCTTCG TAA

This corresponds to the amino acid sequence <SEQ ID 1094; ORF 269>:

m269.pep

1 MVWRVNCAAT AVLIFSSSPW IWAHVWWSR SALSCKPCAT CPRPAPALMV
 51 SPWDFIQNTA SPKVSALMH SFKTRALGRF SSPPVAILLS ERGVKKPLSF
 101 KFSSVQVDT ALLCLSLRSS *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 269 shows 87.6% identity over a 121 aa overlap with a predicted ORF (ORF 269.ng) from *N. gonorrhoeae*:

```

m269 . pep      MVWRVNCAATAVLIFSSSPWIWAAVWVWSRSALSCKPCATCP-RPAPALMVSPWDFIQNT      59
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g269            MVWRVNCAATAALIFSSSPWIWAAVWVWSRSASFCKPCASLDASSAPALAVSPWDFIRNT      60

m269 . pep      ASPKVSAAALMHSFKTRALGRFSSPPVAILLSERGVKKPLSFKFSSVQVDT SALLCLSLRS    119
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g269            ASPKVSAAALMHSFKTRALGRFSAPPVAILLSNRGVKKPLSFKSPSVQVDT SALLCLSLRS    120

m269 . pep      SX      121
                ||
g269            SX      122

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1095>:

```

a269 . seq
1  ATGGTTTGGC GTGTGAATTG CGCGGCAACG GCGGTGCTGA TTTTTCGTC
51 CAGCCCTTGG ATTTGGGCGG CGGTGTGGGT GTGGGCGCGG TCTGCTTTGT
101 CTTGGAGGTT TTGCGCCAGC GTGCCGCGT CCAGCGCGCC GCGTTGACG
151 GTTTCGCCGT GGGACTTTAT CTAGAACACG GCTTCGCCCA AGGTGTCGGC
201 GGCTTTGATG CACAGTTTAA AAACCAGGGC TTTGGGGCGG TTTTCGTCGC
251 CGCCTGTGCG CATTTTGCTG TCCGGGCGCG GGGTTAAAAA GCCGTTGTCG
301 TTAAATTTT CGTCCGTCCA AGTCGATACG AGCGCGCTTC TCTGCCTTTC
351 GTTGTGGTCT TCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1096; ORF 269.a>:

```

a269 . pep
1  MVWRVNCAAT AVLIFSSSPW IWAAVWVWAR SALSWRFCAS VPASSAPALT
51 VSPWDFIQNT ASPKVSAAALM HSFKTRALGR FSSPPVAILL SGRGVKKPLS
101 FKFSSVQVDT SALLCLSLWS S*

```

m269/a269 90.1% identity in 121 aa overlap

```

                10      20      30      40      50      59
m269 . pep      MVWRVNCAATAVLIFSSSPWIWAAVWVWSRSALSCKPCATCP-RPAPALMVSPWDFIQNT
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a269            MVWRVNCAATAVLIFSSSPWIWAAVWVWARSALSWRFCASVPASSAPALTVSPWDFIQNT
                10      20      30      40      50      60

                60      70      80      90      100     110     119
m269 . pep      ASPKVSAAALMHSFKTRALGRFSSPPVAILLSERGVKKPLSFKFSSVQVDT SALLCLSLRS
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a269            ASPKVSAAALMHSFKTRALGRFSSPPVAILLSGRGVKKPLSFKFSSVQVDT SALLCLSLWS
                70      80      90      100     110     120

m269 . pep      120
                SX
                ||
a269            SX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1097>:

```

g270 . seq
1  atgaataaaa accgcaaatt actgcttgcc gcactgctgc tgactgcctt
51 tgccgccttc aagctcgttt tgttgcaatg gtggcaggcg cagcagccgc
101 aagccgtggc ggcgcaatgc gatttgaccg aggggtgcac gctgccggac
151 ggaagccgtg tccgcgcgcg cgccgtttca accaaaaaac cgtttgatat
201 ttatatcgaa cacgcgcccg ccggcacgga acaggtcagc atcagcttca
251 gtatgaaaaa tatggatatg ggtttcaacc gctatatgtt cgagcggcaa
301 ccgtcgggga cttggcaggc agcacgcacg cgctgcccg tctgtgtcga
351 aggcaggcgc gattttacgg cggacattac aatcggcagc cggacatttc
401 agacggcatt taccgccgaa taa

```

This corresponds to the amino acid sequence <SEQ ID 1098; ORF 270.ng>:

618

g270 . pep
 1 MNKNRKLLLA ALLLTAFAAF KLVLLQWWQA QQPQAVAAQC DLTEGCTLPD
 51 GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ
 101 PSGTWQAARI RLPVCVEGRR DFTADITIGS RTFQTAFTAE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1099>:

m270 . seq
 1 ATGAATAAAA ACCGTAAATT ACTGCTTGCC GCACTGCTGC TGATTGCCTT
 51 TGCCGCCGTC AAGCTCGTTT TGTGCAATG GTGGCAGGCG Ca . CAGCCGC
 101 AAGCTGTGGC GGCACAATGC GATTTGACCG AGGGTTGCAC GCTGCCGGAC
 151 GGAAGCCGCG TCCGCGCCGC CGCGTTTCA ACCAAAAAAC CGTTTGATAT
 201 TTATATCGAA CACGCGCCCG CCGGCACGGA ACAGGTCAGC ATCAGCTTCA
 251 GTATGAAAAA TATGGATATG GGTTTCaACC GCTATATGTT CGAGCGGCAA
 301 CCGTCGGGGA CTTGGCAGGC AGTACGCATC CGCCTGCCCA TCTGTGTCGA
 351 AGGCAGGCGC GATTTTACGG CGGACATTAC AATCGGCAGT CGGACATTTC
 401 AGACGGCATT TACCGCCGAA TAA

This corresponds to the amino acid sequence <SEQ ID 1100; ORF 270>:

m270 . pep
 1 MNKNRKLLLA ALLLIAFAAV KLVLLQWWQA XQPQAVAAQC DLTEGCTLPD
 51 GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ
 101 PSGTWQAVRI RLPICVEGRR DFTADITIGS RTFQTAFTAE *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 270 shows 96.4% identity over a 140 aa overlap with a predicted ORF (ORF 270.ng) from *N. gonorrhoeae*:

m270/g270

	10	20	30	40	50	60
m270 . pep	MNKNRKLLLAALLLIAFAAVKLVLLQWWQAXQPQAVAAQCDLTEGCTLPDGSRVRAAAVS					
g270	MNKNRKLLLAALLLTAFAAFCLVLLQWWQAQQPQAVAAQCDLTEGCTLPDGSRVRAAAVS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m270 . pep	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFERQPSGTWQAVRIRLPICVEGRR					
g270	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFERQPSGTWQAARIRLPVCVEGRR					
	70	80	90	100	110	120
	130	140				
m270 . pep	DFTADITIGSRTFQTAFTAEX					
g270	DFTADITIGSRTFQTAFTAEX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1101>:

a270 . seq
 1 ATGAATAAAA ACCGTAAATT ACTGCTTGCC GCACTGCTGC TGATTGCCTT
 51 TGCCGCCGTC AAGCTCGTTT TGTGCAATG GTGGCAGGCG CAGCAGCCGC
 101 AAGCTGTGGC GGCACAATGC GATTTGACCG AGGGTTGCAC GCTGCCGGAC
 151 GGAAGCCGCG TCCGCGCCGC CGCCGTTTCA ACCAAAAAAC CGTTTGATAT
 201 TTATATCGAA CACGCGCCCG CCGGCACGGA ACAGGTCAGC ATCAGCTTCA
 251 GTATGAAAAA TATGGATATG GGTTTCAACC GCTATATGTT CGAGCGGCAA
 301 CCGTCGGGGA CTTGGCAGGC AGTACGCATC CGCCTGCCCA TCTGTGTCGA
 351 AGGCAGGCGC GATTTTACGG CGGACATTAC AATCGGCAGC CGGACATTTC
 401 AGACGGCATT TACCGCCGAA TAA

This corresponds to the amino acid sequence <SEQ ID 1102; ORF 270.a>:

a270 . pep
 1 MNKNRKLLLA ALLLIAFAAV KLVLLQWWQA QQPQAVAAQC DLTEGCTLPD
 51 GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ

101 PSGTWQAVRI RLPICVEGRR DFTADITIGS RTFQTAFTAE *

m270/a270 99.3% identity in 140 aa overlap

	10	20	30	40	50	60
m270.pep	MNKNRKL	LLAALL	IAFAAV	KLVL	LQWQ	AXQPQ
a270	MNKNRKL	LLAALL	IAFAAV	KLVL	LQWQ	AXQPQ
	10	20	30	40	50	60
m270.pep	TKKPF	DIYIE	HAPAG	TEQVS	ISFS	MKNMD
a270	TKKPF	DIYIE	HAPAG	TEQVS	ISFS	MKNMD
	70	80	90	100	110	120
m270.pep	MGFN	RYMF	ERQPS	GTWQ	AVRIR	LPI
a270	MGFN	RYMF	ERQPS	GTWQ	AVRIR	LPI
	70	80	90	100	110	120
m270.pep	DFTAD	ITIGS	RTFQ	TAFT	AEX	
a270	DFTAD	ITIGS	RTFQ	TAFT	AEX	
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1103>:

g271.seq

```

1   atgttcagtt cgcggatggc gaggatttgg gcgacggggg taacgttgtg
51  tatggtcagt cegtgtccgg cgttgacgac caagcccaaa tcgccggcga
101 aatgcgcgcc gttttggatg cgctcgaact gcctgatttg ttcggcgtgg
151 ctttgtgcgt cggcatatgc gccggtgtgc agctcgacaa cgggcgcgcc
201 gacatcacgg gcggcttga tttgcctgtc gtcggcatcg ataaacaagg
251 acacgcgtat gcccgcgtcg gtcaggattt tggcgaattc ggcgattttt
301 tcctgttgcg ccaatacgtc caaacgcct tcggtcgtga tttcctgccg
351 tttttcaggg acgatgcaca cgtcttcgg catcacttta agcgcgtttt
401 cgagcatttc ttccgtcaac gccatttcaa gggtcaggcg cgtgcggatg
451 gcgtttttga cggcaaatac atccgcgtct ttgatgtggc ggcggtcttc
501 gcgcaggtgc atggtaatca ggtctgcacc gtgcgtttcg gcaaccagtg
551 ccgcctccac ggggctggga taa

```

This corresponds to the amino acid sequence <SEQ ID 1104; ORF 271.ng>:

g271.pep

```

1   MFSSRMARIW ATGVTLCMVS PCPALTTKPK SPAKCAPFWM RSNCLICSAW
51  LCASAYAPVC SSTTGAPTSR AAWICLSSAS INKDTRMPAS VRILANSIAIF
101 SCCANTSKPP SVVISCRFSG TMHTSSGITL SAFSSISSVN AISRFRVRM
151 AFLTANTSAS LMWRRSSRRC MVIRSAPCVS ATSAASTGLG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1105>:

m271.seq

```

1   AwGTTcagTT CGCGGATGGC GAGGATTtGG GCGATGGGGG TAACGTTGTG
51  TATGGTCAGT CCGTGTCGGG CGTTGACGAC CAAGCCCAA TCGCCGCGCA
101 AATGCGCGCC GTTTTGGATG CGCTCGAACT GCCTGATTtG TTCGGCGTGG
151 CTGCGCGCGT CGGCATACGC GCCTGTGTGC AGCTCGACAA CGGGCGCGCC
201 GACATCACGG GCGGCTTGA TTTGCCTGTC GTCGGCATCG ATAAACAAAG
251 ACACGCGTAT GCCTGCGTCG GTCAGGATT TGGTGAACCC GCGGATTtTT
301 TCCTGTtGCG CCAATACGTC CAAACCGCCT TCGGTCTGTA TTTCTGACG
351 TTTTTCAGGC ACGATGCACA CGTCTTCCGG CATCACTtTC AAAGCGTTtT
401 CCAACATtTC TTCCGTCAAC GCCATTtCAA GGTTcAGGCG CGTGCGGATG
451 GCGTtTTTGA CGGCAACAC GTCCCGTCT TTGATGTGGC GCGGTCTTc
501 GCGCAGGTGC ATGGTAATCA AATCCGCACC GTGCGTTTCG GCAACCAGTG
551 CCGCTCCAC GGGGCTGGGA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1106; ORF 271>:

m271.pep

```

1   XFSSRMARIW AMGVTLCMVS PCPALTTKPK SPAKCAPFWM RSNCLICSAW
51  LRASAYAPVC SSTTGAPTSR AAWICLSSAS INKDTRMPAS VRILVNPAIF
101 SCCANTSKPP SVVISXRFSG TMHTSSGITF KAFSNISSVN AISRFRVRM
151 AFLTANTSAS LMWRRSSRRC MVIKSAPCVS ATSAASTGLG *

```

Computer analysis of this amino acid sequence gave the following results:

620

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 271 shows 95.2% identity over a 189 aa overlap with a predicted ORF (ORF 271.ng) from *N. gonorrhoeae*:

m271/g271

	10	20	30	40	50	60
m271.pep	XFSSRMARIWAMGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRASAYAPVC					
g271	MFSSRMARIWATGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLCASAYAPVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m271.pep	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNPAIFSCCANTSKPPSVVISXRFSG					
g271	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILANSALFSCCANTSKPPSVVISCRFSG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m271.pep	TMHTSSGITFKAFSNISSVNAISRFRVRMAFLTANTSASLMWRRSSRRRCMVISAPCVS					
g271	TMHTSSGITLSAFSSISSVNAISRFRVRMAFLTANTSASLMWRRSSRRRCMVIRAPCVS					
	130	140	150	160	170	180
	190					
m271.pep	ATSAASTGLGX					
g271	ATSAASTGLGX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1107>:

a271.seq

```

1  ATGTTTCAGTT CGCGGATGGC GAGGATTTGG GCGATGGGGG TAACGTTGTG
51  TATGGTCAGT  CCGTGTCGGG CGTTGACGAC CAAGCCCAA TCGCTGGCAA
101 AATGCGCGCC GTTTTGGATG CGCTCGAACT GCCTGATTTG TTCGGCGTGG
151 CTGCGCGCGT CGGCATACGC GCCTGTGTGC AGCTCGACAA CGGGCGCGCC
201 GACATCACGG GCGGCTTGGA TTTGCCTGTC GTCGGCATCG ATAAACAAGG
251 ACACGCGTAT GCGCGGTCG GTCAGGATTT TGGTGAATTC GGCAATTTTG
301 TCTTGTTCGC CCAATACGTC CAAGCCGCCT TCGGTCGTGA TTTCCTGACG
351 TTTTCCGGC ACGATGCACA CGTCTTCGG CATCACTTTA AGCGCGTTTT
401 CGAGCATTTT TTCCGTCAAC GCCATTTCAA GGTTCAGGCG CGTGCGGATG
451 GCGTTTTTGA CAGCAACAC GTCCGCGTCT TTGATGTGGC GGCGGTCTTC
501 GCGCAGGTGC ATGGTAATCA GGTCGGCACC GTGCGTTTCG GCAACCAGTG
551 CCGCCTCCAC GGGGCTGGGA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1108; ORF 271.a>:

a271.pep

```

1  MFSSRMARIW AMGVTLCMVS PCPALTTKPK SLAKCAPFWM RSNCLICSAW
51  LRASAYAPVC SSTTGAPTSR AAWICLSSAS INKDTRMPAS VRILVNSAIL
101 SCCANTSKPP SVVIS*RFSG TMHTSSGITL SAFSSISSVN AISRFRVRM
151 AFLTANTSAS LMWRRSSRRC MVIRAPCVS ATSAASTGLG *

```

m271/a271 96.3% identity in 189 aa overlap

	10	20	30	40	50	60
m271.pep	XFSSRMARIWAMGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRASAYAPVC					
a271	MFSSRMARIWAMGVTLCMVSPCPALTTKPKSLAKCAPFWMRSNCLICSAWLRASAYAPVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m271.pep	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNPAIFSCCANTSKPPSVVISXRFSG					
a271	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNSAILSCCANTSKPPSVVISXRFSG					

621

	70	80	90	100	110	120
m271.pep	130	140	150	160	170	180
	TMHTSSGITFKAFSNISSVNAISRFRVRMAFLTANTSASLMWRRSSRRCMVIKSAPCVS					
a271	TMHTSSGITLSAFSSISSVNAISRFRVRMAFLTANTSASLMWRRSSRRCMVIRSAPCVS					
	130	140	150	160	170	180
m271.pep	190					
	ATSAASTGLGX					
a271	ATSAASTGLGX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1109>:

g272.seq

```

1  atgactgcaa aggaagaact gttcgcatgg ctgcgccata tgaacaaaaa
51  caaagggttcc gacctgtttg tgacgaccca tttcccgccc gctatgaagc
101 tggacggcaa aatcacccgc atcacggacg aaccgctgac ggcggaaaaa
151 tgtatggaaa tcgccttttc gattatgagt gcgaagcagg cggaagaatt
201 ttcacgcacc aacgagtgca atttcgccat cagcctgccg gacaccagcc
251 gcttcgcgct caatgcgatg atacagcgcg gtgcgacggc gttggtattc
301 cgcgcgatta ccagcaagat tcccaagttt gaaagcctga acctgccgcc
351 ggccttgaag gatgttgccg tgaaaaaacg cgggctggtt atttttgtcg
401 gcggcaccgg ctccgggcaa tcgacttcgc tcgcctcgct tatcgactac
451 cgcaatgaaa attcgttcgg acacatcatc accatcgaag atccgatcga
501 gtttgtccac gaacacaaaa actgcatcat taccagcgcg gaggtcggcg
551 tggacacgga aaactggatg gcggcggtga aaaatacgct gcgtcaggcg
601 ccggatgtga tccttatcgg cgaaatccgc gaccgtgaaa caatggacta
651 cgccatcgcc tttgccgaaa cggggcattt gtgtatggcg acgctgcacg
701 ccaacagcac caatcaggcg ctcgaccgca tcatcaactt cttccccgag
751 gagcggcgcg aacaattgct gacggatttg tcgctcaacc ttcaggcggt
801 tatttcgcaa cgctcgttc cgcgagacgg cggcaaggcg aggggtggcg
851 cagtcgaggt gctgctcaat tcgcccctga tttcggagtt gattcacaa
901 ggcaacatcc atgaaatcaa agaagtgatg aaaaaatcca ctaccctggg
951 tatgcagacc ttcgaccaac acctttacca attgtatgaa aaaggcgaga
1001 tttccttgca ggatgccttg aaaaatgccg attccgcaca tgatttgcg
1051 ttggcggtac agttgcgcag ccgcagggca caaagttccg accccgattt
1101 ggaactgctc tga

```

This corresponds to the amino acid sequence <SEQ ID 1110; ORF 272.ng>:

g272.pep

```

1  MTAKEELFAW LRHMKNKNGS DLFVTTHFPP AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFFSST NECNFAISLP DTSRFRVNAM IQRGATALVF
101 RAITSKIPKF ESLNLPPALK DVALKKRGLV IFVGGTGSCK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYIAA FAETGHLGMA TLHANSTNQA LDRIINFFPE
251 ERREQLLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMQT FDQHLQLYE KGEISLQDAL KNADSAHDLR
351 LAVQLRSRRA QSSDPDLELL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1111>:

m272.seq

```

1  ATGACCGCAA AGGAAGAACT GTTCGCATGG CTGCGCCATA TGAwCCAAAA
51  CAAAGGTTCC GACCTGTTCC TGACAACCCA TTTCCCGCCC GCAATGAAGC
101 TGGACGGCAA AATCACCCGC ATCACGGACG AACCGCTGAC GCGGAAAAAA
151 TGTATGGAAA TCGCCTTTTC GATTATGAGT GCGAAGCAGG CGGAAGAATT
201 TTCATCGACC AACGAGTGCA ACTTCGCCAT CAGCCTGCCG GACACCAGCC
251 GCTTCGCGT CAATGCGATG ATACAGCGCG GCGCGACGGC GTTGGTATTC
301 CGTACGATTA CCAGCAAGAT TCCCAAGTTT GAAAGCCTGA ACCTGCCGCC
351 AGTCTTGAAG GATGTCGCGC TGAAAAAACG CGGGCTGGTT ATTTTGTGCG
401 GCGGCACCGG CTCGGGTAAA TCGACTTCGC TTGCCTCGCT TATCGACTAC
451 CGCAATGAAA ATTCGTTCCG ACACATCATC ACCATCGAAG ACCCGATCGA
501 GTTTGTCCAC GAACACAAAA ACTGCATCAT CACCCAGCGC GAGGTGCGCG

```

622

```

551 TGGATACGGA AAACCTGGATG GcGGCGTTGA AAAACACGCT GCGTCAGGCG
601 CCTGATGTCA TCCTTATCGG CGAAATCCGT GACCGCGAAA CAATGGACTA
651 CGCCATTGCC TTTGCCGAAA CGGGGCATTT GTGTATGGCG ACGCTGCACG
701 CCAACAGCAC CAATCAGGCA CTCGACCGCA TCATCAACTT TTTCCCCGAG
751 GAGCGGCGCG AACAATTGCT GACGGATTG TCGCTCAACC TTCAGGCGTT
801 TATTTTCGCA CGCTCGTTC CGCGAGACGG CGGCAAGGGC AGGGTGGCGG
851 CAGTCGAGGT GCTGCTCAAT TCGCCCCtGA TTTCGGAGTT GATTACAAAC
901 GGCAACATCC ATGAAATCAA AGAAGTGATG AAAAAATCCA CTACCCTGGG
951 TATGCAGACC TTCGATCAAC ACCTTTACCA ATTGTATGAA AAAGGCGATA
1001 TTTCCCTGCA AGAAGCATTG AAAAATGCCG ATTCCGCACA CGATTTCGCT
1051 TTGGCGGTAC AGTTGCGCAG CCGCCGCGCG CAaAGTTyCA GCCCGATT
1101 GGnACTGCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1112; ORF 272>:

m272.pep

```

1  MTAKEELFAW LRHMXQNKGS DLFVTHFPF AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFFSST NECNFAISLP DTSRFRVNAM IORGATALVF
101 RTITSKIPKF ESLNLPVVK DVALKKRGLV IFVGGTGS GK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAIA FAETGHLCA TLHANSTNQA LDRIINFFPE
251 ERREQLLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMMT FDQHLQLYE KGDISLQEAL KNADSAHDLR
351 LAVQLRSRRA QXSPDLXLL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 272 shows 97.6% identity over a 370 aa overlap with a predicted ORF (ORF 272.ng) from *N. gonorrhoeae*:

m272/g272

m272.pep	10	20	30	40	50	60
	MTAKEELFAWLRHMXQNKGS DLFVTHFPFAMKLDGKITRITDEPLTAEK CMEIAFSIMS					
g272	MTAKEELFAWLRHMXQNKGS DLFVTHFPFAMKLDGKITRITDEPLTAEK CMEIAFSIMS					
	10	20	30	40	50	60
m272.pep	70	80	90	100	110	120
	AKQAEFFSSTNECNFAISLPDTSRFRVNAMIORGATALVFRTITSKIPKFESLNLPVVK					
g272	AKQAEFFSSTNECNFAISLPDTSRFRVNAMIORGATALVFRAITSKIPKFESLNLPALK					
	70	80	90	100	110	120
m272.pep	130	140	150	160	170	180
	DVALKKRGLVIFVGGTGS KSTSLASLIDYRNENSFGHII TIEDPIEFVHEHKNCIITQR					
g272	DVALKKRGLVIFVGGTGS KSTSLASLIDYRNENSFGHII TIEDPIEFVHEHKNCIITQR					
	130	140	150	160	170	180
m272.pep	190	200	210	220	230	240
	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETMDYAIAFAETGHLCA TLHANSTNQA					
g272	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETMDYAIAFAETGHLCA TLHANSTNQA					
	190	200	210	220	230	240
m272.pep	250	260	270	280	290	300
	LDRIINFFPEERREQLLTDLSNLQAFISQRLVPRDGGKGRVAAVEVLLN SPLISELIHN					
g272	LDRIINFFPEERREQLLTDLSNLQAFISQRLVPRDGGKGRVAAVEVLLN SPLISELIHN					
	250	260	270	280	290	300
m272.pep	310	320	330	340	350	360
	GNIHEIKEVMKKSTTLGMMTFDQHLQLYE KGDISLQEALKNADSAHDLRLAVQLRSRRA					
g272	GNIHEIKEVMKKSTTLGMMTFDQHLQLYE KGEISLQDALKNADSAHDLRLAVQLRSRRA					
	310	320	330	340	350	360

623

```

                370
m272.pep      QSXSPDLXLLX
                || :||| |||
g272          QSSDPDLELLX
                370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1113>:

```

a272.seq
1   ATGACCGCAA AGGAAGAACT GTTCGCATGG CTGCGCCATA TGAACAAAAA
51  CAAAGGTTCC GACCTGTTCG TGACGACCCA TTTCCCGCCC GCAATGAAGC
101 TGGACGGCAA AATCACCCGC ATCACGGACG AACCGCTGAC GGCGGAAAAA
151 TGTATGGAAG TCGCCTTTTC GATTATGAGT GCGAAGCAGG CGGAAGAATT
201 TTCATCGACC AACGAGTGCA ACTTCGCCAT CAGTCTGCCG GACACCAGCC
251 GCTTCCGCGT CAATGCGATG ATACAGCGCG GTGCGACGGC GTTGGTATTC
301 CGTGCGATTA CCAGCAAGAT TCCCAAGTTT GAAAGCCTGA ACCTGCCGCC
351 GGTCTTGAAG GATGTCGCGC TGAAAAAACG CGGGCTGGTT ATTTTGTGCG
401 CGGGCACC GG CCGGGCAAA TCGACTTCGC TTGCCTCGT TATCGACTAC
451 CGCAATGAAA ATTCGTTTCG ACACATCATC ACCATCGAAG ACCCGATCGA
501 GTTTGTCCAC GAACACAAAA ACTGCATCAT CACCCAGCGC GAGGTCGGCG
551 TGGATACGGA AAACGGATG GCGGCGTTGA AAAACACGCT GCGTCAGGCA
601 CCGGATGTGA TTCTGATCGG CGAAATCCGC GACCGCGAAA CAATGGACTA
651 CGCCATTGCT TTTGCCGAAA CGGGGCATTT GTGTATGGCG ACGCTGCACG
701 CCAACAGCAC CAATCAGGCA CTCGACCGCA TCATCAACTT TTTCCCGGAG
751 GAGCGGCGCG AACAATTGCT GACGGATTTG TCGCTCAACC TTCAGGCATT
801 TATTTGCGAA CGCCTCGTTC CGCGAGACGG CGGCAAGGGC AGGGTGGCGG
851 CAGTCGAGGT GCTGCTCAAT TCGCCCTGTA TTTCGGAGT GATTCACAAC
901 GGCAATATCC ATGAAATCAA AGAAGTGATG AAAAAATCCA CTACCCTGGG
951 TATGCAGACT TTCGACCAAC ACCTTTACCA ATTGTATGAA AAAGGCGAGA
1001 TTTCTTGA GATGCCTTG AAAAATGCCG ATTCCGCACA CGATTTGCGT
1051 TTGGCGGTAC AGTTGCGCAG CCGCCAGGCG CAAAGTCCG GTCCCGATTT
1101 GGAAGTCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1114; ORF 272.a>:

```

a272.pep
1   MTAKEELFAW LRHMNKNKGS DLFVTTHFPP AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFSST NECNFAISLP DTSRFRVNM IQRGATALVF
101 RAITSKIPKF ESLNLPVVK DVALKKRGLV IFVGGTSGSK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAI FAETGHLCA TLHANSTNQA LDRIINFFPE
251 ERREQLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMQT FDQHLYQLYE KGEISLQDAL KNADSAHDLR
351 LAVQLRSRQA QSSGPDLELL *

```

m272/a272 97.6% identity in 370 aa overlap

```

                10      20      30      40      50      60
m272.pep      MTAKEELFAWLRHMNKNKGS DLFVTTHFPPAMKLDGKITRITDEPLTAEK CMEIAFSIMS
                ||||| :|||||
a272           MTAKEELFAWLRHMNKNKGS DLFVTTHFPPAMKLDGKITRITDEPLTAEK CMEIAFSIMS
                10      20      30      40      50      60

                70      80      90      100     110     120
m272.pep      AKQAEFSSTNECNFAISLPDTSRFRVNAMIQRGATALVFRTITSKIPKFESLNLPVVK
                ||||| :|||||
a272           AKQAEFSSTNECNFAISLPDTSRFRVNAMIQRGATALVFRAITSKIPKFESLNLPVVK
                70      80      90      100     110     120

                130     140     150     160     170     180
m272.pep      DVALKKRGLVIFVGGTSGSKSTSLASLIDYRNENSFGHII TIEDPIEFVHEHKNCIITQR
                ||||| :|||||
a272           DVALKKRGLVIFVGGTSGSKSTSLASLIDYRNENSFGHII TIEDPIEFVHEHKNCIITQR
                130     140     150     160     170     180

```

624

	190	200	210	220	230	240
m272.pep	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETMDYIAFAETGHLCMATLHANSTNQA					
a272	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETMDYIAFAETGHLCMATLHANSTNQA					
	190	200	210	220	230	240
m272.pep	LDRIINFFPEERREQLLTDLSLNLAQAFISQRLVPRDGGKGRVAAVEVLLNSPLISELIHN					
a272	LDRIINFFPEERREQLLTDLSLNLAQAFISQRLVPRDGGKGRVAAVEVLLNSPLISELIHN					
	250	260	270	280	290	300
m272.pep	GNIHEIKEVMKKSTTLGMQTFDQHLQYLYEKGDISLQEALKNADSAHDLRLAVQLRSRRA					
a272	GNIHEIKEVMKKSTTLGMQTFDQHLQYLYEKGEISLQDALKNADSAHDLRLAVQLRSRQA					
	310	320	330	340	350	360
m272.pep	GNIHEIKEVMKKSTTLGMQTFDQHLQYLYEKGDISLQEALKNADSAHDLRLAVQLRSRRA					
a272	GNIHEIKEVMKKSTTLGMQTFDQHLQYLYEKGEISLQDALKNADSAHDLRLAVQLRSRQA					
	310	320	330	340	350	360
m272.pep	QSXSPDLXLLX					
a272	QSSGPDLELLX					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1115>:

```

g273.seq
1  atgagtcttc aggcggtatt tatatacccc ccaagccgta ccgcacaata
51  caacgaaat caggaaaacg gcggtaaagc tcataaacag ggacaaagcg
101 gcaaacacac cgaccgccgt caggatatag gcgtattcga ggccggaact
151 ccattcacccg ttttcctgcc gtttcttgtc gcttttgaaa taaaggatga
201 tgccggcaag cagcgcggca gccgcgcccg acattggcat tgtgttcatt
251 gttgttcctt aacggttaaa aaccgcgccg gccgtgcaac cgttttaagg
301 cgggaaattg caaaatttgt ttgcgggcgc gtgcgctga aatcaaggcg
351 gtttgagaag tgtttcnacc gcgcccgcgc tatgtgccga aatattattt
401 gtcgctcacc tgcaaaatcg ccaagaacgc gctttgcgga atttccacgt
451 tgcccacttg tttcatacgg cgtttgccgt ctttttggtt ttcaagcagt
501 tttttcttac gcgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1116; ORF 273.ng>:

```

g273.pep
1  MSLQAVFIYP PSRTAQYNEN QENGGKAHKQ QSGKHTDRR QDIGVFEAGT
51  PFTVFLPFLV AFEIKDDAGK QRGSRARHWH CVHCCSLTVK NPPGRATVLR
101 REIAKFVCGR VPLKSRRFEK CFXRARPMCR NIICRSPAKS PRTRFAEFPR
151 CPLVSYGVCL LFVFQAVFSY A*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1117>:

```

m273.seq
1  ATGAGTCTTC AGGCGGTATT TATATACCCm CCAAGCCGTA CCGCACAAATA
51  CAACGAAAAT CAGGAAAACG GCGGTAAAGC TCAYAAACAG GGACAAAGCG
101 GCAAACACGC CGACCGCTGT CAGGATATAG GCGTATTCAA GGCCGGAAC
151 CCATTCCCCG TTTTCCTGCC GCTTCTTGTC GCTTTTGAAA TAAAGGATGA
201 TGCCGGCAAG CAGCGCGGCA GCCGCGCCCG ACATTAGCAT TGTGTTCATT
251 GTTGTTCCTT AATGCTTAAA AACCCGCCTG TCCGTGCAAC CGTTTAAAGG
301 CGGCAAAATTG CAAAATTGTG TTGCGGGCGC GTGCCCTGA AATCAGGGCG
351 GTTTGAGGGG TGTTCCTGAC GCGCCGCCCT GTGTGCCGGA GTTATTTGTC
401 GCTCACCTGC AAAATCGCCA AGAACGCGCT TTGCGGAATT TCCACATTGC
451 CCACTTGTTT CACACGCGT TTACCTGCCT TTGTkTWTC AAGCAGTTTT
501 TTCTACGCG TAA

```

This corresponds to the amino acid sequence <SEQ ID 1118; ORF 273>:

```

m273.pep
1  MSLQAVFIYP PSRTAQYNEN QENGGKAHKQ QSGKHADRC QDIGVFKAGT
51  PFPVFLPLL V AFEIKDDAGK QRGSRARH*H CVHCCSLMLK NPPVRATVLR
101 RQIAKFVCGR VPLKSGRFEG CSRRAALCAG VICRSPAKSP RTRFAEFPHC
151 PLVSYGVYLP FVXQAVFSY A*

```

Computer analysis of this amino acid sequence gave the following results:

m273/g273

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1119>:

This corresponds to the amino acid sequence <SEQ ID 1120; ORF 273.a>:

m273/a273 80.1% identity in 171 aa overlap

	10	20	30	40	50	60
m273.pep	MSLQAVFIYPPSRTAQYNENQ	ENGGKAHKQGQSGKHADRCQ	DIGVFKA	GTFFP	VFLPL	LV
a273	MSLQAVFIYPPSRTAQYNENQ	ENGGKAHKQGQSGKHADRRQ	DIGVFQTGT	FPFTV	FLPL	LV
	10	20	30	40	50	60
m273.pep	AFEIKDDAGKQGRS	RARHXHCVHCCSLMLKN	PPVRATVL	RRQIAKFV	CGRVPLK	SGRFE
a273	AFEIKDDAGKQGRS	RARHXHNVHCCSLTVKN	PPVRATVFKRRXIT	KFVGGR	ALLQSGR	FEK
	70	80	90	100	110	120
m273.pep	GCSRR	AALCAGVICR	SPAKSPRTRFAEF	PHCPLVSYGVYLP	VFVQAVFSYAX	
a273	GHDALPRV	PDIIICRSPAKL	PRTRFAGFPHCPLV	SYGVCLL	LVFVQAVFSYAX	
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1121>:

g274.seq

```

1   ATGGCGGGGC CGATTTTGT CGTCatCGCC AgcgTCGCTA TGTTTTTGT
51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAGGATG
101 GCAAGCATAT CGACATCCAG CTTCATCGGG ATGAAGAAGC CGTCAGACGG
151 CATATCGGGG TGCAGGTCCT CATTTCTCCC GATATGAATG CGGCAAAAGT
201 GTTTGTCGGC ggCgagtTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251 TGCACCCGAC CCGCAAGGCG GACGATCAAA CCGTCGCCCT CAAGCCCGTC
301 GGCAGCGCGC AGAACGGCAG GGCGGAATAT GAGGCGGTgt tcaaAACCCCT
351 TCCGCCGGCC AACCCTGGT ATGTGCGCGT GGAggacgCG GCAGGCGTGT
401 GGC GCGTCGA GAACAAATGG ATTACCAGCC AGGGCAATGC GGTGATTG
451 ACCCCGATGG ACAAACTTTT CAATAATGCA GGAAGCAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1122; ORF 274.ng>:

g274.pep

```

1   MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR
51  HIGVQVLISP DMNAAKVFGV GEFDGKQPLN LLLMHPTRKA DDQTVALKPV
101 GSAQNGRAEY EAVFKTLPPA NHWYVRVEDA AGVWRVENKW ITSQNAVDL
151 TPMDKLFNNA GSK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1123>:

m274.seq

```

1   ATGGCGGGGC CGATTTTGT CGTCATCGCC AGCGTCGCTA TGTTTTTGT
51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAAGACG
101 GCAAACATAT CGACATCCAG CTTCATCGGG ATGAAGAAGC CGTCAGACGG
151 CATATCGGGG TGCAGGTTCT CATTTCCCCC GATATGAATG CGGCAAAAGT
201 GTTTGTCGGC GCGGAGTTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251 TGCACCCGAC CCGCAAGGCG GACGATCAAA CCGTCGCCCT CAAGCCCGTC
301 GGCAGCGCGC AGAACGGCAG GGCGGAATAT GAGGCGGTGT TCAAACCCT
351 TTCGCCGACC AACCCTGGT ATGTGCGCGT GGAGGACGCG GCAGGCGTGT
401 GGC GCGTCGA GAACAAATGG ATTACCAGCC AAGGCAATGC GGTGATTG
451 ACCCCGATGG ACAAGCTTTT CAATAATACT GAAAGCAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1124; ORF 274>:

m274.pep

```

1   MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR
51  HIGVQVLISP DMNAAKVFGV GEFDGKQPLN LLLMHPTRKA DDQTVALKPV
101 GSAQNGRAEY EAVFKTLSPT NHWYVRVEDA AGVWRVENKW ITSQNAVDL
151 TPMDKLFNNT ESK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 274 shows 97.5% identity over a 163 aa overlap with a predicted ORF (ORF 274.ng) from *N. gonorrhoeae*:

g274/m274

	10	20	30	40	50	60
g274.pep	MAGPIFVVIASVAMFFVAQQHATDLVTDDYYKDGKHIDQLHRDEEAVRRHIGVQVLISP					
m274	MAGPIFVVIASVAMFFVAQQHATDLVTDDYYKDGKHIDQLHRDEEAVRRHIGVQVLISP					
	10	20	30	40	50	60
	70	80	90	100	110	120
g274.pep	DMNAAKVFGGGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTLPPA					
m274	DMNAAKVFGGGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTLSPT					
	70	80	90	100	110	120
	130	140	150	160		
g274.pep	NHWYVRVEDAAGVWRVENKWITSQNAVDLTPMDKLFNNAGSKX					
m274	NHWYVRVEDAAGVWRVENKWITSQNAVDLTPMDKLFNNNTESKX					
	130	140	150	160		

627

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1125>:

```
a274.seq
1   ATGGCGGGGC CGATTTTGT CGTCATCGCC AGCGTCGCTA TGTTTTTTGT
51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAAGACG
101 GCAAGCATAT CGACATCCAG CTTTCATCGGG ATGAAGAAGC CGTCAGACGG
151 CATATCGGGG TGCAGGTTCT CATTTCCTCCC GATATGAATG CGGCAAAAGT
201 GTTGTGTCGGC GGCAGAGTTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251 TGCACCCGAC CCGCAAGGCG GACGATCAAA CCGTCGCCCT CAAGCCCCTC
301 GGCAGCGCGC AGAACGGCAG GCGGGAATAT GAGGCGGTGT TCAAAACCCCT
351 TTCGCCGACC AACCCTGGT ATGTGCGCGT GGAGGACGCG GCAGGCGTGT
401 GCGCGGTCGA GAACAAATGG ATTACCAGCC AAGGCAATGC GGTCGATTTG
451 ACCCCGATGG ACAAACCTTT CAATAATACT GAAAGCAAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 1126; ORF 274.a>:

```
a274.pep
1   MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR
51  HIGVQVLISP DMNAAKVFGV GEFDGKQPLN LLLMHPTRKA DDQTVALKPV
101 GSAQNGRAEY EAVFKTLSPT NHWYVRVEDA AGVWRVENKW ITSQGNVDL
151 TPMDKLFNNT ESK*
```

m274/a274 100.0% identity in 163 aa overlap

	10	20	30	40	50	60
m274.pep	MAGPIFVVIIASVAMFFVAQQHATDLVTDDYYKDGKHIDIQLHRDEEAVRRHIGVQVLISP					
a274	MAGPIFVVIIASVAMFFVAQQHATDLVTDDYYKDGKHIDIQLHRDEEAVRRHIGVQVLISP					
	10	20	30	40	50	60
m274.pep	DMNAAKVFGGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEA VFKTLSPT					
a274	DMNAAKVFGGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEA VFKTLSPT					
	70	80	90	100	110	120
m274.pep	DMNAAKVFGGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEA VFKTLSPT					
a274	DMNAAKVFGGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEA VFKTLSPT					
	70	80	90	100	110	120
m274.pep	NHWYVRVEDAAGVWRVENKWIITSQGNVDLTPMDKLFNNTESKX					
a274	NHWYVRVEDAAGVWRVENKWIITSQGNVDLTPMDKLFNNTESKX					
	130	140	150	160		
m274.pep	NHWYVRVEDAAGVWRVENKWIITSQGNVDLTPMDKLFNNTESKX					
a274	NHWYVRVEDAAGVWRVENKWIITSQGNVDLTPMDKLFNNTESKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1127>:

```
g276.seq
1   atgattttgc cgccatccat gacgatgatg cggtcggcgg attcgacggt
51  ggtcaggcgg tgggcgacga tgatgccggt gcggttttcc atcaggcgtt
101 cgagcgcttg ttggacgagg cggttcggtt cggtgtccaa tgcgctggtg
151 gcttcgtcca ataataatat cggcgcgtct ttcaaaatgg cgcgggcat
201 ggcgacgctg tgccgctgtc cgccggataa gttgctgccg ttcgatccga
251 tgggctggtg cagtcgagc ggggatgcgt cgatcaggct ttgcaggttg
301 gcggcttgga gggcggacag gacttcggct tcgcccgcgt cgggacggct
351 gtatcgagcg ttttcaaca ggggtgcgtc aaacagggaat acgtcttggtg
401 agacgagggc gaattgggcg cgcaggcagt cgagtttgat gtcggcgatg
451 tcgataccgt ctatgcagat gttgccggca gacggttcga caaagcgggg
501 cagaaggttg acgacggttg atttgccgct gccggaacgt ccgaccaggg
551 cgacgcgttc gccttgctg atgtcgaggt tgaagttgtc gagggcttg
601 atgccgtctg aacgggtatc gacatcgacg ttgcggaagc tgatgcgcc
651 ttcgacacgc tgcggcgca gcgtgccttt gtcctgttcg ggcggggtg
701 cgagaaatgc acatacgccg tcggcgcgca ggaacatcgt ctgcataggg
751 atgctgatgt tggcaaggct tttgatgggg gcgtacattt gcagcatcgc
801 gacgatgaat gccataaatt cgccgatggt ggtgtag
```

This corresponds to the amino acid sequence <SEQ ID 1128; ORF 276.ng>:

g276.pep

628

```

1  MILPPSMTMM RSADSTVVRW WATMMPVRFS IRRSSACWTR RSDSLSNALV
51  ASSNNNIGAS FKMARAMATR CRCPDKLLP FDPMGWCSPS GDASIRLCRL
101 AAWRADRTSA SPASGRLYRT FSNRVSSNRN TSWETRANWA RRQSSLMSAM
151 SIPSMQMLPA DGSTKRGRL TTVDLPLPER PTRATRSPCL MSRLKLSRAL
201 MPSERYSTST LRKLMRPSTR CGASVPLSCS GGVSRNAHTP SAARNIVCIG
251 MLMLARLLMG AYICSIATMN AINSPMVV*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1129>:

```

m276.seq
1  ATGATTTTGC CGTCGTCCAT CACGATGATG CGGTCGGCCC CTTCGATGGT
51  GGTACAGCGG TGGGCGACGA TGATGCCGGT GCGGTTTTCC ATCAGGCGTT
101 CGAGCGCCTG TTGGACGAGG CGTTCGGATT CGTTGTCTAA TCGGCTGGTG
151 GCTTCGTCCA ATAATAATAT CGGCGCGTCT TTCAAATGG CGCGGGCAAT
201 GGCACGCGGT TGCCGCTGTC CGCCGGATAA GTTGCTGCCG TTCGATCCGA
251 TGGGCTGGTG CAGTCCGAGC GGGGAGCTGT CAATCAGGCT TTGCAGGTTG
301 GCGGTTTGGA GGGCGAACAG GACTTCGGCT TCGCCCGCGT CGGGACGGCT
351 GTATCGGACG TTTTCAAACA GGGTGTCGTC AAACAGGAAT ACGTCTTGGG
401 AGACGAGGGC GAATTGGGCG CGCAGGCAGT CGAGTTTGAT GTCGGCGATG
451 TCGATACCGT CTATGCAGAT GTTGCCGGCA GACGGTTCGA CAAAGCGGGG
501 CAGCAGGTTG ACGACGGTGG ATTTGCCGCT GCCGGAACGT CCGACCAGGG
551 CGACGCGTTC GCCTTGCTCTG ATGTCGAGGT TGAAGTTGTC GAGGGCTTTG
601 ATGCCGCTCT AACGGTATTC GACATCGACG TTGCGGAAGC TGATGCGCCC
651 TTCGACACGC TCGGTGCGA GCGTGCCCTT GTCCTGTTTC GCGGGGTGTG
701 CGAGAAATGC ACATACACCG TCGGCGGCGA GGAACATCGT CTGCATAGGG
751 ATGCTGATGT TGGCAAGGCT TTTGATGGGG GCGTACATT GCAGCATCGC
801 GACGATGAAT GCCATAAATT CGCCGATGGT GGTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1130; ORF 276>:

```

m276.pep
1  MILPSSITMM RSAPSMVVRW WATMMPVRFS IRRSSACWTR RSDSLSNALV
51  ASSNNNIGAS FKMARAMATR CRCPDKLLP FDPMGWCSPS GELSIRLCRL
101 AVWRANRTSA SPASGRLYRT FSNRVSSNRN TSWETRANWA RRQSSLMSAM
151 SIPSMQMLPA DGSTKGRSRL TTVDLPLPER PTRATRSPCL MSRLKLSRAL
201 MPSERYSTST LRKLMRPSTR CGASVPLSCS GGVSRNAHTP SAARNIVCIG
251 MLMLARLLMG AYICSIATMN AINSPMVV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 276 shows 96.8% identity over a 278 aa overlap with a predicted ORF (ORF 276.ng) from *N. gonorrhoeae*:

m276/g276

	10	20	30	40	50	60
m276.pep	MILPSSITMMRSAPSMVVRWATMMPVRFSIRRSSACWTRRSDSLSNALVASSNNNIGAS					
	:					
g276	MILPSSMTMMRSADSTVVRWATMMPVRFSIRRSSACWTRRSDSLSNALVASSNNNIGAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m276.pep	FKMARAMATRCRCPPDKLLPFDPMGWCSPSGELSIRLCRLAVWRANRTSASPASGRLYRT					
g276	FKMARAMATRCRCPPDKLLPFDPMGWCSPSGDASIRLCRLAAWRADRTSASPASGRLYRT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m276.pep	FSNRVSSNRNTSWETRANWARRQSSLMSAMSIPSMQMLPADGSTKGRSRLTTVDLPLPER					
g276	FSNRVSSNRNTSWETRANWARRQSSLMSAMSIPSMQMLPADGSTKGRRLTTVDLPLPER					
	130	140	150	160	170	180
	190	200	210	220	230	240
m276.pep	PTRATRSPCLMSRLKLSRALMPSERYSTSTLRKLMRPSTRCGASVPLSCSGGVSRNAHTP					
g276	PTRATRSPCLMSRLKLSRALMPSERYSTSTLRKLMRPSTRCGASVPLSCSGGVSRNAHTP					
	190	200	210	220	230	240

629

	250	260	270	279
m276.pep	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX			
g276	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX			
	250	260	270	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1131>:

```
a276.seq
1  ATGATTTTGC CGTCGTCCAT TACGATGATG CGGTCGGCCC CTTGATGGT
51  GGTCAAGCGG TGGGCGACGA TGATGCCGGT GCGGTTTTCC ATCAGGCGTT
101 CGAGCGCCTG TTGGACGAGG CGTTCGGATT CGTTGTCCAA TGCGCTGGTG
151 GCTTCGTCCA ATAATAATAT CGGCGCGTCT TTCAAATGG CGCGGGCAAT
201 GGCAACGCGT TGCCGCTGTC CGCCGGATAA GTTGCTGCCG TTCGATCCGA
251 TGGGCTGGTG CAGTCCGAGC GGTGATGCGT CGATCAGGCT TTGCAGGTTA
301 GCGGCTTGA GGGCGGATAG GACTTCGGCT TCGCCCGCGT CGGGACGGCT
351 ATATCGGACG TTTTCAAACA GGGTGTCTGC AAACAGGAAT ACGTCTTGGG
401 AGACGAGGGC AAATTGGGCG CGCAGGCAGT CGAGTTTGAT GTCGGCGATG
451 TCGATACCGT CTATGCAGAT GTTGCCGGCA GACGGTTCGA CAAAGCGGGG
501 CAGCAGGTTG ACGACGGTGG ATTTGCCGCT GCCGGAACGT CCGACCAGGG
551 CGACGCGTTC GCCTTGTCTG ATGTCGAGGT TGAAGCCGTC GAGGGCTTTG
601 ATGCCGTCCG AACGGTATTC GACATCGACG TTGCGGAAGC TGATGCGCCC
651 TTCGACACGC TGGCGTGCGA GCGTGCCTTT GTCCTGTTCG GGCGGGGTGT
701 CGAGAAATGC ACATACGCCG TCGGCGGCCG GGAACATCGT CTGCATAGGG
751 ATGCTAATGT TGGCAAGGCT TTTGATGGGG GCGTACATT GCAGCATCGC
801 GACGATGAAT GCCATAAATT CGCCGATGGT GGTGTAG
```

This corresponds to the amino acid sequence <SEQ ID 1132; ORF 276.a>:

```
a276.pep
1  MILPSSITMM RSAPSMVVRW WATMMPVRFS IRRSSACWTR RSDSLSNALV
51  ASSNNNIGAS FKMARAMATR CRCPDKLLP FDPMGWCSPS GDASIRLCRL
101 AAWRADRTSA SPASGRLYRT FSNRVSSNRN TSWETRANWA RRQSSLMSAM
151 SIPSMQMLPA DGSTKGRSRL TTVDLPLPER PTRATRSPCL MSRLKPSRAL
201 MPSEYSTST LRLKMRPSTR CGASVPLSCS GGVSRNAHTP SAARNIVCIG
251 MLMLARLLMG AYICSIATMN AINSPMVV*
```

m276/a276 98.2% identity in 278 aa overlap

	10	20	30	40	50	60
m276.pep	MILPSSITMMRSAPSMVVRW WATMMPVRFSIRRSSACWTRRSDSLSNALVASSNNNIGAS					
a276	MILPSSITMMRSAPSMVVRW WATMMPVRFSIRRSSACWTRRSDSLSNALVASSNNNIGAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m276.pep	FKMARAMATRCRCPDKLLPFDPMGWCSPSGELSI RLCRLAVWRANRTSASPASGRLYRT					
a276	FKMARAMATRCRCPDKLLPFDPMGWCSPSGELSI RLCRLAAWRADRTSASPASGRLYRT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m276.pep	FSNRVSSNRNTSWETRANWARRQSSLMSAMSIPSMQMLPADGSTKGRSRLTTVDLPLPER					
a276	FSNRVSSNRNTSWETRANWARRQSSLMSAMSIPSMQMLPADGSTKGRSRLTTVDLPLPER					
	130	140	150	160	170	180
	190	200	210	220	230	240
m276.pep	PTRATRSPCLMSRLKLSRALMPSEYSTSTLRLKMRPSTRCGASVPLSCSGGVSRNAHTP					
a276	PTRATRSPCLMSRLKPSRALMPSEYSTSTLRLKMRPSTRCGASVPLSCSGGVSRNAHTP					
	190	200	210	220	230	240
	250	260	270	279		
m276.pep	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX					
a276	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX					

630

250 260 270

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1133>:

```
g277.seq (partial)
  1 ..atggtacacg tcgccgtagc ttacgggtatt gccgtccggc gtttttgccc
  51 aaacgaggtc atagacgttt tccacgcctt gcagggtacat cgccaagcgt
 101 tcgatgccgt aggtaatctt gccgagtagc ggcgtgcaat cgataccgcc
 151 gacttggttg aaataggtaa actgggttac ttccatgccg ttgagccaga
 201 cttcccagcc caaacccac gcaccgaggg tgggggtttc ccagtcgtct
 251 tcgacaaagc ggatgtcgtg gactttggga tcgatgcca attcgcgcag
 301 ggagtcgaga tagaggtctt ggatattggc gggggcgggt ttgagggcga
 351 cttggaattg gtaatagtgt tgcaggcggg tgggggtgtc gccgtagcgg
 401 ccgtctttgg ggcggcggct gggttggacg taggcggcaa accaaggctc
 451 ggggcccagc gcgcgcaggc aggtggcggg atgggatgtg ccggcaccga
 501 cttccatgtc gaagggttg atgacggtgc agcctttgtc tgcccagaag
 551 gtttgcatgt tgaagatgat ttggtggaag gtaagcatgg cttattgttc
 601 gataaaataa aggtttttatt ttactgtttc catagccgct tgaatagatt
 651 tatctcgaag acagcctga
```

This corresponds to the amino acid sequence <SEQ ID 1134; ORF 277.ng>:

```
g277.pep (partial)
  1 ..MVHVAVAYGI AVRRFCPNEV IDVFHALQVH RQAFDAVGNF AEYGRAIDTA
  51 DLLEIGKLG Y FHAVEPDFPA QTPRTEGGVF PVVFDKADV DFGIDAQFAQ
 101 GVEIEVL DIG GGGFEGDLEL VIVLQAVGVV AVAAVFGAAA GLDVGGKPR L
 151 GAERAQAGG MGCAGTDFHV EGLDDGAAPV CPEGLQFEDD LLEGKHGLLF
 201 DKIKVLFYCF HSRLNRFISK TA*
```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1135>:

```
m277.seq
  1 ATGCCCGCT TTAGGACAA GCTCGTAGGC AGGCAGGGCG AGGGCGGCGT
  51 TTTCTTCGGC AAGCAGGCGT TTGGCTTTCG CTTCTAGTTC GTTGAAGTGG
 101 CGCAGCAGCC AGTCGGCATC GCTGTATTCG AAGTTGTAGG TGGATTGCTC
 151 GACTTCGTTT TGGTGGTACA CGTCGCCGTA GGTGACGGTG TTGCCGTCGA
 201 GCGTTTTTGC CCAAACGAGG TCGTAGACGT TTTCTACACC TTGCAAGTAC
 251 ATCGCCAAGC GTTCGATGCC GTAGGTGATT TCGCCGAGTA CGGGCGTGCA
 301 GTCGATGCCG CCGACTTGTT GGAAATAGGT AAAGTGGGTT ACTTCCATGC
 351 CGTTGAGCCA GACTTCCCAG CCCAAACCCC ACGCGCCGAG GGTGGGGTTT
 401 TCCAGTCGT CTTGACAAA GCGGATGTCG TGGACTTTGG GATCGATGCC
 451 CAATTCGCGC AGAGAGTCGA GATAGAGGTC TTGGATATTG GCGGGAGCGG
 501 GCTTGAGGGC GACTTGAAT TGGTAATAGT GTTGACGGCG GTTGGGGTTG
 551 TCGCCGTAGC GGCCGTCTTT GGGGCGGCGG CTGGGTGGA CGTAGGCGGC
 601 AAACCAAGGC TCGGGGCCGA GTGCGCGCAG GCAGGTGGCG GGATGGGATG
 651 TGCCGGCACC GACTTCCATG TCGAAGGGTT GGATGACGGT GCAGCCTTTG
 701 TCTGCCCAGA ATGTTGCAG TTTGAAGATG ATTTGTTGGA AGGTAAGCAT
 751 GGCTTATGA
```

This corresponds to the amino acid sequence <SEQ ID 1136; ORF 277>:

```
m277.pep
  1 MPRFEDKLVG RQEGGVFFG KQAFGLRFV VELAQQPVG AVFEVVGGLL
  51 DFVLVVHVAV GDGVAVERFC PNEVVDVFT LQVHRQAFDA VGDFAEYGRA
 101 VDAADLLEIG KLG Y FHAVEP DFPAQTPRAE GGVFPVVDK ADVVDFGIDA
 151 QFAQRVEIEV LDIGSGLEG DLELVIVLQA VGVVAVAVF GAAAGLDVGG
 201 KPRLGAECAQ AGGGMGCAGT DFHVEGLDDG AAFVCPECLQ FEDDLLEGKH
 251 GL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 277 shows 90.0% identity over a 221 aa overlap with a predicted ORF (ORF 277.ng) from *N. gonorrhoeae*:

g277/m277

g277.pep

10 20 30
MVHVAVAYGIAVRRFCPNEVIDVFHALQVH

631

```

                                     :|||||: |:|:|||||:|:|:|
m277      GLRFVVVELAQQPVGIAVFEVVGGLLDFVLVVHVAVGDGVAVERFCPNEVVDVFTLQVH
           30      40      50      60      70      80

           40      50      60      70      80      90
g277.pep   RQAFDAVGNFAEYGRAIDTADLLEIGKLGYPHAVEPDFPAQTPRTEGGVFPVVFDDKADV
           |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
m277      RQAFDAVGDFAEYGRAVDAADLLEIGKLGYPHAVEPDFPAQTPRAEGGVFPVVFDDKADV
           90      100     110     120     130     140

           100     110     120     130     140     150
g277.pep   DFGIDAQFAQGVIEVLDIGGGGFEGLDELIVIVLQAVGVVAVAAVFGAAAGLDVGGKPR
           |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
m277      DFGIDAQFAQGVIEVLDIGGSGLEGLDELIVIVLQAVGVVAVAAVFGAAAGLDVGGKPR
           150     160     170     180     190     200

           160     170     180     190     200
g277.pep   GAERAQAGGGMGCAGTDFHVEGLDDGAAFVCPEGLQFEDDLLEGKHGLL
           ||| |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
m277      GAECAQAGGGMGCAGTDFHVEGLDDGAAFVCPECLQFEDDLLEGKHGLX
           210     220     230     240     250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1137>:

```

a277.seq
1  ATGCCCCGCT TTGAGGACAA GCTCGTAGGC AGGCAGGGCG AGGGCGGCGT
51  TTTCTTCGGC AAGCAGGCGT TTGGCTTGCG CTTCGTAGTC GTTGAAGTGG
101 CGCAGCAGCC AATCGGCATC GCTGTATTCG AAGTTGTAGG TGGATTGTTT
151 GACTTCGTTT TGGTGGTACA CGTCGCCGTA AGTTACTGTA TTACCGTCCA
201 GCGTTTTTGC CCAAACGAGG TCATAGACGT TTTCCACGCC TTGCAGGTAC
251 ATCGCCAAGC GTTCGATGCC GTAGGTGATT TCGCCAGTA CGGGGGTGCA
301 TCGATGCCG CCGACTTGTT GGAAATAGGT GAAC TGGGTT ACTTCCATAC
351 CGTTGAGCCA GACTTCCCAG CCCAAACCCC ACGCGCCGAG GGTGGGGTTT
401 TCCCAGTCGT CTTGACAAA GCGGATGTCG TGCAC TTTGG GGTGATGCC
451 CAATTCGCGC AGGGAGTCGA GATAGAGGTC TTGGATATTG GCGGGAGCGG
501 GCTTGAGGGC GACTTGGAAT TGGTAATAGT GTTGCAGGCG GTTGGGGTTG
551 TCGCCGTAGC GACCGTCTTT GGGGCGGCGG CTGGGTTGGA CGTAGGCGGC
601 AAACCAAGGC TCGGGGCCGA GTGCGCGCAG ACAGGTGGCG GGATGGGATG
651 TGCCGGCACC GACTTCCATG TCGAAGGGT GGATGACGGT GCAGCCTTTG
701 TCTGCCCAGA ATGTTTGCAG TTTGAAGATG ATTTGTTGGA AGGTAAGCAT
751 GGCTTATGA

```

This corresponds to the amino acid sequence <SEQ ID 1138; ORF 277.a>:

```

a277.pep
1  MPRFEDKLVG RQEGGVVFFG KQAFGLRFVV VELAQQPIGI AVFEVVGGLF
51  DFVLVVHVAV SYCITVQRFC PNEVIDVFHA LQVHRQAFDA VGDFAEYGGA
101 VDAADLLEIG ELGYFHTVEP DFPAQTPRAE GGVFPVVFDD ADVVHFGVDA
151 QFAQGVIEV LDIGGSGLEG DLELVIVLQA VGVVAVATVF GAAAGLDVGG
201 KPRLGAECAQ TGGGMGCAGT DFHVEGLDDG AAFVCPECLQ FEDDLLEGKH
251 GL*

```

m277/a277 92.5% identity in 252 aa overlap

```

           10      20      30      40      50      60
m277.pep   MPRFEDKLVGRQEGGVVFFGKQAFGLRFVVVELAQQPVGIAVFEVVGGLLDFVLVVHVAV
           |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
a277      MPRFEDKLVGRQEGGVVFFGKQAFGLRFVVVELAQQPVGIAVFEVVGGLDFVLVVHVAV
           10      20      30      40      50      60

           70      80      90      100     110     120
m277.pep   GDGVAVERFCPNEVVDVFTLQVHRQAFDAVGDFAEYGRAVDAADLLEIGKLGYPHAVEP
           : :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
a277      SYCITVQRFCPNEVIDVFHALQVHRQAFDAVGDFAEYGGAVDAADLLEIGELGYFHTVEP
           70      80      90      100     110     120

           130     140     150     160     170     180

```

632

```

m277.pep      DFPAQTPRAEGGVFPVVFVKADVVDFGIDAQFAQRVEIEVLDIGGSGLEGDLVLVQLQA
                |||||
a277          DFPAQTPRAEGGVFPVVFVKADVVHFGVDAQFAQGVIEVLDIGGSGLEGDLVLVQLQA
                130      140      150      160      170      180

                190      200      210      220      230      240
m277.pep      VGVVAVAAVFGAAAGLDVGGKPRLLGAECAQAGGGMGCAGTDFHVEGLDDGAAAFVCPCECLQ
                |||||
a277          VGVVAVATVFGAAAGLDVGGKPRLLGAECAQTGGGGMGCAGTDFHVEGLDDGAAAFVCPCECLQ
                190      200      210      220      230      240

                250
m277.pep      FEDDLLEGKHGLX
                |||||
a277          FEDDLLEGKHGLX
                250

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1139>:

```

g278.seq (partial)
1   ttgcgtgcaa tcacgcccgg tgcgattttt tcgacagggg cgggtcaaagt
51  tgtattaatc ggacctttgc cgtcgatagg ccgacccaat gcatcgacga
101 cgcgtccgac caattcgcg ttcgaccgga cttctaaat acggccggta
151 caggtaaccg tgcgccttc ttaatatgt tcgtactcgc ccaacactac
201 ggcaccgacg gagtgcgcgt ccaggttcat cgccaagcct aaagtgttac
251 ccgggaattc gagcatctca ccttgcatg catctgacaa accatggatg
301 cgaacgatac cgtcagttac cgaaatcacc gtaccacggg tactcacttc
351 ggcattttaca gacagatttt cgatcttggc ttaatcaga tcgctaattt
401 cagcaggatt aagctgcatg aaaactctcc taattcgta tagtcgtgta
451 caaagcactc agttgcctt gtacagacaa atccaaaacc tgatcaccca
501 cttcaacttt ta...

```

This corresponds to the amino acid sequence <SEQ ID 1140; ORF 278.ng>:

```

g278.pep (partial)
1   LRAITPGAIF STGAVKVVLI GPLPSIGRPN ASTTRPTNSR PTGTSKIRPV
51  QVTVSPSLIC SYSPNTTAPT ESRSRFIAKP KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPRVLTSFT DRFSILALIR SLISAGLSCM KTLIRHSRV
151 QSTQFALYRQ IQNLITHFNF...

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1141>:

```

m278.seq..
1   TTGCGCGCAA TCACGCCCCG TGCGATTTT TCGATAGGGG CGGTCAAAGT
51  TGTATTAATC GGGCCTTTGC CGTCGATAGG CCGACCCAAT GCATCAACGA
101 CGCGTCCGAC CAGTTCGCGT CCGACCGGCA CTTCCAAGAT ACGACCGGTA
151 CAGGTAACCG TGTCGCCTTC TTTAATGTGT TCGTACTCGC CCAACACTAC
201 GGCGCCGACG GAGTCGCGCT CCAGGTTTAT CGCCAAGCCG AAAGTGTTAC
251 CCGGGAATTC GAGCATCTCA CCTTGATTTG CATCTGACAA ACCATGGATG
301 CGAACGATAC CGTCAGTTAC CGAAATTACC GTACCACAGG TACGCACTTC
351 GGCATTTACA GACAGATTTT CGATCTTGGC TTTAATCAAA TCGCTAATTT
401 CAGCAGGATT AAGCTGCATG AAAACTCTCC TAATTCGTCA TAGTCGTGTA
451 CAAGGCACTC AATTTCCTT GTACAGACAA ATCCAAAACC TGATCACCCA
501 CTTCAACTTT TATGCCGCCA ATCAGCTCCG GTTCGATTTC GACAGAGATT
551 TTCAGCTCGC TGTCGAAACG CTTATTCAGC ATTTGCACCA ACTCGCCGAC
601 CTGTTTGTGC GTCAACGGAT AGGCACTGTA AATGACGGCA GATTGTATAT
651 GGTGGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1142; ORF 278>:

```

m278.pep
1   LRAITPGAIF SIGAVKVVLI GPLPSIGRPN ASTTRPTSSR PTGTSKIRPV
51  QVTVSPSLMC SYSPNTTAPT ESRSRFIAKP KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPQVRTSAFT DRFSILALIK SLISAGLSCM KTLIRHSRV
151 QGTQFALYRQ IQNLITHFNF YAANQLRFDF DRDFQLAVET LIQHLHLAD
201 LFVGQRIGTV NDGRFDMVE*

```

Computer analysis of this amino acid sequence gave the following results:

633

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 278 shows 95.9% identity over a 170 aa overlap with a predicted ORF (ORF 278.ng) from *N. gonorrhoeae*:

g278/m278

	10	20	30	40	50	60
g278.pep	LRAITPGAIFSTGAVKVVLI	GPLPSIGRPNASTTRPTNSRPTGT	SKIRPVQVT	VSPSLIC		
m278	LRAITPGAIFSIGAVKVVLI	GPLPSIGRPNASTTRPTSSRPTGT	SKIRPVQVT	VSPSLMC		
	10	20	30	40	50	60
	70	80	90	100	110	120
g278.pep	SYPNNTAPT	ESRSRFIAKPKVLP	GNSSISPCIASDKP	WMRTIPSVTEIT	VPRVLTSAFT	
m278	SYPNNTAPT	ESRSRFIAKPKVLP	GNSSISPCIASDKP	WMRTIPSVTEIT	VPRVLTSAFT	
	70	80	90	100	110	120
	130	140	150	160	170	
g278.pep	DRFSILALIRSLISAGL	SCMKTLLIRHSRVQSTQ	FALYRQIQNLITHFNF			
m278	DRFSILALIKSLISAGL	SCMKTLLIRHSRVQSTQ	FALYRQIQNLITHFNF	YAAQLRFDF		
	130	140	150	160	170	180
m278	DRDFQLAVETLIQHLHQLADLFV	QGRIGTVNDGRFDMVE*				
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1143>:

a278.seq

1	TTGCGCGCAA	TCACGCCCGG	TGCGATTTTT	TCGATAGGGG	CGGTCAAAGT
51	TGTATTAATC	GGGCCTTTGC	CGTCGATAGG	CCGACCCAAT	GCATCAACGA
101	CGCGTCCGAC	CAGTTCGCGT	CCGACCGGCA	CTTCCAAGAT	ACGACCGGTA
151	CAGGTAACCG	TGTCGCCTTC	TTTAATATGT	TCGTGCTCGC	CCAACACTAC
201	GGCGCCGACG	GAGTCGCGCT	CCAGGTTCAT	CGCCAAGCCG	AAAGTGTTAC
251	CCGGGAATTC	GAGCATCTCA	CCTTGCAATTG	CATCTGACAA	ACCATGGATG
301	CGAACGATAC	CGTCAGTTAC	CGAAATCACC	GTACCACGGG	TACGCACTTC
351	GGCATTTACA	GACAGATTTT	CGATCTTGGC	TTTAATCAAA	TCGCTAATTT
401	CAGCAGGATT	AAGCTGCATG	AAACTCTCC	TAATTCGTCA	TAGTCGTGTA
451	CAAGGCACTC	AATTTGCCTT	GTACAGACAA	ATCCAAAACC	TGATCACCCA
501	CTTCAACTTT	TATGCCGCCA	ATCAGCTCCG	GTTTCGATTTC	GACAGAGATT
551	TTCAGCTCGC	TGTCGAAACG	CTTATTCAGC	ATTTGCGCCA	ACTCGCCGAC
601	CTGTTTGTCG	GTCACGGAT	AGGCACTGTA	AATGACGGCA	GATTTGATAT
651	GGTTGAATGA				

This corresponds to the amino acid sequence <SEQ ID 1144; ORF 278.a>:

a278.pep

1	LRAITPGAIF	SIGAVKVVLI	GPLPSIGRPN	ASTTRPTSSR	PTGTSKIRPV
51	QVTVSPSLIC	SCSPNNTAPT	ESRSRFIAKP	KVLPGNSSIS	PCIASDKPWM
101	RTIPSVTEIT	VPRVRTSAFT	DRFSILALIK	SLISAGLSCM	KTLLIRHSRV
151	QGTQFALYRQ	IQNLITHFNF	YAAQLRFDF	DRDFQLAVET	LIQHLRQLAD
201	LFVGQRIGTV	NDGRFDMVE*			

m278/a278 98.2% identity in 219 aa overlap

	10	20	30	40	50	60
m278.pep	LRAITPGAIFSIGAVKVVLI	GPLPSIGRPNASTTRPTSSRPTGT	SKIRPVQVT	VSPSLMC		
a278	LRAITPGAIFSIGAVKVVLI	GPLPSIGRPNASTTRPTSSRPTGT	SKIRPVQVT	VSPSLIC		
	10	20	30	40	50	60
	70	80	90	100	110	120
m278.pep	SYPNNTAPT	ESRSRFIAKPKVLP	GNSSISPCIASDKP	WMRTIPSVTEIT	VPRVRTSAFT	
a278	SCSPNNTAPT	ESRSRFIAKPKVLP	GNSSISPCIASDKP	WMRTIPSVTEIT	VPRVRTSAFT	
	70	80	90	100	110	120

634

	130	140	150	160	170	180
m278.pep	DRFSILALIKSLISAGLSCKMTLLIRHSRVQGTQFALYRQIQNLITHFNFYAANQLRFDF					
a278	DRFSILALIKSLISAGLSCKMTLLIRHSRVQGTQFALYRQIQNLITHFNFYAANQLRFDF					
	130	140	150	160	170	180
	190	200	210	220		
m278.pep	DRDFQLAVETLIQHLHQLADLFVGGQRIGTVNDGRFDMVEX					
a278	DRDFQLAVETLIQHLHQLADLFVGGQRIGTVNDGRFDMVEX					
	190	200	210	220		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1145>:

g279.seq

```

1  atgacgcgga tttgcggctg cttgatttca acggttttga gtgtttcggc
51  aagtttgctg gcggcgggtt tcatcaggct gcaatgggaa ggaacggata
101 ccggcagcgg cagggcgctg ttggctccgg cttctttggc ggcagccatg
151 gtgcgtccga cggcgccggc gttgcctgca atcacgactt gtccgggcga
201 gttgaagttg acggcttcga ccacttcgcc ctgtgcggat tcggcacaaa
251 tctgcctgac ctgttcattc tccaaaccca aaatggccgc cattgcgcct
301 acgccttgcg gtacggcgga ctgcatcagt tcggcgcgca ggcggacgag
351 tttgacggca tcggcaaaat ccaatgcttc ggcggcgaca agcgcggtgt
401 attcgccgag gctgtgtccg gcaacggcgg caggcgtttt gccgcccact
451 tccaaatag

```

This corresponds to the amino acid sequence <SEQ ID 1146; ORF 279.ng>:

g279.pep

```

1  MTRICGCLIS TVLSVSASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  VRPTAAALPA ITTCPGELKL TASTTSPCAD SAQICLTCSS SKPKMAAIAP
101 TPCGTADCIS SARRRSLTA SAKSNASAAT SAVYSPRLCP ATAAGVLPPT
151 SK*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1147>:

m279.seq

```

1  ATAACGCGGA TTTGCGGCTG CTTGATTCA ACAGTTTTCG GGGCTTCGGC
51  AAGTTTGTCG GCGGCGGGTT TCATCAGGCT GCAATGGGAA GGTACGGACA
101 CGGCAGCGG CAGGCGCGGT TTGGCACCGG CTTCTTTGGC GGCAGCCATG
151 GCGCGTCCGA CGGCGCGGCG GTTGCTGCA ATCACGATT GTCCGGGTGA
201 GTTGAAGTTG ACGGCTTCGA CCACCTCGCT TTGGGCGGCT TCGGCACAAA
251 TGGCTTTAAC CTGCTCATCT TCCAAGCCGA GAATCGCCGC CATTGCGCCC
301 ACGCCTTGCG GTACGGCGGA CTGCATCAGT TCGGCGCGCA GGCGCACGAG
351 TTTGACCGCG TCGGCAAAAT TCAATGCGCC GCGGCAACG AGTGCGGTGT
401 ATTCGCCGAG GCTGTGTCCG GCAACGCGCG CAGGCGTTT GCCGCCCGCT
451 TCTAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 1148; ORF 279>:

m279.pep

```

1  ITRICGCLIS TVFRASASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  ARPTAAALPA ITICPGELKL TASTTSLWAA SAQMALTCSS SKPRIAAIAP
101 TPCGTADCIS SARRRSLTA SAKFNAPAA SAVYSPRLCP ATAAGVLPPT
151 SK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 279 shows 89.5% identity over a 152 aa overlap with a predicted ORF (ORF 279.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m279.pep	ITRICGCLISTVFRASASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMARPTAAALPA					
g279	MTRICGCLISTVLSVSASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMVRPTAAALPA					
	10	20	30	40	50	60
	70	80	90	100	110	120

```

m279.pep      ITICPGELKLTASTTSLWAASAQMALTCSSSKPRIAAIAPTPCGTADCISSARRRTSLTA
                ||||||||||||||| | |||: |||||||||::||| |||||||||||||||
g279          ITTCPGELKLTASTTSPCADSAQICLTSSSKPKMAAIAPTPCGTADCISSARRRTSLTA
                70          80          90          100          110          120

                130          140          150
m279.pep      SAKFNAPAATSAVYSPRLCPATAAGVLP PASKX
                ||| || ||||||||||| |||||||||: |||
g279          SAKSNASAATSAVYSPRLCPATAAGVLP PPTSKX
                130          140          150

```

a279.seq

1	ATGACNCNGA	TTTGCGGGTG	CTTGATTTCA	ACGGTTTNNNA	GGGCTTCGGC
51	GAGTTTGTCG	GCGGCGGGTT	TCATGAGGCT	GCAATTGGGAA	GGTACNGACA
101	CNNGCAGCGG	CAGGGCGCGT	TTGGCGCCGG	CTCTTTTGGC	GGCAAGCATA
151	GCGCGCTCGA	CGGCGGCGGC	ATTGCTTGCA	ATCACGACTT	GTCGCGGCGA
201	GTTGAAGTTG	ACGGCTTCAA	CCACTTCATC	CTGTGCGGAT	TCGGCGCAAA
251	TTTGTTTTAC	CTGTTTCATCT	TCCAAGCCGA	GAATCGCCGC	CATTGCGCCC
301	ACGCCTTGCG	GTACGGCGGA	CTGCATCAGT	TCGGCGCGCA	NGCGCACGAG
351	TTTGACCGCG	TCGGCAAAAT	CCAATGCGCC	GGCGGCAACN	AGTGCGGTGT
401	ATTCGCCGAN	GCTGTGTCCG	GCAACGGCGG	CAGGCGTTTT	GCCGCCCGCT
451	TCCGAATAG				

a279.pep					
1	MTXICGCLIS	TVXRASASLS	AAGFMRLQWE	GTDTGSGRAR	LAPASLAASI
51	ARSTAAALPA	ITTCPGELKL	TASTTSSCAD	SAQICFTCSS	SKPRIAAIAP
101	TPCGTADCIS	SARXRTSLTA	SAKSNAAPAAT	SAVYSPXLCP	ATAAGVLPPA
151	SE*				

		10	20	30	40	50	60
m279.pep		ITRICGCLISTVFRASASLSAAGFIRLOWEGTDTGSGRARLAPASLAAAMARPTAAALPA					
		:					
a279		MTXICGCLISTVXRASASLSAAGFMRLQWEGTDTGSGRARLAPASLAASIARSTAAALPA					
		10	20	30	40	50	60
		70	80	90	100	110	120
m279.pep		ITICPGELKLTASTTSLWAASAQMALTCSSSKPRIAAIAPTTCGTADCISSARRRTSLTA					
a279		ITTCPGELKLTASTTSSCADSAQICFTCSSSKPRIAAIAPTTCGTADCISSARXRTSLTA					
		70	80	90	100	110	120
		130	140	150			
m279.pep		SAKFNAPAATSAVYSPRLCPATAAGVLPASKX					
a279		SAKSNAPAATSAVYSPXLCPPASEX					
		130	140	150			

The primer described in Table 1 for ORF 279 was used to locate and clone ORF 279. ORF 279 was cloned in pET and pGex vectors and expressed in E.coli as above-described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 2A shows the results of affinity purification and Figure 2B shows the expression in E.coli. Purified GST-fusion protein was used to immunize mice whose sera were used for ELISA (positive result), FACS analysis (Figure 2C), western blot (Figure 2D). These experiments confirm that 279 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 279 are provided in Figure 6. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al.

1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 279 and the amino acid sequence encoded thereby is provided herein.

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1151>:

g280.seq

```

1  atgaaacacc tcaaacttac ccttattgcc gcattgctgg ccaccgccgc
51  aactgccgca ccccttccgg ttgtaaccag tttagcgatt ttaggcgacg
101 tagccaaaca aatcggcggt gagcgcgtag ccgtacaaag cctcgtcggg
151 gccaaaccaag atactcatgc ctatcacatg accagtggcg acattaaaaa
201 aatccgcagt gcaaaactcg tcctgctcaa cggcttggga cttgaagccg
251 ccgacatcca acgcgccgtc aaacagagca aagtatccta tgccgaagcg
301 accaaaggca tccaaccctt caaagccgaa gaagaaggcg gacaccatca
351 cgaccaccat cagaccacg atcatgacca cgaaggacac caccacgacc
401 acggcgaata tgaccccccac gtctggaacg accctgttct tatgtccgac
451 tatgcccata acgtcgctga aaccctgata aaggccgatc ccgaaggcaa
501 agtttattat caacaacgct tgggcaacta ccaaattgcag cttaaaaaac
551 tgcacagcga cgcacaagcc gcatttaatg ccgtccctgc cgccaaacgc
601 aaagtcctga cggggcacga cgcattttcc tacatgggca accgctacaa
651 catcagcttc atcgccccgc aaggcgtgag cagcgaagcc gagccgtccg
701 ccaaacaagt cgcgcccatc atccggcaaa tcaaacgcga aggcatacaa
751 gccgtattta ccgaaaatat caaagacacc cgcattggtg accgcatcgc
801 caaagaaacc ggcgtcaacg tcagcggcaa actgtattcc gacgcactcg
851 gcaacgcgcc cgcagacacc tacatcgcca tgtaccgcca caacgtcgaa
901 gccttgacca acgcatgaa gcaataa

```

This corresponds to the amino acid sequence <SEQ ID 1152; ORF 280.ng>:

g280.pep

```

1  MKHLKLTLIA ALLATAATAA PLPVVTSFSI LGDVAQIGG ERVAVQSLVG
51  ANQDTHAYHM TSGDIKKIRS AKLVLLNGLG LEAADIQRAV KQSKVSYAEA
101  TKGIQPLKAE EEGHHHDHHD HDHHDHDEGH HHDHGEYDPH VWNDPVLMSD
151  YAQNVAETLI KADPEGKVYY QQLGNVYQMQ LKKLHSDAQA AFNAVPAKR
201  KVLTHGDAFS YMGNRYNISF IAPQVSSEA EPSAKQVAI IRQIKREGIK
251  AVFTENIKDT RMVDRIAKET GVNVSGLKLYS DALGNAPADT YIGMYRHNVE
301  ALTNAMKQ*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1153>:

m280.seq

```

1  ATGAAACACC TCAAACACAC CCTTATTGCC GCATTGCTGA CCGCCTCCGC
51  AACTGCCGCC CCCCTGCCGG TTGTAACCAG CTTCAGCATT TTAGGCGACG
101 TAGCCAAACA AATCGGCGGA GAGCGCGTAT CCATACAAAG TTTGGTCGGA
151 GCCAACCAAG ATACGCACGC CTATCATATG ACCAGTGGCG ACATTAAAAA
201 AATCCGCAGT GCAAAACTCG TCCTGTCTAA CGGCTTAGGA CTTGAAGCTG
251 CCGATGTGCA ACGCGCCGTC AAACAAAGCA AAGTATCCTA TACCGAAGCG
301 ACCAAAGGCA TCCAACCCCT CAAAGCCGAA GAAGAAGGCG GACACCATCA
351 CGACCACGAT CATGACCACG AAGGACACCA CCATGACCAC GCGGAATATG
401 ACCCGCACGT CTGGAACGAC CCCGTCCTTA TGTCCGCTTA TGCCCAAAAC
451 GTTGCCAAAG CCCTGATAAA GGCCGATCCC GAAGGCAAAG TTTATTATCA
501 ACAACGCTTG GGCAACTACC AAATGCAGCT CAAAAAAGT CACAGCGACG
551 CACAAGCCGC ATTTAATGCC GTCCCTGCTG CCAAACGCAA AGTCCTGACC
601 GGGCACGATG CCTTTTCCTA TATGGGCAA CATTACCATA TCGAATTCAT
651 CGCCCCGCAA GCGGTGAGCA GCGAAGCCGA GCCTTCGGCC AAACAAGTCG
701 CCGCCATCAT CCGACAAATC AAACGCGAAG GCATCAAAGC CGTCTTACC
751 GAAAACATCA AGGACACCCG TATGGTTGAC CGTATCGCCA AAGAAACCGG
801 TGTCAACGTC AGCGGCAAAC TGTATTCCGA CGCACTCGGC AACCGCCCCG
851 CAGACACCTA CATCGGAATG TACCGCCACA ACATCAAAGC CTTGACCAAC
901 GCGATGAAGC AATAA

```

This corresponds to the amino acid sequence <SEQ ID 1154; ORF 280>:

m280.pep

```

1  MKHLKLTLIA ALLTASATAA PLPVVTSFSI LGDVAQIGG ERVSIQSLVG
51  ANQDTHAYHM TSGDIKKIRS AKLVLLNGLG LEAADVQRAV KQSKVSYTEA
101  TKGIQPLKAE EEGHHHDHHD HDHEGHHHDH GEYDPHVWND PVLMSAYQON
151  VAKALIKADP EGKVYYQQL GNYQMLKKL HSDAQA AFNA VPAKRKVL

```

ORF 280 shows 93.8% identity over a 308 aa overlap with a predicted ORF (ORF 280.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m280.pep	MKHLKLTLIAALLTASATAAPLPVVT	SFSILGDVAKQIGGERVSIQSLVGANQDTHAYHM				
g280	MKHLKLTLIAALLATAATAAPLPVVT	SFSILGDVAKQIGGERVAVQSLVGANQDTHAYHM				
	10	20	30	40	50	60
	70	80	90	100	110	119
m280.pep	TSGDIKKIRS	AKLVLLNGLGLEAADVQRAVKQSKVSYTEATKGIQPLKAE	EEGGHHHDH-			
g280	TSGDIKKIRS	AKLVLLNGLGLEAADIQRAVKQSKVSYAEATKGIQPLKAE	EEGGHHHDH			
	70	80	90	100	110	120
	120	130	140	150	160	170
m280.pep	---	DHDHEGHHHDHGEYDPHVWNDPVLMSAYAQN	VAKALIKADPEGKVYYQ	QRLGNYQMQ		
g280	HDHDHD	HEGHHHDHGEYDPHVWNDPVLMSDYAQN	VAETLIKADPEGKVYYQ	QRLGNYQMQ		
	130	140	150	160	170	180
	180	190	200	210	220	230
m280.pep	LKKLHSDAQA	AFNAVPAAKRKVLTGHDAFSYMGKRYHIEFIAPQGSSEAEPSAKQVA	AI			
g280	LKKLHSDAQA	AFNAVPAAKRKVLTGHDAFSYMGNRYNISFIAPQGSSEAEPSAKQVA	AI			
	190	200	210	220	230	240
	240	250	260	270	280	290
m280.pep	IRQIKREGIKAVFTENIKDTRMVDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHN	IK				
g280	IRQIKREGIKAVFTENIKDTRMVDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHN	VE				
	250	260	270	280	290	300
	300					
m280.pep	ALTNAMKQX					
g280	ALTNAMKQX					

a280.seq

1	ATGAAACACC	CCAAACTCAC	CCTTATCGCC	GCATTGCTGA	CCACTGCCGC
51	AACTGCCGCC	CCCCTGCCGG	TTGTAACCAG	CTTCAGCATT	TTAGGCGACG
101	TAGCCAAACA	AATCGGCGGA	GAGCGCGTAT	CCATACAAG	TTTGGTCGGA
151	GCCAACCAAG	ATACGACAGC	CTATCATATG	ACCAGCGGCG	ACATAAAAA
201	AATCCGCAGT	GCAAAACTCG	TCTGTATTAA	CGGCTTAGGA	CTTGAAGCTG
251	CCGACATCCA	ACGTGCCGTC	AAACAGAGCA	AAGTATCCTA	TGCCGAAGCG
301	ACCAAAGGCA	TCCAACCCCT	CAAAGCCGAA	GAAGAAGGCG	GACACCATCA
351	CGACCACGAT	CATGACCACG	ACCATGACCA	CGAAGGACAC	CACCACGACC
401	ACGGCGAATA	TGACCCCCAC	GTCTGGAACG	ACCCCTCTCT	TATGTCCGCG
451	TATGCCCAAA	ACGTCCGCGA	AGCCCTGATA	AAGCCGACCC	CCGAAGGCAA
501	AGTTTATTAT	CAACAACGCT	TGGGCAACTA	CCAAATGCAG	CTCAAAAAAC
551	TGCACAGTGA	CGCACAAGCC	GCATTTAATG	CCGTCCCTGC	CGCCAAACGC
601	AAAGTCTCTG	CCGGGACAGA	TGCCTTTTCC	TATATGGGCA	AACGTTACCA
651	TATCGAATTC	ATCGCCCCAC	AAGGTGTGAG	CAGCGAAGCC	GAGCCTTACG
701	CCAACAAGT	CGCCGCGATC	ATCCGACAAA	TCAAACGCGA	AGGCATCAAA
751	GCCGTATTTA	CCGAAATAT	CAAAGACACC	CGCATGGTTG	ACCGCATCGC

638

801 CAAAGAAACC GGTGTCAACG TCAGCGGCAA ACTGTATTCC GACGCACTCG
 851 GCAACGCACC CGCAGACACC TACATCGGCA TGTACCGCCA CAACATCAAA
 901 GCCTTAACCA ACGCGATGAA GCAATAA

This corresponds to the amino acid sequence <SEQ ID 1156; ORF 280.a>:

a280.pep
 1 MKHPKLTLIA ALLTTAATAA PLPVVTSFSI LGDVAQIGG ERVSIQSLVG
 51 ANQDTHAYHM TSGDIKKIRS AKLVLLINGLG LEAADIQRAV KQSKVSYAEA
 101 TKGIQPLKAE EEGGHHHDHD HDHDHDHEGH HHDHGEYDPH VWNDFVLMSA
 151 YAQNVAEALI KADPEGKVYY QQRLGNYQMQ LKKLHSDAQA AFNAVPAAKR
 201 KVLTHGDAFS YMGKRYHIEF IAPQGVSSA EPSAKQVA AI IRQIKREGIK
 251 AVFTENIKDT RMVDRIAKET GVNVSGLYS DALGNAPADT YIGMYRHNK
 301 ALTNAMKQ*

m280/a280 96.4% identity in 308 aa overlap

	10	20	30	40	50	60
m280.pep	MKHLKLTLIAALLTASATAAPLPVVTFSI	LGDVAQIGGERVSIQSLV	GANQDTHAYHM			
a280	MKHPKLTLIAALLTTAATAAPLPVVTFSI	LGDVAQIGGERVSIQSLV	GANQDTHAYHM			
	70	80	90	100	110	120
m280.pep	TSGDIKKIRSAKLVLNGLGLEAADVQRAVKQSKVSYEAT	TKGIQPLKAE	EEGGHHHDHD			
a280	TSGDIKKIRSAKLVLNGLGLEAADVQRAVKQSKVSYEAT	TKGIQPLKAE	EEGGHHHDHD			
	130	140	150	160	170	
m280.pep	HDH---EGHHHDHGEYDPHVWNPVLM	SAYAQNVAKALIKADPEGKVYYQ	QRLGNYQMQ			
a280	HDHDHDHEGHHHDHGEYDPHVWNPVLM	SAYAQNVAEALIKADPEGKVYYQ	QRLGNYQMQ			
	180	190	200	210	220	230
m280.pep	LKKLHSDAQA AFNAVPAAKRKVLTGHDAFSYMGKRYHIEFI	APQGVSSA	EPSAKQVA	AI		
a280	LKKLHSDAQA AFNAVPAAKRKVLTGHDAFSYMGKRYHIEFI	APQGVSSA	EPSAKQVA	AI		
	240	250	260	270	280	290
m280.pep	IRQIKREGIKAVFTENIKDTRMVDRIAKETGVNVSGKLYSD	DALGNAPADTYIGMYRHNK				
a280	IRQIKREGIKAVFTENIKDTRMVDRIAKETGVNVSGKLYSD	DALGNAPADTYIGMYRHNK				
	300					
m280.pep	ALTNAMKQX					
a280	ALTNAMKQX					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1157>:

g281.seq
 1 atgcactacg ccctcgcac cgtcttctgc ctgtccctca gcgcgcacc
 51 cgtcggcgta ttcctcgtca tgcgcgctat gagcctgata ggcgacgcat
 101 tgagccacgc cgtcctgccc ggtgcgcgcg tcggctacat gtttgccggc
 151 ttgagcctgc ccgctatggg tgtgggcggg tttgccgccc gtatgctgat
 201 ggcgctgctt gccggactcg tcagccgctt taccaccctg aaagaagatg
 251 ccaactttgc cgccttttac ctgagcagcc tcgccatcgg cgtaatcctc
 301 atcagcaaaa acggcagcag cgtcgattta ctccacctcc ttttcggatc
 351 tgtgcttgcc gtcgatattc ccgactgca actcatcgcc gccgtctccg
 401 gcctcacgct cattaccctt gccgtcatct accgcccctt ggtgctagaa
 451 agcatagacc cccttttctt caagtccgtc aacggcaaa gcgggctttg

501 gcacgtcatt ttctctcatcc tcgtcgttat gaacctcgta tccggcttcc
551 aagctctcgg catcctgatg tcggtcggaa ttatgatgct gcccgccatt
601 accgcccggt tatgggcaag aaatatgggg acgctcattc tgttgtccgt
651 cctcatcgcc ctttttttgcg gtttgatcgg gctgctcatt tcctaccaca
701 tcgaaatccc ttccggcccc gccatcatcc tctgttgca gtcctttat
751 ctttttttccg tcatcatcgg caaagaaggc ggcatcttgc ccaaatgggt
801 caaaaaccac cgccaccaca ccacctga

g281.pcp

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1159>:

1	ATGCGCTACG	CCCTCGCATC	CGTCTTCTGC	CTGTCCCTCA	GTGCCGCACC
51	CGTCGCGGTA	TTCTCTGTCA	TGCGCCGTAT	GAGCCTGATA	GGCGACGCAT
101	TGAGCCACGC	CGTCCTGCCC	GGTGCCGCCG	TCGGCTACAT	GTTTGCCGGC
151	TTGAGCTTGC	CCGCATCTGG	TTTGGGCGCG	GTAGCCGCAG	GCATGCTGAT
201	GGCATTGCTT	GCCGGACTCG	TCAGCCGCTT	CACCACCTGT	AAAGAAGATG
251	CCAACCTTGC	CGCCTTTTAT	CTCAGCAGCC	TCGCCATCGG	CGTAGTCCTC
301	GTCAGCAAAA	ACGGGAGCAG	CGTCGATTTG	CTCCACCTCC	TTTTCGGCTC
351	TGTACTTGCC	GTGATATTTT	CTGCCCTGAT	GCTCATCGCC	GCCGTCTCCA
401	GCCTACGCCT	CATTACCTTC	GCCCTCATCT	ACCGCCCGCT	CGTATCTGAA
451	AGCATCGACC	CCTGTTTTCT	CAATCCGTG	AGCGGCAAAG	CGGGCTTTTG
501	GCACGTCTCT	TTTCTCGTCC	TGGTCGTGAT	GAACCTCGTA	TCCGGCTTTT
551	AAGCCCTCGG	CACACTCATG	TCCGTCCGAC	TCATGATGCT	GCCAGCCATT
601	ACCGCCCGCC	TGTGGGCGAA	GCATATGGGC	GCACTCATCT	TCCTATCCGT
651	CTTGACACGC	CTGCTGTGGC	GCTTGAGCGG	ACTGCTCATT	TCCTACCACA
701	TCGAAATTCC	TTCCGCTCCC	GCCATCATCC	TCGTTGTCAG	CGTCTTTTAT
751	CTCTTTTCCG	TCATACTCGG	CAAAGAAGGC	GGCATTCTGA	CC...

m281.pep (partial)

Computer analysis of this amino acid sequence gave the following results:

ORF 281 shows 93.5% identity over a 263 aa overlap with a predicted ORF (ORF 281.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m281.pep	MRYALASVFCLSL	SAAPVGVLV	MRRMSLI	GDALSHAVL	PGA	AVGYMFAGLSLPAMGLGG
	:					
g281	MHYALASVFCLSL	SAAPVGVLV	MRRMSLI	GDALSHAVL	PGA	AVGYMFAGLSLPAMGVGG
	:					
	10	20	30	40	50	60
	70	80	90	100	110	120
m281.pep	VAAGMLMALLAGL	VS	RFTTLKEDAN	FAAFYLSS	LAIGVVLV	SKNGSSVDLLHLLFGSVLA
g281	FAAGMLMALLAGL	VS	RFTTLKEDAN	FAAFYLSS	LAIGVILISK	NGSSVDLLHLLFGSVLA
	70	80	90	100	110	120
	130	140	150	160	170	180
m281.pep	VDIPALQLIAA	VSSSLTLITL	AVIYRPLV	LESIDPLFL	SKSVGGK	GGLWHVFLVLVVMNLV

	: : : :
g281	VDIPALQLIAAAVSGLTTLITLAVIYRPLVLESIDPLFLKSVNGKGGLWHVIFLIILVVMNLV
	130 140 150 160 170 180
	190 200 210 220 230 240
m281.pep	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTTALLCGLSGLLISYHIEIPSGP
	: : :
g281	SGFQALGIILMSVGIMMLPAITARLWARNMGTLILLSVLIALFCGLIGLLISYHIEIPSGP
	190 200 210 220 230 240
	250 260
m281.pep	AIILCCSVLYLFSVILGKEGGILT
g281	AIILCCSVLYLFSVILGKEGGILPKWFKNHRHHTTX
	250 260 270

```

a281.seq
1  ATGCGCTACG CCCTCGCATC CGTCTTCTGC CTGTCCCTCA GTGCCGCACC
51  CGTCGGCGTA TTCCTCGTCA TGCGCCGTAT GAGCCTGATA GGGCAGCAGT
101 TGAGCCACGC CGTCTGCCCC GGTGCCGCCG TCGGCTACAT GTTTCGCCGG
151 TTAAGCCTGC CCGCCATGGG TTTGGGCGGC GTAGCCGCAG GTATGCTGAT
201 GGCAGTGCTT GCCGGATCTG TCAGCCGCTT CACCACCCTG AAAGAAGATG
251 CCAACTTTGC CGCCTTTTAT CTCAGCAGCC TCGCCATCGG TGTAGTCCTC
301 GTCAGCAAAA ACGGCAGCAG CGTCGATTTG CTCCACCTCC TTTCGGCTC
351 CGTACTTGCC GTCGATATTC CTGCCCTGCA ACTCATCGCC GCCGTATCCA
401 CCCTCACACT GCTTACCCTT GCCGTCATCT ACCGCCCGCT CGTACTCGAA
451 AGCATCGACC CCCTGTTTTCT CAAATCTGTC GGCGGCAAAG GCGGGCTTTG
501 GCACGTCCTC TTTCTCGTCT TGGTCGTGAT GAACCTCGTA TCCGGCTTTC
551 AAGCCCTCGG CACACTCATG TCCGTCGGAC TTATGATGCT GCCAGCCATT
601 ACCGCCCGCC TATGGGCGAA GCACATGGGC GCACTCATCC TCCTATCCGT
651 TCTGACAGCG CTGCTGTGCG GCTTGAGCGG ACTGCTCATT TCCTACCACA
701 TCGAAATTCC TTCCGGTCCC GCCATCATCC TCTGTTGCAG CGTCCTTTAT
751 CTCTTTTCCG TCATACTCGG CAAAGAAGGC GGCATTCTGA CCAAATGGCT
801 CAAAAACCAC CGCACCACA CCACCTGA

```

a281.pep

1	<u>MRYALASVFC</u>	<u>LSLSAAPGV</u>	<u>FLVMRRMSLI</u>	<u>GDALSHAVLP</u>	<u>GAAGVGYMFAG</u>
51	<u>LSLPAMGLGG</u>	<u>VAAGMLMALL</u>	<u>AGLSRFTTL</u>	<u>KEDANFAAFY</u>	<u>LSSLAIGVVL</u>
101	<u>VSKNGSSVDL</u>	<u>LHLLFGSVLA</u>	<u>VDIPALQLIA</u>	<u>AVSTLTLLTL</u>	<u>AVIYRPLVLE</u>
151	<u>SIDPLFLKSV</u>	<u>GGKGGLWHVL</u>	<u>FLVLVVMNLV</u>	<u>SGFQALGTL</u>	<u>SVGLMMLPAI</u>
201	<u>TARLWAKHMG</u>	<u>ALILLSVLTA</u>	<u>LLCGLSGLLI</u>	<u>SYHIEIPSGP</u>	<u>AIILCCSVLY</u>
251	<u>LFSVILGKEG</u>	<u>GILTKWLKNH</u>	<u>RHHTT*</u>		

	10	20	30	40	50	60
m281.pep	MRYALASVFCLSLSAAPVGVLVMMRRMSLIGDALSHAVLPGAAVGYMFAGLSLPAMGLGG					
a281	MRYALASVFCLSLSAAPVGVLVMMRRMSLIGDALSHAVLPGAAVGYMFAGLSLPAMGLGG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m281.pep	VAAGMLMALLAGLVSRFTTLKEDANFAAFYLSSLAIGVVLVSKNGSSVDLLHLLFGSVLA					
a281	VAAGMLMALLAGLVSRFTTLKEDANFAAFYLSSLAIGVVLVSKNGSSVDLLHLLFGSVLA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m281.pep	VDIPALQLIAAVSSLTTLTAVIYRPLVLESIDPLFLKSVGGKGGLWHVFLVLVVMNLV					
a281	VDIPALQLIAAVSTLTLLTAVIYRPLVLESIDPLFLKSVGGKGGLWHVFLVLVVMNLV					
	130	140	150	160	170	180

641

	190	200	210	220	230	240
m281.pep	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP					
a281	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP					
	190	200	210	220	230	240
	250	260				
m281.pep	AIILCCSVLYLFSVILGKEGGILT					
a281	AIILCCSVLYLFSVILGKEGGILTKWLKNHRHHTTX					
	250	260	270			

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1163>:

g282.seq

```

1  atgggattgg gtatggaaat cggcaagctg attgtggctc ttttgggtgct
51  gatcaatccg tttagcgcgt tgtcgcttta ccttgacctg accaacggac
101 acagcacgaa ggagcgcagg aaggtcgcgc ggacggccgc cgtcgccgtg
151 tttgccgtga ttgcggtatt tgcgctgata ggcggtgcgc tattgaaggt
201 tttgggcata agcgtcgggt cgtttcaggt cggcggcggg attttgggtgc
251 tgctgatcgc catttcgatg atgaacggca acgacaatcc cgccaagcag
301 aatctcggcg cgcagccgga aacggggcaa gcgcgccccg cccgcaatgc
351 aggggacgatt gccgtcgtgc ccatcgccat accgatcacc atcggtcggg
401 gcggtatttc gactgtgatt atttatgctt cggcagccaa aacgtacagc
451 gatatcgcg tgattatcgc ggccggtttg gtggtcagtg cgatttggtta
501 tgccatttta atcgttgccg ggaaggtcag ccgcctgctg ggcgcgacgg
551 ggctgacgat tttaaaccgc attatgggta tgatgctggc ggcggtatcg
601 gtggagatta ttgtgtcggg actgaaaacg atattccccg aactggcagg
651 ttga

```

This corresponds to the amino acid sequence <SEQ ID 1164; ORF 282.ng>:

g282.pep

```

1  MGLGMEIGKL IVALLVLINP FSALSPLYLDL TNGHSTKERR KVARTAAVAV
51  FAVIAVFALI GGALLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101 NLGAQPETGQ ARPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYS
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLI GATGLTILNR IMGMLLAAYS
201 VEIIVSGLKT IFPQLAG*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1165>:

m282.seq

```

1  ATGGGATTGG GCATGGAAAT CGGCAAGCTG ATTGTGGCTT TTTTGGTGCT
51  GATTAATCCG TTTAGCGCGT TGTGCTTTA CCTTGACCTG ACCAACGGGC
101 ACAGCACGAA GGAGCGCAGG AAGGTCGCGC GGACGGCCGC CGTTGCCGTG
151 TTTGCCGTGA TTGCGGTATT TGCCTGATC GCGGTACGC TGCTGAAGGT
201 TTTGGGCATC AGCGTCGGTT CGTTTCAGGT CGGCGGCGGG ATTTTGGTGC
251 TGCTGATCGC CATTTCGATG ATGAACGGCA ACGACAATCC CGCCAAGCAG
301 AATCTCGGCG CGCAGCCGGA AACGGGGCAG GCGCGCCCCG CCCGCAATGC
351 CGGAGCGATT GCCGTCGTGC CCATCGCCAT ACCGATCACC ATCGGCCCGG
401 GCGGTATTTC GACCGTGATT ATTTACGCTT CGGCGGCTAA AACATACGGC
451 GACATCGCGT TGATTATCGC GGCCGGTTTG GTGGTCAGTG CGATTTGTTA
501 TGCCATTTTA ATCGTTGCCG GGAAGGTCAG CCGCCTGCTG GGC GCGACGG
551 GGCTGACGAT TTTAAACCGC ATTATGGGTA TGATGCTGGC GCGGTATCG
601 GTGGAGATTA TTGTGTCGGG ACTGAAAACG ATATTCCCCG AACTGGCAGG
651 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1166; ORF 282.ng>:

m282.pep

```

1  MGLGMEIGKL IVAFLVLINP FSALSPLYLDL TNGHSTKERR KVARTAAVAV
51  FAVIAVFALI GGTLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101 NLGAQPETGQ ARPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYG
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLI GATGLTILNR IMGMLLAAYS
201 VEIIVSGLKT IFPQLAG*

```

Computer analysis of this amino acid sequence gave the following results:

642

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 282 shows 98.6 % identity over a 217 aa overlap with a predicted ORF (ORF 282.ng) from *N. gonorrhoeae*:

m282/g282

	10	20	30	40	50	60
m282 . pep	MGLGMEIGKLIVAFVLINPFSALSPLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
	:					
g282	MGLGMEIGKLIVALLVLINPFSALSPLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m282 . pep	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI					
	:					
g282	GGALLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m282 . pep	AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL					
	:					
g282	AVVPIAIPITIGPGGISTVIIYASAAKTYSDIALIIAAGLVVSAICYAILIVAGKVSRL					
	130	140	150	160	170	180
	190	200	210			
m282 . pep	GATGLTILNRIMGMLAAVSVEIIVSGLKTIFPQLAGX					
g282	GATGLTILNRIMGMLAAVSVEIIVSGLKTIFPQLAGX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1167>:

a282 . seq

```

1  ATGGGATTGG GCATGGAAAT CGGCAAGCTG ATTGTGGCTT TTTTGGTGCT
51  GATTAATCCG TTTAGCGCGT TGTCGCTTTA CCTTGACCTG ACCAACGGGC
101 ACAGCACGAA GGAGCGCAGG AAGGTCGCGC GGACGGCCGC CGTTGCCGTG
151 TTTGCCGTGA TTGCGGTATT TGCGCTGATC GGCGGTACGC TGCTGAAGGT
201 TTTGGGCATC AGCGTCGGTT CGTTTCAGGT CGGCGGCGGA ATTTTGGTGT
251 TGCTGATTGC CATTTCGATG ATGAACGGCA ACGACAATCC CGCCAAGCAG
301 AATCTCGGCG CGCAGCCGGA AACGGGGCAG GTGCGCCCCG CCCGCAATGC
351 CGGAGCGATT GCCGTCGTGC CCATCGCCAT ACCGATCACC ATCGGCCCCG
401 GCGGTATTTT GACCGTGATT ATTTACGCTT CGGCGGCTAA AACATACGGC
451 GACATCGCGT TGATTATCGC GGCCGGTTTG GTGGTCAGTG CGATTTGTTA
501 TGCCATTTTA ATCGTTGCCG GGAAGGTCAG CCGCCTGCTG GGTGCGACGG
551 GGCTGACGAT TTAAACCGT ATCATGGGTA TGATGCTGGC GGCGGTATCG
601 GTGGAGATTA TTGTGTCGGG ACTGAAAATG ATATCCCGC AACTGGCAGG
651 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1168; ORF 282.a>:

a282 . pep

```

1  MGLGMEIGKL IVAFLVLINP FSALSPLYLDL TNGHSTKERR KVARTAAVAV
51  FAVIAVFALI GGTLLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101 NLGAQPETGQ VRPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYG
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLG GATGLTILNR IMGMLAAVS
201 VEIIVSGLKM IFPQLAG*

```

m282/a282 99.1% identity in 217 aa overlap

	10	20	30	40	50	60
m282 . pep	MGLGMEIGKLIVAFVLINPFSALSPLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
a282	MGLGMEIGKLIVAFVLINPFSALSPLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
	10	20	30	40	50	60

643

	70	80	90	100	110	120
m282 . pep	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI					
a282	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQVRPARNAGAI					
	70	80	90	100	110	120
m282 . pep	AVVPPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL					
a282	AVVPPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL					
	130	140	150	160	170	180
m282 . pep	GATGLTILNRIMGMLAAVSVEIIVSGLKTIFFPQLAGX					
a282	GATGLTILNRIMGMLAAVSVEIIVSGLKMIFFPQLAGX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1169>:

g283 . seq

1	atgaactttg	ctttatccgt	catcacattt	accctcgctt	ctttcctgcc
51	cgtcccgccct	gccggaaccg	ccgtcttttac	ttggaagac	ggcggcggca
101	acagctattc	ggatgtgccg	aaacagcttc	atcccgacca	gagccaaatc
151	ctcaacctgc	ggacgctcca	aaccaaaccg	gcggtcaagc	ccaaacctgc
201	cgtcgatagc	aatgcggaca	gtgcgaagga	aaacgaaaag	gatatcgccg
251	agaaaaacg	gcagcttgag	gaagaaaaga	aaaaaattgc	cgaaaccgaa
301	cggcagaaca	aagaagaaaa	ctgccggatt	tcaaaaatga	acctgaaggc
351	ggtgggaaac	tcaaatgcga	aaaacaagga	tgatttgatc	cgtaaatata
401	ataacgccgt	aaacaaatac	tgccgttaa		

This corresponds to the amino acid sequence <SEQ ID 1170; ORF 283.ng>:

g283 . pep

1	MNFALSVITF	TLASFLPVPP	AGTAVFTWKD	GGGNSYS DVP	KQLHPDQSQI
51	LNLRTLQTKP	AVKPKPAVDT	NADSAKENEK	DIAEKNGQLE	EEKKKIAETE
101	RQNKEENCRI	SKMNLKAVGN	SNAKNKDDLI	RKYNNNAV NKY	CR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1171>:

m283 . seq

1	ATGAACTTTG	CTTTATCCGT	CATTATGTTG	ACCCTCGCCT	CTTTCCTGCC
51	CGTCCCGCCT	GCCGGAGCCG	CCGTCTTTAC	TTGGAAGGAC	GGCGGCGGCA
101	ACAGCTATTC	GGATGTACCG	AAACAGCTTC	ATCCCGACCA	AAGCCAAATC
151	TTAAACCTGC	GGACGCGCCA	AACCAAACCG	GCGGTCAAAC	CCGCCCAAGC
201	CGACGCAGGG	AAGCGCACAG	ACGGCGCGGC	ACAGGAAAAC	AATCCCGACA
251	CTGCCGAGAA	AAACCGGCAG	CTTGAGGAAG	AAAAGAAAAG	AATTGCCGAA
301	ACCGAACGGC	AGAACAAAGA	AGAAACTGTC	CGGATTTCAA	AAATGAACCT
351	GAAGGCGGTG	GGAAATTCAA	ATGCAAAAAA	CAAGGATGAT	TTGATTCGGA
401	AATACAATAA	CGCCGTAAAC	AAATACTGCC	GTAA	

This corresponds to the amino acid sequence <SEQ ID 1172; ORF 283>:

m283 . pep

1	MNFALSVIML	TLASFLPVPP	AGAAVFTWKD	GGGNSYS DVP	KQLHPDQSQI
51	LNLRTQTQTKP	AVKPAQADAG	KRTDGAAQEN	NPDTAEKNRQ	LEEEKKRIAE
101	TERQNKEENC	RISKMNLKAV	GNSNAKNKDD	LIRKYNNAV N	KYCR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m283/g283 86.1% identity in 144 aa overlap

	10	20	30	40	50	60
m283 . pep	MNFALSVIMLTLASFLPVPPAGAAVFTWKDGGGNSYS DVPKQLHPDQSQILNLRTQTKP					
g283	MNFALSVITFTLASFLPVPPAGTAVFTWKDGGGNSYS DVPKQLHPDQSQILNLRTLQTKP					
	10	20	30	40	50	60

	70	80	90	100	110	120
m283.pep	AVKPAQADAGKRTDGAAQENNPDTAENRQLEEEKKRIAETERQNKEENCRISKMNLKAV					
		:	:	:	:	:
g283	AVKPKPA-VDTNAD-SAKENEKDIAEKNGQLEEEKKKIAETERQNKEENCRISKMNLKAV					
	70	80	90	100	110	
	130	140				
m283.pep	GNSNAKNKDDLIRKYNNAVNKYCRX					
g283	GNSNAKNKDDLIRKYNNAVNKYCRX					
	120	130	140			

```
a283.seq
1  ATGAACTTTG CTTTATCCGT CATTATGTTG ACCCTCGCCT CTTTCCTGCC
51  CGTCCCGCCT GCCGGAGCCG CCGTCTTTAC TTGGAAGGCA GCGCGCGGCA
101 ACAGCTATT C GGATGTACCG AAACAGCTTC ATCCCGACCA AAGCCAAATC
151 TTAAACCTGC GGACGCGCCA AACCAAACCG GCGGTCAAAC CGCCCAAGC
201 CGACGCAGGG AAGCGCACAG ACGGCGCGGC ACAGGAAAAC AATCCCGACA
251 CTGCCGAGAA AAACCGGCAG CTTGAGGAAG AAAAGAAAAG AATTGCCGAA
301 ACCGAACGGC AGAACAAAGA AGAAAAC TGC CGGATTTCAA AAATGAACCT
351 GAAAGCGGTG GGAAATTCAA ATGCAAAAAA CAAGATGAT TTGATTCGGA
401 AATACAATAA CGCCGTAAAC AAATACTGCC GTTAA
```

a283.pap

1	MNFALSVIML	TLASFLPVPP	AGAAVFTWKD	GGGSYSYDVP	KQLHPDQSQI
51	LNLRTQTQK	AVKPAQADAG	KRTDGAQEN	NPDTAEKNRQ	LEEEKKRIAE
101	TERQNKENC	RISKMNKAV	GNSNAKNKDD	LIRKYNNAVN	KYCR*

	10	20	30	40	50	60
m283.pep	MNFALSVMIMLTLASFLPVP	PAGAAVFTWKDGGGNSYSDV	PKQLHPDQSQILNLR	TRQT	KP	
a283	MNFALSVMIMLTLASFLPVP	PAGAAVFTWKDGGGNSYSDV	PKQLHPDQSQILNLR	TRQT	KP	
	10	20	30	40	50	60
	70	80	90	100	110	120
m283.pep	AVKPAQADAGKRTDGA	AQENNPDTAEKNRQLEEE	EKKRIAETERQNKE	ENC	RISKMN	LKAV
a283	AVKPAQADAGKRTDGA	AQENNPDTAEKNRQLEEE	EKKRIAETERQNKE	ENC	RISKMN	LKAV
	70	80	90	100	110	120
	130	140				
m283.pep	GNSNAKNKDDLIRKY	NNAVNKYCRX				
a283	GNSNAKNKDDLIRKY	NNAVNKYCRX				
	130	140				

g284.seq.

1	atgccgtctg	aaactcgaaa	tcggtttcag	acggcattgg	tttacgcggc
51	aggttggggc	ttagcggctc	ttgtaacggc	attcgctttt	gctgcaaaa
101	gagtcgcggc	ctttgcgttt	gcctttgaag	ccttcgcggc	tttttttgaa
151	actgtctttc	ttaaagcctt	ctttcttgaa	accttcgcgc	cgcggtttgc
201	cgcggaagcc	ttctttgccc	ggtttatgat	cgcgcgcggc	gccgcgggat
251	ttcctatcgc	cccagccgcc	tttgcccttc	ggcttgccgc	ctgcggattt
301	gcgtttgcgg	gccggctcca	tgccctcgat	ggtcagttcg	ggcagtttgc
351	ggttaatgta	ttttctgatt	ttgtggactt	tgacgtattc	gttcacctcg
401	gcaaacgtaa	tgcgaatacc	cgtgcggcct	cgcgcgcggc	tgcccccgat
451	gcggtggacg	tagtcttccg	ctcgtttccg	caggtcgtaq	tttatgaacg

645

```

501  gggtaatggt  cggtagctca  ataccgcgtg  cggcaacgtc  ggtggcaacc
551  aaaattttgc  agcggccttt  acgcaaattc  gtcagcgtgc  ggttgcgcca
601  gccctgcggc  atatcgccgt  gcaggcagtt  ggccgcgaaa  cctttttcgt
651  acaattcatc  cgcgatgact  tcggtcatcg  ctttggtgga  cgtgaaaatc
701  acacattggt  cgatgttggc  atcgcgcagg  atgtggtcga  gcaggcggtt
751  tttgtggcgc  atatcgtcgc  agtacaacaa  ctgctcttcg  attttgcctt
801  ggccgtccac  gcgttcgact  tcgataattt  cagagtcctt  ggtcagtttg
851  cgcgccagtt  tgccgactgc  gccgtcccaa  gtggcggaga  acaataa

```

This corresponds to the amino acid sequence <SEQ ID 1176; ORF 284.ng>:

```

g284.pep
  1  MPSETRNRFO  TALVYAAGWG  LAVFVTAF  ACKRVAGFAF  AFEAFAGFFE
51  TVFLKAFFLE  TFAARFAAEA  FFARFMIAAP  AAGFPIAPAA  FAFRLAACGF
101 AFAGRLHAFD  GQFGQFVNV  FFDFVDFDVF  VHFGRNRNT  RAACAAGAPD
151 AVDVVFRLEF  QVVVDVNG  RYVNTACGNV  GGNQNFAAAF  TQIRQRAVAP
201 ALRHIAVQAV  GGETFFVQFI  RDDFGHRFGG  RENHTLVDVG  IAQDVVEQAV
251 FVAHIVAVQQ  LLFDLALAVH  AFDFDNFRVF  GQFARQFADC  AVPSGGEQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1177>:

```

m284.seq..
  1  ATGCCGCTCTG  AAACCTCGAAA  TCGGTTTCAG  ACGGCATTGG  TTTATGCGGC
51  AGGTTGGGGC  TTAGCGGTCT  TTGTAACGGC  GTTCGCCTTT  GCCTGCAAAA
101 GAATCGCCGG  CTTTGCCTTT  GCCTTTGAAG  CCTTCGCCGG  TTTTTCGAA
151 ACCGTCTCTC  TTAAAGCCTT  CTTTCTTGAA  ACCTTCGCCG  CGCGTTTTCG
201 CGCCGAAGCC  TTCTTTGCTC  GGTTTATGAT  CGCCGCGCCA  ACCGCCGGAT
251 TTACGATCGC  CCCAGCCGCC  TTTGCCTTTC  GGCTTGCCGC  CTGCGGATTT
301 GCGTTTGGCG  GTCGGTTCCA  TGCCTTCGAT  GGTGAGTTCG  GGCAGTTTTC
351 GGTTAATGTA  TTTTTCGATT  TTGTGGACTT  TGACGTATTC  GTTCACTTCG
401 GCAAACGTAA  TCGCAATACC  CGTGCAGCCT  GCGCGGCCGG  TCGCGCCGAT
451 GCGGTGGACG  TAGTCTTCGG  CCTGTTTCGG  CAGGTCGTAG  TTGATAACGT
501 GGGTAATGGT  CGGTACGTCG  ATACCGCGTG  CGGCAACATC  GGTGGCAACC
551 AAAATTTTGC  AGCGGCCTTT  ACGCAAATCC  ATCAGCGTGC  GGTGCGCCA
601 GCCTTGCGGC  ATATCGCCGT  GCAGGCAGTT  TGCGCGGAAA  CCTTTTTCGT
651 ACAGTTCATC  CGCAATGACT  TCGGTCATGG  CTTTGGTGGA  CGTGAAAATC
701 ACGCATTGAT  CGATATTGGC  ATCGCGCAAG  ATATGATCGA  GCAGCGGGTT
751 TTTGTGGCGC  ATATCGTCGC  AGTACAGCAG  TTGTTCTTCG  ATTTTGCCTT
801 GATCGTCCAC  GCGTTCGACT  TCGATGATT  CAGGTCCTTT  GGTGAGTTTG
851 CGCGCCAGTT  TGCCGACCGC  GCCGTCCCAA  GTGGCGGAGA  ACAACAAAGT
901 CTGACGGTCG  CTCGGCGTGT  CTTCCACGAT  GGTTCGATG  TCGTCGATAA
951 AGCCCATATC  CAACATACGG  TCGGCTTCGT  CCAAATCAG  CACTTCCAAA
1001 CGTTCAAAAT  CAACTTTGCC  GCTTTGCATC  AGGTCCATCA  GACGGCCCCG
1051 CGTGCGGACA  ATCAGATCGA  CCGGTTTGCT  CAGGCGACGG  GTTGGTAGC
1101 CGAAAGACGC  GCCGCCGACG  ATGCTGACGG  TCGGGAACCA  ACGCATATTT
1151 TTGGCATAAC  CCAGCGCGTT  TTTCTCGACT  TGAGCCGCCA  GTTCGCGGGT
1201 CGGGGTCAAC  ACCAAAGCAC  GCGGGCCTTT  GCCCGGTTTT  TCCTGCGGTT
1251 TGGTCAGTTT  TTGCAAAGTC  GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1178; ORF 284>:

```

m284.pep
  1  MPSETRNRFO  TALVYAAGWG  LAVFVTAF  ACKRIAGFAF  AFEAFAGFFE
51  TVSLKAFFLE  TFAARFAAEA  FFARFMIAAP  TAGFTIAPAA  FAFRLAACGF
101 AFAGRFHAFD  GQFGQFSVNV  FFDFVDFDVF  VHFGRNRNT  RAACAAGAPD
151 AVDVVFRLEF  QVVVDVNG  RYVDTACGNI  GGNQNFAAAF  TQIHQRAVAP
201 ALRHIAVQAV  CGETFFVQFI  RNDFGHGF  RENHALIDIG  IAQDMIEQAV
251 FVAHIVAVQQ  LFFDFALIVH  AFDFDDFRVF  GQFARQFADR  AVPSGGEQQS
301 LTVARRCFHD  GFDVVDKAHI  QHTVGFVQNO  HFQTFKINFA  ALHQVHQATAR
351 RGDNQIDRFA  QGTGLVAERR  AADDADGAEP  THIFGIRQRV  FLDLSRQFAG
401 RGQHQSTRAF  ARFFAAGQF  LQSR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m284/g284 92.3% identity in 298 aa overlap

646

	10	20	30	40	50	60
m284.pep	MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE					
g284	MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRVAGFAFAFEAFAGFFETVFLKAFFLE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m284.pep	TFAARFAAEAFFARFMIAAPTAGFTIAPAAFAFRLAACGFAGRFHAFDGGQFGQFSVNV					
g284	TFAARFAAEAFFARFMIAAPAGFP IAPAAFAFRLAACGFAGRLHAFDGGQFGQFAVNV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m284.pep	FFDFVDFDV FVHFGRNRNTRAACAAGAPDAVDVFR LFRQVVVDNVGNRGYVDTACGNI					
g284	FFDFVDFDV FVHFGRNRNTRAACAAGAPDAVDVFR LFRQVVVDNVGNRGYVNTACGNV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m284.pep	GGNQNF AAAFTQIHQRAVAPALRHIAVQAVCGETFFVQFIRNDFGHGFGGRENHALIDIG					
g284	GGNQNF AAAFTQIRQRAVAPALRHIAVQAVGGETFFVQFIRDDFGHREFGGRENHTLVDVG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m284.pep	IAQDMIEQAVFVAHIVAVQQLFFDFALIVHAFDFFDRVFGQFARQFADRAVPSGGEQQS					
g284	IAQDVVEQAVFVAHIVAVQQLFFDFALAVHAFDFFDRVFGQFARQFADCAVPSGGEQX					
	250	260	270	280	290	
	310	320	330	340	350	360
m284.pep	LTVARRCFHDGFDVVDKAHIQHTVGFVQNQHFTFKINFAALHQVHQ TARRGDNQIDRFA					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1179>:

```

a284.seq
1  ATGCCGCTCTG  AAACCTCGAAA  TCGGTTTCAG  ACGGCATTGG  TTTATGCGGC
51  AGGTTGGGGC  TTAGCGGTCT  TTGTAACGGC  GTTCGCCTTT  GCCTGCAAAA
101  GAATCGCCGG  CTTTGCGTTT  GCCTTTGAAG  CCTTCGCCGG  TTTTGTGAA
151  ACCGTCTCTC  TTAAAGCCTT  CTTTCTTGAA  ACCTTCGCCG  CGCGTTTTC
201  CGCCGAAGCC  TTCTTTGCTC  GGTTTATGAT  CGCCGCGCCA  ACCGCCGGAT
251  TTACGATCGC  CCCAGCCGCC  TTTGCCTTTC  GGCTTGCCGC  CTGCGGATTT
301  GCGTTTGCGG  GTCGGTTCCA  TGCCTTCGAT  GGTCAGTTTC  GGCAGTTTTC
351  GGTTAATGTA  TTTTTCGATT  TTGTGGACTT  TGACGTATTC  GTTCACTTCG
401  GCAAACGTAA  TCGCAATACC  CGTGCGGCCT  GCGCGGCCGG  TCGGCCCGAT
451  GCGGTGGACG  TAGTCTTCCG  CCTGTTTCGG  CAGGTCGTAG  TTGATAACGT
501  GGTAATGGT  CCGTACGTCG  ATACCGCGTG  CGGCAACGTC  GGTGGCAACC
551  AAAATTTTGC  AGCGGCCTTT  GCGCAAATCC  ATCAGCGTGC  GGTTCGCGCA
601  GCCTTGCGGC  ATATCGCCGT  GCAGGCAGTT  GCGGCGGAAA  CCTTTTTCGT
651  ACAATTCATC  CGCGATGACT  TCGGTCATGG  CTTTGGTGGA  CGTGAAAATC
701  ACGCATTGAT  CGATGTCGGC  ATCGCGCAAG  ATATGATCGA  GCAGGCGGTT
751  TTTGTGGCGC  ATATCGTCGC  AGTACAGCAG  TTGTTCTTCG  ATTTTGCCTT
801  GGTCGTCCAC  GCGTTCGACT  TCGATGATTT  CAGGGTCTTT  GGTCAGTTTG
851  CGCGCCAGTT  TGCCGACCGC  GCCGTCCCAA  GTGGCGGAGA  ACAACAAAGT
901  CTGACGGTCT  TCCGGCGTGG  CTTGACGAT  GGTTCGATG  TCGTCGATAA
951  AGCCCATATC  CAACATACGG  TCGGCTTCGT  CCAAATCAG  CACTTCCAAG
1001  CGGGCGAAAT  CGACTTTGCC  GCTTTGCATC  AAGTCCATCA  GACGGCCCGG
1051  CGTGCGGACA  ATCAGATCGA  CCGGTTTGCT  CAGGGCGCGG  GTTTGGTAGC
1101  CGAACGATGC  ACCACCGACG  ATGCTGACGG  TACGGAACCA  ACGCATATTT
1151  TTGGCATACG  CCAGCGCGTT  TTTCTCGACT  TGAGCCGCCA  ATTCGCGGGT
1201  CGGCGTCAAC  ACCAACGCGC  GCGGGCCTTT  GCCCGGTTTT  TCGCTGCGTT
1251  TGTCAGTCG  CTGCAAAGTC  GGTA

```

This corresponds to the amino acid sequence <SEQ ID 1180; ORF 284.a>:

```

a284.pep
1  MPSETRNRFO  TALVYAAGWG  LAVFVTAFAF  ACKRIAGFAF  AFEAFAGFFE

```

647

```

51 TVSLKAFFLE TFAARFAAEA FFARFMIAAP TAGFTIAPAA FAFRLAACGF
101 AFAGRFAHFD GQFGQFSVNV FFDFVDFDVF VHEGKRNRNT RAACAAGAPD
151 AVDVVFRLEF QVVVDNVGNG RYVDTACGNV GGNQNFAAAF AQIHQRAVAP
201 ALRHIAVQAV GGETFFVQFI RDDEFGHGGG RENHALIDVG IAQDMIEQAV
251 FVAHIVAVQQ LFFDFALVVH AFDFDDFRVF GQFARQFADR AVPSGGEQQS
301 LTVFRRGFDD GFDVVDKAHI QHTVGFVQNO HFQAGEIDFA ALHQVHQTAR
351 RGDNQIDRFA QGAGLVAERC TTDDADGTEP THIFGIRQRV FLDLSRQFAG
401 RRQHQRRARAF ARFFAAGQS LQSR*

```

m284/a284 94.8% identity in 424 aa overlap

```

              10      20      30      40      50      60
m284.pep      MPSETRNRFQTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE
              |||
a284           MPSETRNRFQTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE
              10      20      30      40      50      60

              70      80      90      100     110     120
m284.pep      TFAARFAAEAFFAREFMIAAPTAGFTIAPAAFAFRLAACGFAGRFHAFDGGQFGQFSVNV
              |||
a284           TFAARFAAEAFFAREFMIAAPTAGFTIAPAAFAFRLAACGFAGRFHAFDGGQFGQFSVNV
              70      80      90      100     110     120

              130     140     150     160     170     180
m284.pep      FFDFVDFDVFVHFGKRNRNTRAACAAGAPDAVDVFRLEFRQVVVDNVGNRGYVDTACGNI
              |||
a284           FFDFVDFDVFVHFGKRNRNTRAACAAGAPDAVDVFRLEFRQVVVDNVGNRGYVDTACGNV
              130     140     150     160     170     180

              190     200     210     220     230     240
m284.pep      GGNQNFAAAFTQIHQRAVAPALRHIAVQAVCGGETFFVQFIRNDFGHGFGGRENHALIDIG
              |||
a284           GGNQNFAAAFAQIHQRAVAPALRHIAVQAVGGETFFVQFIRDDFGHGGGRENHALIDVG
              190     200     210     220     230     240

              250     260     270     280     290     300
m284.pep      IAQDMIEQAVFVAHIVAVQQLFFDFALIVHAFDFDDFRVFGQFARQFADRAVPSGGEQQS
              |||
a284           IAQDMIEQAVFVAHIVAVQQLFFDFALVVHAFDFDDFRVFGQFARQFADRAVPSGGEQQS
              250     260     270     280     290     300

              310     320     330     340     350     360
m284.pep      LTVARRCFHDGFDVVDKAHIQHTVGFVQNHQHFQTFKINFAALHQVHQTARRGDNQIDRFA
              |||
a284           LTVFRRGFDDGFDVVDKAHIQHTVGFVQNHQFQAGEIDFAALHQVHQTARRGDNQIDRFA
              310     320     330     340     350     360

              370     380     390     400     410     420
m284.pep      QGTGLVAERRAADDADGAEPHTHIFGIRQRVFLDLSRQFAGRGHQSTRAFARFFAAGQF
              |||
a284           QGAGLVAERCTTDDADGTEPHTHIFGIRQRVFLDLSRQFAGRRQHQRRARAFARFFAAGQS
              370     380     390     400     410     420

m284.pep      LQSRX
              |||
a284           LQSRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1181>:

```

g285.seq
1  atgaccgata ccacaccgac agataccgat ccgaccgaaa acggcgacgcg
51 caaaatgccg tctgaacacc gcccgcgcc gccggcaaaa aaacgccgcc
101 cgctgctgaa gctgtcggcg gcactgctgt ctgtcctgat tttggcagta

```

```

151  tgtttcctcg gctggatcgc cggtagcgaa gcaggtttgc gcttcgggct
201  gtaccaaata ccgtcctggt tcggcgtaaa catttcctcc caaaacctca
251  aaggcacact gctcgacggc ttcgacggcg acaactgggt gatagaaacc
301  gagggggcag accttaaaat cagccgcttc cgcttcgctg gaaaccgtc
351  cgaactgatg cggcgacgcc tgacatcac cgacatctcc gccggcgaca
401  tcgccatcgt aaccaaaccc actccgccta aagaagaacg cccgcctcaa
451  ggctgcccgc acagcataga cctgcccgcg gctgtctatc tcgaccgctt
501  cgagacgggc aaaatcagca tgggcaaaac cttgacaaa caaacgtct
551  atctcgaacg cctcaacgcg gcataccggt acgaccgtaa agggcacccg
601  ctcgacctga agggcgccga cacgccgtgg agcagttcgt cggggtcagc
651  ctcggtcggc ttgaaaaaac cgtttgccct cgataccgcc atttacacca
701  aaggcggatt cgaaggcgaa accatacaca gtacggcgcg gctgagcggc
751  agcctgaagg atgtgcgcgc cgaactgacg atcgacggcg gcaatatccg
801  cctctcgga aaatccgtca tccaccggtt tgccgaatca ttggataaaa
851  cattggaaga agtactggtc aaaggattca acatcaatcc gtccgccttc
901  gtgccttccc tgccgatgac cgggctgaat ttcgacctga ccgccatccc
951  gtcgttttca gacggcatcg cgttggaagg ctgctcgat ttggaaaaca
1001 ccaaagccgg ctttgccgac cgcaacggca tcccgtccg tcaggttttg
1051 ggcggttttg tcatccggca ggacggcacg gtgcatatcg gcaatacgtc
1101 cgccgccttg ctcgacggg gcggcatcag gctgtcgggc aaaaacgaca
1151 ccgaaaaaga catccttgat ttaaatatag gcatacaact cgtcggcgcg
1201 gaagacgtgc tgcaaacccg gttaaaggc aggttggacg gcagcatcgg
1251 catcggcgcc acgaccgcct cgccaaaat ctcttggcaa ctcgccaccg
1301 gcacggcacg cacggacggc agcctcccca tcgaagcga ccccgcaaac
1351 gaacagcgga aactggtgtt cgacaccgtc aacatctccg ccggggaagg
1401 cagcctgacc gcgcaaggct atctcgagct gtttaaagac cgctgctca
1451 agctggacat cgttcccgc gcattcgacc ctccgcgat cgatccgcaa
1501 tttccggcag gcaatatcaa cgttcgatt catcttgccg gtgaactggc
1551 aaaagagaaa ttacgggca aaatgcgtt tttgccggt acgttcaacg
1601 gcgtgccgat tgccggcagc gccgacattg ttacgagtc ccgccacctt
1651 ccgcgcgcgc cgctcgattt gcggttgggg cggaaacatc taaaacaga
1701 cggcggttcc ggcaaaaaag gcgaccggct taacctcaat ataccgcac
1751 ccgatttatc ccgtttcggt ttcggactcg cggggtcttt aatgtacgc
1801 ggacaccttt ccggcgattt ggacggcggc atccgaacct ttgaaaccga
1851 cctttccggc acggcgcgca acttacacat cggcaaacg gcagacatcc
1901 gttcgctcga tttaccctc aaaggctcac ccggcacaag ccgcccgatg
1951 cgcccgata tcaaggcggc ccgcctttcc ctgtcggcg gcgcggcggt
2001 tctcgatacc gccggcctga cgttggaagg tacgggcgcg cagcagcga
2051 tccgcacaca cgcgcgatg acgctggacg gcaaacggt caaactcgat
2101 ttggacgctt caggcgcat caacaggga cttaccgat ggaaggcag
2151 catcggcatc ctgacatcg gcggcgcat caacctcaag ctgcaaaacc
2201 gtatgacgct cgaagccggt gcggaacacg tggcggaag tgcggcaaat
2251 tggcaggcaa ttggcggcag cctcaacctg caaaccttt ctgggacag
2301 gaaaaccggc atatcggcaa aaggcggcgc acgcggcctg cacatcgccg
2351 agttgcacaa tttcttcaa ccgccttcg aacacaatct ggttttaaac
2401 ggcgactggg atgtcgcta cgggcacaa gcgcgcggct acctcaatat
2451 cagccggcaa agcggcgatg ccgtattgcc cggcgggcag gctttgggtt
2501 tgaacgcatt ttccctgaaa acgcgctttc aaaacgaccg catcggaatc
2551 ctgcttgacg gcggcgcgcg tttcgacggg attaacgcgg atttgggcat
2601 cggaacgcc ttcgggcgca atatggcaaa tacaccgctc ggcggcagga
2651 ttacagcctc cttcccgcac ttgggcgat tgaagccctt tctgccgcg
2701 gccgcgcaaa acattaccgg cagcctgaat gcctccgcgc aaatcggcg
2751 acgggtaggc tctccgtccg tcaatgccgc cgtcaacggt agcagcaact
2801 acgggaaaat caacggcaat ataccgctc ggcaaacgcg ctcttcgat
2851 accgcacctt tggcgggcag gctcaacctg accgttgccg atgccgaagc
2901 attccgcaac ttctaccgg tcggacaaac cgtcaaaggc agcctgaatg
2951 ccgccgtaac cctcgcgccg agcatcgccg acccgcaact ggcggcgagt
3001 atcaacggcg acaagctcta ttaccgcaac caaacccaag gcatcatctt
3051 ggacaacggc tcgtgctgt cgcatattgc aggcaggaaa tgggtaatcg
3101 acagcctgaa attccggcac gaaggacgg cggaaactct cggcacggtc
3151 agcatggaaa acagcgtgcc cgatgtcgat atcggcggcg tgttcgacaa
3201 ataccgcatc ctgtcccgcc ccaaccgcgc cctgacgggt tccggcaaca
3251 cccgcctgcg ctattcgccg caaaaaggca tatccgttac cggtatgatt
3301 aaaactgatc aggggctgtt cggttcgcaa aaatcctcga tgcgctccgt
3351 cggcgacgat gtcgtcgtat tgggcgaagt caagaaagag gcggcgcat
3401 cgtcccccgt caatatgaac ctgactttag acctcaatga cggcatccgc

```


649

```

3451 ttctccggct acggcgcgga cgttaccata ggcggcaaac tgaccctgac
3501 cgcgcaaccg ggcggaaatg tgcgtggggg ggcacgggtc cgcgtcatca
3551 aaggcggtta caaagcatat gggcaggatt tagacattac caaaggcaca
3601 gtctcctttg tcggcccgct caacgacccc aacctgaaca tccgcgccga
3651 acgcccgcct tccccgcgtg gtgcgggctg ggaaatattg ggcagcctca
3701 acagcccgcg cattacgctg acggcaaacg aaccgatgag tgaaaaagac
3751 aagctctcct ggctcatcct caaccgtgcc ggcagcgcca gcagcgcgga
3801 caatgccgcc ctgtccgcag ccgcaggcgc gctgcttgcc gggcaaatca
3851 acgaccgcat cgggctggtg gatgatttgg gctttaccag caagcgcgagc
3901 cgcaacgcgc aaaccggcga actcaacccc gccgaacagg tgctgaccgt
3951 cggcaaacaa ctgaccggca aactctacat cggctacgaa tacggcatct
4001 ccagcgcgga acagtccgtc aaactgattt accggctgac ccgcgccata
4051 caggcggttg cccgtatcgg cagccggttc tcgggcggcg agctgacata
4101 caccatacgt ttcgaccgcc tcttcggttc ggacaaaaaa gactccgcag
4151 gaaacggcaa agggaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1182; ORF 285.ng>:

```

g285.pep
  1  MTDTTPTD TD PTENGTRKMP SEHRPAPPK KRRPLKLKSA ALLSVLILAV
 51  CFLGWIAGTE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGNWNSIET
101  EGADLKISRF RFAWKPELSE RSLHITDIS AGDIAIVTKP TPPKEERPPQ
151  GLPDSIDLPA AVYLDRFETG KISMGTDFDK QTVYLERLNA AYRYDRKGHR
201  LDLKAADTPW SSSSGSASVG LKKPFALDTA IYTKGGFEGE TIHSTARLSG
251  SLKDVRAELT IDGNIIRLSG KSVIHPFAES LDKTLEEVLV KGFNIQNSAF
301  VPSLPDAGLN FDLTAIPSFS DGIALEGS LD LENTKAGFAD RINGIPVRQVL
351  GGFVIRQDGT VHIGNTSAAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
401  EDVLQTAFKG RLDGSIGIGG TTASPKISWQ LGTGTARTDG SLPIASDPAN
451  EQRKLVFDTV NISAGEGSLT AQGYLELFKD RLLKLDIRSR AFDPSRIDPQ
501  FPAGNINGSI HLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
551  PRAAVDLRLG RNIVKTDGGF GKKGDRLNLN ITAPDLSRFG FGLAGSLNVR
601  GHLSGDLDDG IRTFETDLSE TARNLHIGKA ADIRSLDFTL KGSPGTSRPM
651  RADIKGGRLS LSGGAAVVDT AGLTLEGTGA QHRIRTHAAM TLDGKPFKLD
701  LDASGGINRE LTRWKSGSIGI LDIGGAFNLK LQNRMTLEAG AEHVAASAAN
751  WQAMGGSLNL QHFSWDRKTG ISAKGGARGL HIAELHNFFK PPFHNLVLN
801  GDWDVAYGHN ARGYLNISRQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRIGI
851  LLDGGARFGR INADLGIGNA FGGNMANTPL GGRITASLPD LGALKPFLPA
901  AAQNTGSLN ASAQIGGRVG SPSVNAAVNG SSNYGKINGN ITVQGSRSFD
951  TAPLGGRNLN TVADAEAFRN FLVPGQTVKG SLNAAVTLGG SIADPHLGGS
1001  INGDKLYYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAEISGTV
1051  SMENSVPDND IGAVFDKYRI LSRPNRRLTV SGNTRLRYSP QKGISVTGMI
1101  KTDQGLFSGS KSMPSVGDD VVVLGEVKKE AAASLPVNMN LTLDLNDGIR
1151  FSGYGADVTI GKKLTLTAQP GGNVRGVGTV RVIKGRYKAY GQDLIDITKGT
1201  VSFVGPLNDP NLNIRAERRL SPVGAGVEIL GSLNSPRITL TANEPMSKED
1251  LSWLILNRA GSGSSGDNAAL LSAAAGALLA GQINDRIGLV DDLGFTSKRS
1301  RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YGISSAEQSV KLIYRLTRAI
1351  QAVARIGSRS SGGELTYTIR FDRLFGSDKK DSAGNGKKGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1183>:

```

m285.seq
  1  ATGACCGATA CCGACCGAC AGATACCGAT CCGACCGAAA ACGGCACGCG
 51  CAAAATGCCG TCTGAACACC GCCCTACCCC GCCGGCAAAA AAACGCCGCC
101  CGTTGCTGAA GCTGTCGGCG GCACTGCTGT CTGTCCTGAT TTTGGCAGTA
151  TGTTTCCTCG GCTGGCTCGC CGGTACGGAA GCAGGTTTGC GCTTCGGGCT
201  GTACCAAATC CCGTCTTGGT TCGGCGTAAA CATTTCCTCC CAAAACCTCA
251  AAGGCACGCT GCTCGACGGC TTCGACGGCG ACAACTGGTC GATAGAAACC
301  GAGGGGGCAG ACCTTAAAT CAGCCGCTTC CGCTTCGCGT GGAAACCGTC
351  CGAACTGATG CGCCGCAGCC TGCACATTAC CGAAATTTCG GCCGGCGACA
401  TCGCCATCGT TACCAAACCG ACTCCGCTTA AAGAAGAACG CCCGGCGCTC
451  AGCCTTCCCG ACAGCATAGA CCTGCCTGCC GCCGTCTATC TCGAGCGCTT
501  CGAGACGGGC AAAATCAGCA TGGGCAAAGC CTTTGACAAA CAAACCGTCT
551  ATCTCGAACG GCTGGATGCT TCATACCGTT ACGACCGCAA AGGACACCGC
601  CTTGACCTGA AGGCCGCCGA CACGCCGTGG AGCAGTTCGT CGGGGGCGGC
651  CTCGGTCGGC TTGAAAAAAC CGTTTGCCCT CGATACCGCC ATTTACACCA
701  AAGCGGACT CGAAGGCAAA ACCATACACA GTACGGCTCG GCTGACGGCG
751  AGCCTGAAGG ATGTGCGCGC CGAACTGGCG ATCGACGGCG GCAATATCCG

```

801	CCTCTCGGGA	AAATCCGTCA	TCCACCCGTT	TGCCGAATCA	TTGGATAAAA
851	CATTGGAAGA	AGTACTGGTC	AAAGGGTTCA	ACATCAATCC	GGCCGCCTTC
901	GTGCTTCCC	TGCCCGATGC	CGGACTGAAT	TTCGACCTGA	CCGCCATCCC
951	GTCGTTTTCA	GACGGCATCG	CGCTGGAAGG	TTCGCTCGAT	TTGGAAAACA
1001	CCAAAGCCGG	CTTTGCCGAC	CGCAACGGCA	TCCCCGTCCG	TCAGGTTTTA
1051	GGCGGCTTTG	TCATCCGGCA	GGACGGCACG	GTGCATATCG	GCAATACGTC
1101	CGCCGCCCTG	CTCGGACGGG	GCGGCATCAG	GCTGTCGGGC	AAAATCGACA
1151	CCGAAAAAGA	CATCCTCGAT	TTAAATATAG	GCATCAACTC	CGTCGGCGCG
1201	GAAGACGTAC	TGCAAACCGC	GTTCAAAGGC	AGGTTGGACG	GCAGCATCGG
1251	CATCGGTGGC	ACGACCGCCT	CGCCAAAAT	CTCTTGGAAC	CTCGGCATCG
1301	GCACGGCGCG	CACGGACGGC	AGCCTCGCCA	TTGCAAGCGA	CCCAGCAAAC
1351	GGACAGCGGA	AACTGTTGCT	CGACACCGTC	AACATCGCCG	CCGGGCAAGG
1401	CAGCCTGACC	GCGCAAGGCT	ATCTCGAGCT	GTTTAAAGAC	CGCCTGCTCA
1451	AGCTGGACAT	CCGTTCCCGC	GCATTGACAC	CTTCGCGCAT	CGATCCGCAA
1501	CTTCCGGCAG	GCAATATCAA	CGGCTCAATA	AACCTTGCCG	GCGAACTGGC
1551	AAAAGAGAAA	TTACACAGGCA	AAATGCGGTT	TTTACCCGGC	ACGTTCAACG
1601	CGGTACCGAT	TGCCGGCAGT	GCCGACATTG	TTTACGAGTC	CCGCCACCTT
1651	CCGCGTGCCG	CCGTCGATTT	GCGGCTGGGG	CGGAACATTA	TTAAAACAGA
1701	CGGCGGCTTC	GGCAAAAAAG	GCGACCGGCT	TAACCTCAAT	ATCACCGCAC
1751	CCGATTTATC	CCGTTTCGGT	TTCGGACTCG	CGGGGTCTTT	AAATGTACGC
1801	GGACACCTTT	CCGGTGATTT	GGACGGCGGC	ATCCGAACCT	TTGAAACCGA
1851	CCTTTCCGGC	GCGGCGCGCA	ACCTGCACAT	CGGCAAGGCG	GCAGACATCC
1901	GTTCGCTCGA	TTTACGCTC	AAAGGTTGCG	CCGACACAAG	CCGCCCGATA
1951	CGCGCCGACA	TCAAAGGCAG	CCGCCTTTCG	CTGTGCGGCG	GAGCGGCGGT
2001	TGTCGATACC	GCCGACCTGA	TGCTGGACGG	CACGGGCGTG	CAGCACCGCA
2051	TCCGCACACA	CGCCGCCATG	ACGCTGGATG	GCAAACCGTT	CAAATTTCAT
2101	TTGGACGCTT	CAGGCGGCAT	CAACAGGGAA	CTTACCCGAT	GGAAAGGCAG
2151	CATCGGCATC	CTCGACATCG	GCGGCGCATT	CAACCTCAAG	CTGCAAAACC
2201	GTATGACGCT	CGAAGCCGGT	GCGGAACGCG	TGGCGGCAAG	TGCGGCAAAT
2251	TGGCAGGCAA	TGGGCGGCAG	CCTCAACCTG	CAACACTTTT	CTTGGGATAA
2301	AAAACCGGC	ATATCGGCAA	AAGGCGGCGC	ACACGGTCTG	CATATCGCCG
2351	AGTTGCACAA	TTTCTTCAAA	CCGCCCTTCG	AACACAATCT	GGTTTTAAAC
2401	GGCGACTGGG	ATGTCGCCTA	CGGGCGCAAC	GCGCGCGGCT	ACCTCAATAT
2451	CAGCCGGCAA	AGCGGCGATG	CCGTATTGCC	CGGCGGGCAG	GCTTTGGGTT
2501	TGAACGCATT	TTCCCTGAAA	ACGCGCTTTC	AAAACGACCG	CATCGGAATC
2551	CTGCTTGACG	GCGGCGCGCG	TTTCGGGCGG	ATTAACGCCG	ATTTGGGCAT
2601	CGCCAACGCC	TTCGGCGGCA	ATATGGCAAA	TGCACCGCTC	GGCGGCAGGA
2651	TTACCGCCTC	CCTTCCCGAC	TTGGGCGCAT	TGAAGCCCTT	TCTGCCCGCC
2701	GCCGCGCAAA	ACATTACCGG	CAGCCTGAAT	GCCGCGCGCG	AAATCGGCGG
2751	ACGGGTAGGC	TCTCCGTCGG	TCAATGCCGC	CGTCAACGGC	AGCAGCAACT
2801	ACGGGAAAAT	CAACGGCAAC	ATCACCGTCG	GGCAAAGCCG	CTCTTTCGAT
2851	ACCGCGCCTT	TGGGCGGCAG	GCTCAACCTG	ACCGTTGCCG	ATGCCGAAGT
2901	ATTCCGCAAC	TTCTTACCGG	TCGGACAAAC	CGTCAAAGGC	AGCCTGAATG
2951	CCGCCGTAAAC	CCTCGGCGGC	AGCATCGCCG	ATCCGCACTT	GGGCGGCAGC
3001	ATCAACGGCG	ACAAACTCTA	TTACCGCAAC	CAAACCCAAG	GCATCCTTCT
3051	GGACAACGGC	TCGCTGCGTT	CGCATATCGC	GGGCAGGAAA	TGGGTAATCG
3101	ACAGCCTGAA	ATTCCGGCAC	GAAGGGACGG	CGGAACCTCT	CGGTACGGTC
3151	GGTATGGAAA	ACAGCGGACC	CGATGTCGAT	ATCGGCGCGG	TGTTTCGACAA
3201	ATACCGCATC	CTGTCCCGCC	CCAACCGCCG	CCTGACGGTT	TCCGGCAACA
3251	CCCGCCTGCG	CTATTGCGCG	CAAAAAGGCA	TATCCGTTAC	CGGGATGATT
3301	AAAACGGATC	AGGGGCTGTT	CGGTTTCGAA	AAATCCTCGA	TGCCGTCCGT
3351	CGGCGACGAT	GTGTCGTAT	TAGGCGAAGT	CAAAAAGAG	GCGGCGGCAC
3401	CGTCCCGCT	CAATATGAAC	CTGACTTTAG	ACCTCAATGA	CGGCATCCGC
3451	TTCCGCGGCT	ACGGCGCGGA	CGTTACCATA	GCGGCGAAAC	TGACCTGAC
3501	CGCCAATCG	GGCGGAAGCG	TACGGGGCGT	GGGCACGGTC	CGCGTCATCA
3551	AAGGGCGTTA	TAAGGCATAC	GGGCAGGATT	TGGACATTAC	CAAAGGCACG
3601	GTCTCCTTTG	TCGGCCCGCT	CAACGATCCC	AACCTCAACA	TCCGCGCCGA
3651	ACGCCGCCTT	TCCCCCGTCG	GTGCGGGCGT	GGAAATATTG	GGCAGCCTCA
3701	ACAGCCCGCG	CATTACGCTG	ACGGCAAACG	AACCGATGAG	TGAAAAGAC
3751	AAGCTCTCTT	GGCTCATCCT	CAACCGCGCC	GGCAGCGGCA	GCAGCGGCGA
3801	CAATGCCGCC	CTGTCTGCAG	CCGCAGGTGC	GCTGCTTGCC	GGGCAAATCA
3851	ACGACCGCAT	CGGGCTGGTG	GATGATTTGG	GCTTTACCAG	CAAGCGCAGC
3901	CGCAACGCGC	AAACCGGCGA	ACTCAACCCC	GCCGAACAGG	TGCTGACCGT
3951	CGCAAAACAA	CTGACCGGCA	AACTCTACAT	CGGCTACGAA	TACAGCATCT
4001	CCAGCGCGGA	ACAGTCCGTC	AAACTGATTT	ACCGGCTGAC	CCGCGCCATA
4051	CAGGCGGTTG	CCCGTATCGG	CAGCCGTTTC	TCGGGCGGCG	AGCTGACATA

651

4101 CACCATACGT TTCGACCGCT TCTCCGGTTC GGACAAAAA GACTCCGCCG
 4151 GAAACGGCAA AGGAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1184; ORF 285>:

m285.pep
 1 MTDTAPTDTD PTENGTRKMP SEHRPTPPAK KRRPLLKLSA ALLSVLILAV
 51 CFLGWLAGE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET
 101 EGADLKISRF RFAWKPSSELM RRS�HITEIS AGDIAIVTKP TPPKEERPPL
 151 SLPDSIDLPA AVYLDRLFETG KISMKGAFDK QTVYLERLDA SYRYDRKGHR
 201 LDLKAADTPW SSSSGAASVG LKKPFALDTA IYTKGGLEGK TIHSTARLSG
 251 SLKDVRAELA IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPAAF
 301 VPSLPDAGLN FDLTAIPSF S DGIALEGS LD LENTKAGFAD RNGIPVRQVL
 351 GGFVIRQDGT VHIGNTSAA LGRGGIRLSG KIDTEKDILD LNIGINSVGA
 401 EDVLQTAFKG RLDGSIGIGG TTASPKISWQ LGIGTARTDG SLAIASDPAN
 451 GQRKLVLDTV NIAAGQGS LT AQGYLELFKD RLLKLDIRS AFDPSRIDPQ
 501 LPAGNINGSI NLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
 551 PRAAVDLRLG RNIIKT DGGF GKKGDRNLN ITAPDLSRFG FGLAGSLNVR
 601 GHLSGDL DGG IRTFETDLSG AARNLHIGKA ADIRSLDFTL KGSPDTSRPI
 651 RADIKGSRLS LSGGA AVVD ADLMLDGTGV QHRIRTHAAM TLDGKPFKFD
 701 LDASGGINRE LTRWKSGSIGI LDIGGAFNLK LQNRMTLEAG AERVAASAAN
 751 WQAMGGS LN LH QHFSWDKKTG ISAKGGAHGL HIAELHNFFK PPFEHNLVLN
 801 GDWDVAYGRN ARGYLNISRQ SGDAVLP GGQ ALGLNAFSLK TRFQNDRIGI
 851 LLDGGARFGR INADLGIANA FGGNMANAPL GGRITASLPD LGALKPFLLPA
 901 AAQNITGSLN AAAQIGGRVG SPSVNAAVNG SSNYGKINGN ITVGQSRSEF
 951 TAPLGGRLNL TVADAEVFRN FLPVGQTVKG SLNAAVTLGG SIADPHLGGS
 1001 INGDKLYYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSCTV
 1051 GMENSGPDVD IGAVFDKYRI LSRPNRRLTV SGNTRLRYSP QKGISVTGMI
 1101 KTDQGLFGSQ KSSMP SVGDD VVVLGEVKKE AAAPLPVNMN LTLDLNDGIR
 1151 FAGYGADV TI GGKLT LTAQS GGSVRGVGT V RVIKG RYKAY QQDL DITKGT
 1201 VSFVGPLNDP NLNIRAERRL SPVGAGVEIL GSLNSPRITL TANEPMSEKD
 1251 KLSWLILNRA GSGSSGDNA LSAAGALLA GQINDRIGLV DDLGFTSKRS
 1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YSISAEQSV KLIYRLTRAI
 1351 QAVARIGSRS SGGELTYTIR FDRFSGSDKK DSAGNGKKGK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m285/g285 96.5% identity in 1389 aa overlap

	10	20	30	40	50	60
m285.pep	MTDTAPTDTDPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE					
g285	MTDTTPTDTDPTENGTRKMPSEHRPAPPAKRRPLLKLSAALLSVLILAVCFLGWIAGE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m285.pep	AGLRFGLYQIPSWFGVNISSQNLKGTLLDGF DGDNWSIETEGADLKISRFRFAWKPSSELM					
g285	AGLRFGLYQIPSWFGVNISSQNLKGTLLDGF DGDNWSIETEGADLKISRFRFAWKPSSELM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m285.pep	RRSLHITEISAGDIAIVTKPTTPKEERPPLSLPDSIDLPAAVYLDRLFETGKISMKGAFDK					
g285	RRSLHITDISAGDIAIVTKPTTPKEERPQGLPDSIDLPAAVYLDRLFETGKISMKGTFDK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m285.pep	QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGAASVGLKPPFALDTAIYTKGGLEGK					
g285	QTVYLERLNAAARYDRKGHRDLKAADTPWSSSSGSASVGLKPPFALDTAIYTKGGFEGE					
	190	200	210	220	230	240
	250	260	270	280	290	300
m285.pep	TIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIHPFAESLDKTLEEVLVKGFNINPAAF					

[illegible]

[illegible]

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1185>:

a285.seq	1	ATGACCGATA	CCGCACCGAC	AGATACCGAT	CCGACCGAAA	ACGGCACGCG
	51	CAAATGCGG	TCTGAACACC	GCCCTACCCC	GCCGGCAAAA	AAACGCCGCC
	101	CGTGCTGAA	GCTGTCGGCG	GCACTGCTGT	CTGTCTGTAT	TTTGGCAGTA
	151	TGTTTCTCG	GCTGGCTCGC	CGGCACGGAA	GCGGGTTTGC	GCTTCGGGCT
	201	GTACCAAATC	CCGTCTTGGT	TCGGCGTAAA	CATTTCTCTC	CAAAACCTCA
	251	AAGGCACGCT	GCTCGACGGC	TTCGACGGCG	ACAACTGGTC	GATAGAAACC
	301	GAGGGGGCAG	ACCTTAAAA	CAGCCGCTTC	CGCTTCGGCT	GGAAACCGTC
	351	CGAACTGATG	CGCCGCAGCC	TGCACATTAC	CGAAATTTCC	CCCGCCGACA
	401	TCGCCATCGT	TACCAAACCG	ACTCCGCCTA	AAGAAGAACG	CCCGCCGCTC
	451	AGCCTTCCCG	ACAGCATAGA	CCTGCCTGCC	GCCGTCTATC	TCGACCGCTT
	501	CGAGACGGGC	AAAATCAGCA	TGGGCAAAGC	CTTTGACAAA	CAAACCGTCT
	551	ATCTCGAAGC	GCTGGATGCT	TCATACCGTT	ACGACGCCAA	AGGACACCGC
	601	CTCGACCTGA	AGGCTGCCGA	CACCGCGTGG	AGCAGTTTCT	CGGGTCTCAG

```

651 CTCGGTCGGC TTGAAAAAAC CGTTTGCCCT CGATACCGCC ATTTACACCA
701 AAGGCGGACT CGAAGGCAAA ACCATACACA GTACGGCTCG GCTGAGCGGC
751 AGCCTGAAGG ATGTGCGCGC CGAACTGGCG ATCGACGGCG GCAATATCCG
801 CCTCTCGGGA AAATCCGTCA TCCACCCGTT TGCCGAATCA TTGGATAAAAA
851 CATTGGAAGA AGTACTGGTC AAAGGGTTCA ACATCAATCC GTCCGCCTTC
901 GTGCCTTCCC TGCCCGATGC CGGGCTGAAT TTCGACCTGA CCGCCATCCC
951 GTCGTTTTCA GACGGCATCG CGCTGGAAGG CTCGCTCGAT TTGGAACAACA
1001 CCAAAGCCGG CTTTGCCGAC CGCAACGGCA TCCCGTCCG TCAGGTTTTA
1051 GGCAGCTTTG TCATCCGGCA GGACGGCAG GTGCATATCG GCAATACGTC
1101 CGTCGCCCTG CTCGGACGGG GCGGCATCAG GCTGTCGGGC AAAATCGACA
1151 CCGAAAAAGA CATCCTCGAT TTAAATATAG GCATCAACTC CGTCGGCGCG
1201 GAAGACGTAC TGCAAACCGC GTTCAAAGGC AGGTTGGACG GCAGCATCGG
1251 CATCGGTGGC ACGACCGCCT CGCCAAAAT CTCTTGCAA CTCGGCATCG
1301 GCACGGCGCG CACGGACGGC AGCCTCGCCA TTGCAAGCGA CCCCAGAAC
1351 GGACAGCGGA AACTGGTGCT CGACACCGTC AACATCGCCG CCGGGCAAGG
1401 CAGCCTGACC GCGCAAGGCT ATCTCGAGCT GTTTAAAGAC CGCTGCTCA
1451 AGCTGGACAT CCGTTCCCGC GCATTGACAC CTTGCGCAT CGATCCGCA
1501 CTTCCGGCAG GCAATATCAA CGGCTCAATA AACCTTGCCG GCGAACTGGC
1551 AAAAGAGAAA TTCACAGGCA AAATGCGGTT TTTACCCGGC ACGTCAACG
1601 GCGTACCGAT TGCCGGCAGT GCCGACATTG TTTACGAGTC CCGCCACCTT
1651 CCGCGTGCCG CCGTCGATTT GCGGCTGGGG CGGAACATTA TTAAACAGA
1701 CGGCGGCTTC GGCAAAAAG GCGACCGGCT TAACCTCAAT ATCACCAC
1751 CCGATTTATC CCGTTTCGGT TTCGGACTCG CCGGGTCTTT AAATGTACGC
1801 GGACACCTTT CCGGCGATTT GGACGGTGGC ATCCGAACCT TTGAAACCGA
1851 CCTTTCCGGC GCGGCGCGCA ACCTGCACAT CGGCAAGGCG GCAGACATCC
1901 GTTCGCTCGA TTTCACGCTC AAAGTTTCGC CCGACACAAG CCGCCGATA
1951 CGCGCCGACA TCAAAGGCAG CCGCCTTTCG CTGTCGGGCG GAGCGGAGGT
2001 TGTCGATACC GCCGACCTGA TGCTGGACGG CACGGGCGTG CAGCACCAGC
2051 TCCGCACACA CGCCGCCATG ACGCTGGATG GCAAACCGTT CAAATTCGAT
2101 TTGGACGCTT CAGGCGGCAT CAACAGGGAA CTTACCCGAT GGAAGGCAG
2151 CATCGGCATC CTCGACATCG GCGGCGCATT CAACCTCAAG CTGCAAAACC
2201 GTATGACGCT CGAAGCCGGT GCGGAACGCG TGGCGGCAAG TCGGCAAAAT
2251 TGGCAGGCAA TGGGCGGCAG CCTCAACCTG CAACACTTTT CTTGGGATAA
2301 AAAAACCAGC ATATCGGCAA AAGGCGGCGC ACACGGTCTG CATATCGCCG
2351 AGTTGCACAA TTTCTTCAAA CCGCCCTTCG AACACAATCT GGTTTTAAAC
2401 GGCGACTGGG ATGTGCGCTA CCGGCGAAAC GCGCGCGGCT ACCTCAATAT
2451 CAGCCGGCAA AGCGGCGATG CCGTATTGCC CCGCGGGCAG GCTTTGGGTT
2501 TGAACGCATT TTCCCTGAAA ACGCGCTTTC AAAACGACCG TATCGGAATC
2551 CTGCTTGACG GCGGCGCGCG TTTCGGGCGG ATTAACGCCG ATTTGGACAT
2601 CGGCAACGCC TTCGGCGGCA ATATGGCAA TGCACCGCTC GCGGCGAGGA
2651 TTACCGCCTC CTTTCCCGAC TTGGGCACAT TGAAGCCCTT TCTGCCCGCC
2701 GCCGCGCAAA ACATTACCGG CAGCCTGAAT GCCGCGCGC AAATCGGCGG
2751 ACGGGTCGGC TCTCCGTCCG TCAATGCCGC CGTCAACGGC AGCAGCAACT
2801 ACGGGAAAT CAACGGCAAC ATCACCCTCG GGCAAGCCG CTCTTTCGAT
2851 ACCGCGCCTT TGGGCGGCAG GCTCAACCTG ACCGTTGCCG ATGCCGAAGT
2901 ATTCGCAAC TTCTACCGG TCGGACAAAC CGTCAAAGGC AGCCTGAATG
2951 CCGCCGTAAC CCTCGGCGGC AGCATCGCCG ATCCGCACTT GGGCGGACG
3001 ATCAACGGCG ACAAACCTTA TTACCGCAAC CAAACCCAAG GCATCATCTT
3051 GGACAACGGC TCGCTGCGTT CGCATATCGC GGGCAGGAAA TGGGTAATCG
3101 ACAGCCTGAA ATTCCGGCAC GAAGGGACGG CGGAACCTC CGGTACGGTC
3151 GGTATGAAA ACAGCGGACC CGATGTCGAT ATCGGCGCGG TGTTCGACAA
3201 ATACCGCATC CTGTCCCGCC CCAACCGCCG CCTGACGGTT TCCGGCAACA
3251 CCCGCTGCG CTATTCGCCG CAAAAGGCA TATCCGTTAC CGGGATGATT
3301 AAAACGATC AGGGGCTGTT CGGTTTCGCA AAATCCTCGA TGCCGTCCGT
3351 CGGCGACGAT GTCGTCGTAT TAGGCGAAGT CAAAAAGAG GCGGCGGCAC
3401 CGCTCCCGT CAATATGAAC CTGACTTTAG ACCTCAATGA CGGCATCCG
3451 TTCGCCGGCT ACGGCGCGGA CGTTACCATA GCGGCAAAAC TGACCTGAC
3501 CGCCCAATCG GCGGAAGCG TGCGGGGCGT GGGCACGGTC CGCGTCATCA
3551 AAGGGCGTTA TAAGGCATAC GGGCAGGATT TGGACATTAC CAAAGGCACG
3601 GTCTCCTTTG TCGGCCCGCT CAACGACCCC AACCTCAACA TCCGCGCCGA
3651 ACGCGCCTT TCCCCGTCG GTGCGGGCGT GGAATATTG GGCAGCCTCA
3701 ACAGTCCGCG CATTACGCTG ACGGCAAACG AACCGATGAG TGAAAAAGAC
3751 AAGCTCTCCT GGCTCATCCT CAACCGCGCC GGCAGTGGCA GCAGCGGCGA
3801 CAATGCCGCC CTGTCCGCGA CCGCCGGCGC GCTGCTTGCC GGGCAAATCA
3851 ACGACCGCAT CGGGCTGGTG GATGATTTGG GCTTTACCAG CAAGCGCAGC
3901 CGCAACGCGC AAACCGCGCA ACTCAACCCC GCCGAACAGG TGCTGACCGT

```

655

```

3951 CGGCAAACAA CTGACCGGCA AACTCTACAT CGGCTACGAA TACAGCATCT
4001 CCAGCGCGGA ACAGTCCGTC AAAGTATT ACCGGCTGAC CCGCGCCATA
4051 CAGGCGGTTG CCCGTATCGG CAGCCGTTTC TCGGGCGGCG AGCTGACATA
4101 CACCATACGT TTCGACCGCT TCTCCGGTTC GGACAAAAAA GACTCCGCCG
4151 GAAACAGCAA AGGAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1186; ORF 285.a>:

```

a285.pep
  1 MTDAPTDTD PTENGTRKMP SEHRPTPPAK KRRPCLKLSA ALLSVLILAV
  51 CFLGWLAGE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET
 101 EGADLKISRF RFAWKPSSELM RRSLLHITEIS AGDIAIVTKP TPPKEERPPL
 151 SLPDSIDLPA AVYLDREFETG KISMKGAFDK QTVYLERLDA SYRYDRKGHR
 201 LDLKAADTPW SSSSGSASVG LKKPFALDTA IYTKGGLEGK TIHSTARLSG
 251 SLKDVRAELA IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPSAF
 301 VPSLPDAGLN FDLTAIPSEF DGIALEGLSD LENTKAGFAD RNGIPVRQVL
 351 GSFVIRQDGT VHIGNTSVAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
 401 EDVLQTAFCG RLDGSIGIGG TTASPKISWQ LGIGTARTDG SLAIASDPAN
 451 GQRKLVLDTV NIAAGQGSILT AQGYLELFKD RLLKLDIRSR AFDPSRIDPQ
 501 LPAGNINGSI NLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
 551 PRAAVDLRLG RNIIKTDGGF GKKGDRLNLN ITAPDLRFSG FGLAGSLNVR
 601 GHLSGDLGG IRTFETDLSE AARNLHIGKA ADIRSLDFTL KGSPDTSRPI
 651 RADIKGSRLS LSGGAEVVDI ADLMLDGTGV QHRIRTHAAM TLDGKPFKFD
 701 LDASGGINRE LTRWKGSIIGI LDIGGAFNLK LQNRMTLEAG AERVAASAAN
 751 WQAMGGSLNL QHFSWDKKTG ISAKGGAHGL HIAELHNFFK PPFENLVLN
 801 GDWDVAYGRN ARGYLNISRQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRIGI
 851 LLDGGARFGR INADLDIGNA FGGNMANAPL GGRITASLPD LGTLKPFPLPA
 901 AAQNTGSLN AAAQIGGRVG SPSVNAAVNG SSNYGKINGN ITVQSRSFSD
 951 TAPLGGRLNL TVADAEVFRN FLPVGQTVKG SLNAAVTLGG SIADPHLGGS
1001 INGDKLYYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV
1051 GMENSGPDVD IGAVFDKYRI LSRPNRRLTV SGNTRLRYSP QKGISVTGMI
1101 KTDQGLFSGQ KSSMPSVGDD VVVLGEVKKE AAAPLPVNMN LTLDLNDGIR
1151 FAGYGADVTI GGKLTTLTAQS GGSVRGVGTV RVIKGRYKAY GQDLDTKGT
1201 VSFVGPLNDP NLNIRAERRL SPVGAGVEIL GSLNSPRITL TANEPMSKED
1251 KLSWLILNRA GSGSSGDNA LSAAGALLA GQINDRIGLV DDLGFTSKRS
1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YSISSAEQSV KLIYRLTRAI
1351 QAVARIGSRS SGGELTYTIR FDRFSGSDKK DSAGNSKKG*

```

m285/a285 99.4% identity in 1389 aa overlap

```

              10      20      30      40      50      60
m285.pep      MTDAPTDTDPTENGTRKMPSEHRPTPPAKKRRPCLKLSAALLSVLILAVCFLGWLAGE
              |||||
a285           MTDAPTDTDPTENGTRKMPSEHRPTPPAKKRRPCLKLSAALLSVLILAVCFLGWLAGE
              10      20      30      40      50      60

              70      80      90      100     110     120
m285.pep      AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGDNWSIETEGADLKISRFRFAWKPSSELM
              |||||
a285           AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGDNWSIETEGADLKISRFRFAWKPSSELM
              70      80      90      100     110     120

              130     140     150     160     170     180
m285.pep      RRSLLHITEISAGDIAIVTKPTPPKEERPPLSLPDSIDLPAAVYLDREFETGKISMKGAFDK
              |||||
a285           RRSLLHITEISAGDIAIVTKPTPPKEERPPLSLPDSIDLPAAVYLDREFETGKISMKGAFDK
              130     140     150     160     170     180

              190     200     210     220     230     240
m285.pep      QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGAASVGLKKPFALDTAIYTKGGLEGK
              |||||
a285           QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGSASVGLKKPFALDTAIYTKGGLEGK
              190     200     210     220     230     240

              250     260     270     280     290     300
m285.pep      TIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIHPFAESLDKTLEEVLVKGFNINPAAF
              |||||

```

656

a285	TIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIHPFAESLDKTLLEEVLVKGFNINPSAF
	250 260 270 280 290 300
m285.pep	310 320 330 340 350 360
	VPSLPDAGLNFDLTAIPSFSDGIALEGSLENTKAGFADRNGIPVRQVLGGFVIRQDGT
a285	VPSLPDAGLNFDLTAIPSFSDGIALEGSLENTKAGFADRNGIPVRQVLGSFVIRQDGT
	310 320 330 340 350 360
m285.pep	370 380 390 400 410 420
	VHIGNTSAALLGRGGIRLSGKIDTEKDILDNLNIGINSVGAEDVLQTAFKGRLDGSIGIGG
a285	VHIGNTSVALGRGGIRLSGKIDTEKDILDNLNIGINSVGAEDVLQTAFKGRLDGSIGIGG
	370 380 390 400 410 420
m285.pep	430 440 450 460 470 480
	TTASPKISWQLGIGTARTDGLAIASDPANGQRKLVLDTVNIAAGQGSILTAQGYLELFKD
a285	TTASPKISWQLGIGTARTDGLAIASDPANGQRKLVLDTVNIAAGQGSILTAQGYLELFKD
	430 440 450 460 470 480
m285.pep	490 500 510 520 530 540
	RLKLDIRSRAFDPSRIDPQLPAGNINGSINLAGELAKEKFTGKMRFLPGTFNGVPIAGS
a285	RLKLDIRSRAFDPSRIDPQLPAGNINGSINLAGELAKEKFTGKMRFLPGTFNGVPIAGS
	490 500 510 520 530 540
m285.pep	550 560 570 580 590 600
	ADIVYESRHLPRAAVDLRLGRNIIKTDGGFGKKGDRNLNLNITAPDLRSRFGFGLAGSLNVR
a285	ADIVYESRHLPRAAVDLRLGRNIIKTDGGFGKKGDRNLNLNITAPDLRSRFGFGLAGSLNVR
	550 560 570 580 590 600
m285.pep	610 620 630 640 650 660
	GHLSGDLGGIRTFFETDLGAARNLHIGKAADIRSLDFTLKGSPTSRPIRADIKGSRLS
a285	GHLSGDLGGIRTFFETDLGAARNLHIGKAADIRSLDFTLKGSPTSRPIRADIKGSRLS
	610 620 630 640 650 660
m285.pep	670 680 690 700 710 720
	LSGGAHVDTADLMLDGTGVQHRIRTHAAMTLDGKPFKFDLDASGGINRELTRWKSGSIGI
a285	LSGGAHVDTADLMLDGTGVQHRIRTHAAMTLDGKPFKFDLDASGGINRELTRWKSGSIGI
	670 680 690 700 710 720
m285.pep	730 740 750 760 770 780
	LDIGGAFNLKLQNRMTLEAGAERVAASAANWQAMGGSNLQHFSWDKKTGISAKGGAHGL
a285	LDIGGAFNLKLQNRMTLEAGAERVAASAANWQAMGGSNLQHFSWDKKTGISAKGGAHGL
	730 740 750 760 770 780
m285.pep	790 800 810 820 830 840
	HIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYLNISRQSGDAVLPGGQALGLNAFSLK
a285	HIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYLNISRQSGDAVLPGGQALGLNAFSLK
	790 800 810 820 830 840
m285.pep	850 860 870 880 890 900
	TRFQNDRIGILLDGGARFGRINADLGIANAFGGNMANAPLGGRITASLPDLGALKPFLPA
a285	TRFQNDRIGILLDGGARFGRINADLGIANAFGGNMANAPLGGRITASLPDLGALKPFLPA
	850 860 870 880 890 900
m285.pep	910 920 930 940 950 960
	AAQNITGSLNAAQIGGRVGSFVNAAVNGSSNYGKINGNITVGQSRSFDTAPLGGRNLNL
a285	AAQNITGSLNAAQIGGRVGSFVNAAVNGSSNYGKINGNITVGQSRSFDTAPLGGRNLNL

657

a285	AAQNITGSLNAAAQIGGRVGS	PSVNAAVNGSSNYGKINGNITVGQSR	SFDTAPLGGRLNL		
	910	920	930	940	950 960
m285.pep	970	980	990	1000	1010 1020
	TVADAEVFRNFLPVGQTVKGS	LNAAVTLGGSIADPHLGG	SINGDKLYYRNQTQGI	ILDNG	
a285	TVADAEVFRNFLPVGQTVKGS	LNAAVTLGGSIADPHLGG	SINGDKLYYRNQTQGI	ILDNG	
	970	980	990	1000	1010 1020
m285.pep	1030	1040	1050	1060	1070 1080
	SLRSHIAGRKWVIDSLKFR	HEGTAELSGTVGMENSG	PDVDIGAVFDKYRILSR	PNRRLTV	
a285	SLRSHIAGRKWVIDSLKFR	HEGTAELSGTVGMENSG	PDVDIGAVFDKYRILSR	PNRRLTV	
	1030	1040	1050	1060	1070 1080
m285.pep	1090	1100	1110	1120	1130 1140
	SGNTRLRYS	PQKGISVTGMIKTDQGL	FGSQSSMPSVGD	DDVVVLGEVKKEAA	APLPVNMN
a285	SGNTRLRYS	PQKGISVTGMIKTDQGL	FGSQSSMPSVGD	DDVVVLGEVKKEAA	APLPVNMN
	1090	1100	1110	1120	1130 1140
m285.pep	1150	1160	1170	1180	1190 1200
	LTLDLNDGIRFAGYGADVT	IGGKLTTLTAQSGGS	VRGVGTVRVIKGRY	KAYQDLDITKGT	
a285	LTLDLNDGIRFAGYGADVT	IGGKLTTLTAQSGGS	VRGVGTVRVIKGRY	KAYQDLDITKGT	
	1150	1160	1170	1180	1190 1200
m285.pep	1210	1220	1230	1240	1250 1260
	VSVFVGPLNDPNL	NIRAERRLSPVGAG	VEILGSLNSPRIT	LTANEPMSEKDKL	SWLIILNRA
a285	VSVFVGPLNDPNL	NIRAERRLSPVGAG	VEILGSLNSPRIT	LTANEPMSEKDKL	SWLIILNRA
	1210	1220	1230	1240	1250 1260
m285.pep	1270	1280	1290	1300	1310 1320
	GSGSSGDNAALSAA	AAGALLAGQINDRIG	LVDDLGF	TSKRSRNAQTGEL	NPAEQVLT
a285	GSGSSGDNAALSAA	AAGALLAGQINDRIG	LVDDLGF	TSKRSRNAQTGEL	NPAEQVLT
	1270	1280	1290	1300	1310 1320
m285.pep	1330	1340	1350	1360	1370 1380
	LTGKLYIGYEYSIS	SAEQSVKLIYRLTRAI	QAVARIGSRSSG	GELTYTIRFDR	FSGSDKK
a285	LTGKLYIGYEYSIS	SAEQSVKLIYRLTRAI	QAVARIGSRSSG	GELTYTIRFDR	FSGSDKK
	1330	1340	1350	1360	1370 1380
m285.pep	1390				
	DSAGNGKGKX				
a285	DSAGNSKGKX				
	1390				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1187>:

g285-1.seq

```

1  CTGAAGCTGT  CGGCGGCACT  GCTGTCTGTC  CTGATTTTGG  CAGTATGTTT
51  CCTCGGCTGG  ATCGCCGGTA  CGGAAGCAGG  TTTGCGCTTC  GGGCTGTACC
101 AAATCCCGTC  CTGGTTCGGC  GTAAACATTT  CCTCCCAAAA  CCTCAAAGGC
151 ACGCTGCTCG  ACGGCTTCGA  CGGCGACAAC  TGGTCGATAG  AAACCGAGGG
201 GGCAGACCTT  AAAATCAGCC  GCTTCCGCTT  CGCGTGGAAC  CCGTCCGAAC
251 TGATGCGCCG  CAGCCTGCAC  ATCACCAGCA  TCTCCGCCGG  CGACATCGCC
301 ATCGTAACCA  AACCGACTCC  GCCTAAAGAA  GAACGCCCGC  CTCAAGGCCT
351 GCCCACAGC  ATAGACCTGC  CCGCCGCCGT  CTATCTCGAC  CGCTTCGAGA
401 CGGGCAAAAT  CAGCATGGGC  AAAACCTTTG  ACAAACAAAC  CGTCTATCTC
451 GAACGCCTCA  ACGCGGCATA  CCGTTACGAC  CGTAAAGGGC  ACCGCCTCGA
501 CCTGAAGGCC  GCCGACACGC  CGTGAGCAG  TTCGTCGGGG  TCAGCCTCGG

```

```

551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGATTCTGAAG GCGAAACCAT ACACAGTACG GCGCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CGCGCCGAAC TGACGATCGA CGGCGGCAAT ATCCGCCTCT
701 CGGGAATATC CGTCATCCAC CCGTTTGCCG AATCATTTGA TAAACATTG
751 GAAGAAGTAC TGGTCAAAGG ATTCAACATC AATCCGTCCG CCTTCGTGCC
801 TTCCCTGCCC GATGCCGGGC TGAATTTCGA CCTGACCGCC ATCCCGTCGT
851 TTTTCAGACGG CATCGCGCTG GAAGGCTCGC TCGATTTGGA AAACACCAAA
901 GCCGGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTCAGG TTTTGGGCGG
951 CTTTGTCTATC CGGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGCCG
1001 CCCTGCTCGG ACGGGGCGGC ATCAGGCTGT CGGGCAAAAT CGACACCGAA
1051 AAAGACATCC TTGATTTAAA TATAGGCATC AACTCCGTCG GCGCGGAAGA
1101 CGTGCTGCAA ACCGCTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GCGGCACGAC CGCCTCGCCC AAAATCTCTT GGCAACTCGG CACCGGCACG
1201 GCACGCACGG ACGGCAGCCT cgcCATCGCA AGCGACCCCG CAAACGAACA
1251 GCGGAACTAG GTGTTGACAC CCGTCAACAT CTCCGCGGGG GAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCCGCGCATT CGACCCCTCG CGCATCGATC CGCAATTTCC
1401 GGCAGGCGat atCAACGGTT CGATTCATCT TGCCGGTGAA CTGGCAAAAG
1451 AGAAATTTAC GGGCAAAATG CGTTTTTTGC CCGGTACGTT CAACGGCGTG
1501 CCGATTGCCG GCAGCGCCGA CATTGTTTAC GAGTCCCGCC ACCTTCCGCG
1551 CGCCGCGCTC GATTTGCGGT TGGGGCGGAA CATCGTCAAA ACAGACGGCG
1601 GCTTCGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGCACCCGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CCTTTCGGGC GATTTGGACG GCGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CCGGCACGGC GCGCAACTTA CACATCGGCA AAGCGGCAGA CATCCGTTCC
1801 CTCGATTTTA CCTCAAAAGG CTCACCCGGC ACAAGCCGCC CGATGCGCGC
1851 CGATATCAAG GGGGGCCGCC TTTCCCTGTC GGGCGGCGCG GCGGTGTGCG
1901 ATACCGCCGG CCTGACGCTG GAAGGTACGG GCGCGCAGCA CCGCATCCGC
1951 ACACACGCGC CCATGACGCT GGACGGCAAA CCGTTCAAA TCATTGGA
2001 CGCTTCAGGC GGCATCAACA GGGAACTTAC CCGATGGAAG GGCAGCATCG
2051 GCATCTCTGA CATCGCGGGC GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACACGTGGCG GCAAGTGGCG CAAATGGCA
2151 GCAATGGGC GGCAGCCTCA ACCTGCAACA CTTTCTTGG GACAGGAAAA
2201 CCGGCATATC GGCAAAAGGC GGCACGCGC GCCTGCACAT CGCCGAGTTG
2251 CACAATTTCT TCAAACCGCC CTTGCAACAC AATCTGGTTT TAAACGGCGA
2301 CTGGGATGTC GCCTACGGGC ACAACGCGCG CGGCTACCTC AATATCAGCC
2351 GGCAAAGCGG CGATGCCGTA TTGCCCGGCG GGCAGGCTTT GGGTTGAAC
2401 GCATTTTCCC TGAAAACGCG CTTTCAAAAC GACCGCATCG GAATCCTGCT
2451 TGACGGCGGC GCGCGTTTCG GACGGATTAA CGCCGATTG GGCATCGGCA
2501 ACGCCTTCGG CGGCAATATG GCAAATACAC CGCTCGGCGG CAGGATTACA
2551 GCCTCCCTTC CCGACTTGGG CGCATGGAAG CCCTTTCTGC CCGCCGCCGC
2601 GCAAAACATT ACCGGCAGCC TGAATGCCTC CGCGCAATC GCGGACGGG
2651 TAGGCTCTCC GTCCGTCAAT GCCGCGTCA ACGGTAGCAG CAACTACGGG
2701 AAAATCAACG GCAATATCAC CGTCGGGCAA AGCCGCTCCT TCGATACCGC
2751 ACCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGCATTC
2801 GCAACTTCCT ACCGGTCGGA CAAACCGTCA AAGGCAGCCT GAATGCCGCC
2851 GTAACCTTCG GCGGCAGCAT CGCCGACCCG CACTTGGGCG GCAGTATCAA
2901 CGGCGACAAG CTCTATTACC GCAACCAAA CCAAGGCATC ATCTTGGACA
2951 ACGGCTCGCT GCGTTGCGAT ATTGCAGGCA GGAAATGGGT AATCGACAGC
3001 CTGAAATTTCC GGCACGAAGG GACGGCGGAA CTCTCCGGCA CGGTACGAT
3051 GGAACACAGC GTGCCCGATG TCGATATCGG CGCGGTGTTT GACAAATACC
3101 GCATCTGTGC CCGCCCAAC CGCCGCTGA CCGTTTCCGG CAACACCCGC
3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGTA TGATTAAAA
3201 TGATCAGGGG CTGTTGCGTT CGCAAAAATC CTCGATGCCG TCCGTGCGCG
3251 ACGATGTCGT CGTATTGGGC GAAGTCAAGA AAGAGCGCGG GGCATCGCTC
3301 CCCGTCAATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGTTCTC
3351 CGGCTACGGC GCGGACGTTA CCATAGGCGG CAAACTGACC CTGACCGCGC
3401 AACCGGGCGG AAATGTGCGT GGGGTGGGCA CCGTCCGCGT CATCAAAGGG
3451 CGTTACAAAG CATACGGGCA GGATTAGAC ATTACCAAAG GCACAGTCTC
3501 CTTTGTGCGC CCGCTCAACG ACCCAACCT GAACATCCG GCCGAACGCC
3551 GCCTTTCCCG CGTCGGTGCG GCGTGGAATA TATTGGGCGG CCTCAACAGC
3601 CCGCGCATTA CGCTGACGGC AAACGAACCG ATGAGTGAAG AAGACAAGCT
3651 CTCCTGGCTC ATCCTCAACC GTGCCGGCAG CGGCAGCAGC GGCACAATG
3701 CGCCCTGTGC CGCAGCCGCA GCGCGCTGCT TTGGCGGGCA AATCAACGAC
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 CGCGCAAAAC GCGCAACTCA ACCCGCCGA ACAGGTGCTG ACCGTGCGCA
3851 AACAACTGAC CGGCAAACTC TACATCGGCT ACGAATACGG CATCTCCAGC
3901 GCGGAACAGT CCGTCAAACT GATTTACCGG CTGACCCGCG CCATACAGGC
3951 GGTTCGCCGT ATCGGCAGCC GTTCGTGCGG CGGCGAGCTG ACATACACCA
4001 TACGTTTCGA CCGCCTCTTC GGTTCGGACA AAAAGACTC CGCAGGAAAC
4051 GGCAAAAGGA AATAA

```

This corresponds to the amino acid sequence <SEQ ID 1188; ORF 285-1.ng>:
g285-1.pep

```

1  LKLSAALLSV LILAVCFLGW IAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51  TLLDGFEDGDN WSIETEGADL KISRFRFAWK PSELMRRSLH ITDISAGDIA
101 IVTKPTPPKE ERPPQGLPDS IDLPAAVYLD RFETGKISMG KTFDKQTVYL
151 ERLNAAYRYD RKGHRDLKA ADTPWSSSSG SASVGLKPPF ALDTAIYTKG
201 GFEGETIHST ARLSGSLKDV RAELTIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP VRQVLGGFVI RQDGTVHIGN TSAALLGRGG IRLSGKIDTE
351 KDILDLNIGI NSVGAEDVLQ TAFKGRLDGS IGIGGTTASP KISWQLGTGT
401 ARTDGSIAIA SDPANEQRKL VFDTVNISAG EGSLTAQGYL ELFKDRLLKL
451 DIRSRAFDPS RIDPQFPAGD INGSIHLAG EAKEFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIVK TDGGFGKKGD RLNLNITAPD
551 LSRFGFGLAG SLNVRGHL SG DLDGGIRTFE TDLSGTARNL HIGKAADIRS
601 LDFTLKSGPG TSRPMRADIK GGRLSLSGGA AVVDTAGLTL EGTGAQHRIR
651 THAAMTLDGK PFKLDLDASG GINRELTRWK GSIGILDIGG AFNLKLQNRM
701 TLEAGAEHVA ASANWQAMG GSLNLQHFSW DRKTGISAKG GARGLHIAEL
751 HNFFKPPFEH NLVLNGDWDV AYGHNARGYL NISRQSGDAV LPPGQALGLN
801 AFSLKTRFQN DRIGILLDGG ARFGRINADL GIGNAFGGNM ANTPLGGRIT
851 ASLPDLGALK PFLPAAAQNI TGSLNASHAQI GGRVGSPSVN AAVNGSSNYG
901 KINGNITVGQ SRSFDTAPLG GRLNLTVADA EAFRNFPLVG QTVKGSINAA
951 VTGGSGIADP HLGGSINGDK LYYRNQTQGI ILDNGLSLRSH IAGRKWVIDS
1001 LKFRHEGTAE LSGTVSMENS VPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGSY VTGMIKTDQG LFGSQKSSMP SVGDDVVVLG EVKKEAAASL
1101 PVMNMLTLDL NDGIRFSGYG ADVTIGGKLT LTAQPGGNVR GVGTVRVIK
1151 RYKAYGQDLD ITKGTVSFVG PLNDPNLNIR AERRLSPVGA GAILGSLNS
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAA GALLAQIND
1251 RIGLVDDLGF TSKRSRNAQT GELNPAEQVL TVGKQLTGKL YIGYEGISS
1301 AEQSVKLIYR LTRAIQAVAR IGSRSSGGEL TYTIRFDRLF GSDKKDSAGN
1351 KGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1189>:

m285-1.seq

```

1  CTGAAGCTGT CGGCGGCACT GCTGTCTGTC CTGATTTTGG CAGTATGTTT
51  CCTCGGCTGG CTCGCCGTA CGGAAGCAGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCCTC TTGGTTCGGC GTAAACATTT CCTCCCAAAA CCTCAAAGGC
151 ACCTGCTCGC ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAC CCGTCCGAAC
251 TGATGCGCCG CAGCCTGCAC ATTACCGAAA TTTCCGCCGG CGACATCGCC
301 ATCGTTACCA AACCGACTCC GCCTAAAGAA GAACGCCCGC CGCTCAGCCT
351 TCCCGACAGC ATAGACCTGC CTGCCGCCGT CTATCTCGAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAGCCTTTG ACAAACAACG CGTCTATCTC
451 GAACGGCTGG ATGCTTCATA CCGTTACGAC CGCAAAGGAC ACCGCCTTGA
501 CCTGAAGGCC GCCGACACGC CGTGGAGCAG TTCGTCGGGG GCGGCCTCGG
551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGACTCGAAG GCAAAACCAT ACACAGTACG GCTCGGCTGA CGGCGAGCCT
651 GAAGGATGTG CGCGCCGAAC TGGCGATCGA CGGCGGCAAT ATCCGCTCT
701 CGGGAAAAAT CGTCATCCAC CCGTTTGCCG AATCATTGGA TAAACATTG
751 GAAGAAGTAC TGGTCAAAGG GTTCAACATC AATCCGGCCG CCTTCGTGCC
801 TTCCCTGCCC GATGCCGGAC TGAATTTCTG CCTGACCGCC ATCCCGTCGT
851 TTTCAGACGG CATCGCGCTG GAAGGTTCGC TCGATTTGGA AAACACCAAA
901 GCCGGCTTTC CCGACCGCAA CGGCATCCCC GTCCGTCAGG TTTTAGGCGG
951 CTTTGTATC CGCGAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGCG
1001 CCCTGCTCGG ACGGGGCGGC ATCAGGCTGT CGGGCAAAAT CGACACCGAA
1051 AAAGACATCC TCATTTTAAA TATAGGCATC AACTCCGTCG CGCGGGAAGA
1101 CGTACTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GTGGCACGAC CGCCTCGCCC AAAATCTCTT GGCAACTCGG CATCGGCACG
1201 GCGCGCACGG ACGGCAGCCT CGCCATTGCA AGCGACCCAG CAAACGGACA
1251 GCGGAACTG GTGCTCGACA CCGTCAACAT CGCCGCGGGG CAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCGCGCATTT CGACCCTTCG CGCATCGATC CGCAACTTCC
1401 GGCAGGCAAT ATCAACGGCT CAATAAACCT TGCCGGCGAA CTGGCAAAAG
1451 AGAAATTAC AGGCAAAATG CGGTTTTTAC CCGGCACGTT CAACGGCGTA
1501 CCGATTGCCG GCAGTGCCGA CATTGTTTAC GAGTCCCGCC ACCTTCCGCG
1551 TGCCCGCGTC GATTTGCGGC TGGGGCGGAA CATTATTAAT ACAGACGGCG
1601 GTTTCGGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGCACCAGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGT TCTTTAAATG TACGCGGACA
1701 CTTTTCGGGT GATTTGGACG GCGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CCGGCGCGCG GCGCAACCTG CACATCGGCA AGGCGGCAGA CATCGGTTCC
1801 CTCGATTTCG CGCTCAAAGG TTCGCCCGAC ACAAGCCGCC CGATACGCGC
1851 CGACATCAAA GGCAGCCGCC TTTGCTGTCT GGGCGGAGCG GCGGTTGTCT
1901 ATACCGCGCA CCTGATGCTG GACGGCACGG GCGTGCAGCA CCGCATCCGC
1951 ACACACGCGG CCATGACGCT GGATGGCAAA CCGTTCAAT TCGATTGGA
2001 CGCTTCAGGC GGCATCAACA GGGAACTTAC CCGATGGAAT GGCAGCATCG
2051 GCATCCTCGA CATCGGCGGC GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACGCGTGGCG GCAAGTGCGG CAAATTGGCA

```

660

```

2151 GGCAATGGGC GGCAGCCTCA ACCTGCAACA CTTTCTTTGG GATAAAAAAA
2201 CCGGCATATC GGCAAAAGGC GGCACACACG GTCTGCATAT CGCCGAGTTG
2251 CACAATTTCT TCAAACCGCC CTTGCAACAC AATCTGGTTT TAAACGGCGA
2301 CTGGGATGTC GCCTACGGGC GCAACGCGCG CGGCTACCTC AATATCAGCC
2351 GGCAAGAGCG CGATGCCGTA TTGCCCGGCG GGCAGGCTTT GGGTTTGAA
2401 GCATTTTCCC TGAAAACGCG CTTTCAAAAC GACCGCATCG GAATCCTGCT
2451 TGACGGCGCG GCGCGTTTCG GCGGATTAA CGCCGATTG GGCATCGCCA
2501 ACGCCTTCGG CGGCAATATG GCAAATGCAC CGCTCGGCG CAGGATTACC
2551 GCCTCCCTTC CCGACTTGGG CGCATTGAAG CCCTTTCTGC CCGCCGCGCG
2601 GCAAAACATT ACCGGCAGCC TGAATGCCGC CGCGCAAATC GCGGACGCGG
2651 TAGGCTCTCC GTCCGTCAT GCCGCCGTC ACGGCAGCAG CAACTACGGG
2701 AAAATCAACG GCAACATCAC CGTCGGGCAA AGCCGCTCTT TCATACCGC
2751 GCCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGTATTCC
2801 GCAACTTCTC ACCGGTCGGA CAAACCGTCA AAGGCAGCCT GAATGCCGCC
2851 GTAACCCCTC GCGCAGCAT CGCGATCCG CACTTGGGCG GCAGCATCAA
2901 CCGCGACAAA CTCTATTACC GCAACCAAAC CCAAGGCATC ATCTTGACA
2951 ACGGCTCGCT GCGTTCGAT ATCGCGGCGA GGAATGGGT AATCGACAGC
3001 CTGAAATTCC GGCACGAAG GACGGCGGAA CTCTCCGTA CGTCCGTAT
3051 GTAAAAACAG GGACCCGATG TCATATCGG CGCGGTGTT GACAAATACC
3101 GCATCCTGTC CCGCCCCAAC CGCGCCTGA CGGTTCCGG CAACACCGCG
3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGGA TGATTAATAA
3201 GCATCAGGGG CTGTTCCGTT CGCAAAATC CTCGATGCC TCCGTCGCG
3251 ACGATGTCGT CGTATTAGG GAAGTCAAAA AAGAGGCGGC GGCACCGCTC
3301 CCCGTCAATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGCTTCG
3351 CGGCTACGGC GCGGACGTTA CCATAGGCGG CAACTGACC CTGACCGCCC
3401 AATCGGGCGG AAGCGTACGG GCGTGGGCA CGTCCGCGT CATCAAAGGG
3451 CGTTATAAGG CATACGGGCA GGATTGGAC ATTACCAAAG GCACGGTCTC
3501 CTTTGTCCGG CCGCTCAACG ATCCCAACCT CAACATCCGC GCCGAACGCC
3551 GCCTTTCCCG CGTCGGTGC GCGTGGGAA TATTGGGCG CCTCAACAGC
3601 CCGCGCATTA CGTGACGGC AACGAACCG ATGAGTGAAA AAGACAAGCT
3651 CTCTTGGGTC ATCCTCAACC GCGCCGGCAG CGGCAGCAGC GGCAGCAATG
3701 CCGCCCTGTC TGCAGCCGCA GGTGCGCTG TTGCCGGGCA AATCAACGAC
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTT ACCAGCAAGC GCAGCCGCAA
3801 CCGCGAAACC GCGGAACCTA ACCCGCCGCA ACAGGTGCTG ACCGTCGCA
3851 AACAACTGAC CCGCAAATC TACATCGGCT ACGAATACAG CATCTCCAGC
3901 CGGGAACAGT CCGTCAAAT GATTACCAG CTGACCCGCG CCATACAGGC
3951 GGTGCCCCGT ATCGGCAGCC GTTCGTCGGG CGGCGAGCTG ACATACACCA
4001 TACGTTTCGA CGCTTCTCC GGTTCGGACA AAAAAGACTC CGCCGGAAC
4051 GGCAAGGAA AATAA

```

This corresponds to the amino acid sequence <SEQ ID 1190; ORF 285-1>:

m285-1.pep

```

1 LKLSAALLSV LILAVCF LGW LAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51 TLLDGFDDGN WSIETEGADL KISRFRFAWK PSELMRRSLH ITEISAGDIA
101 IVTKPTPPKE ERPLSLPDS IDLPAAVYLD RFETGKISMV KAFDKQTVYL
151 ERLDASYRYD RKGHRLDLKA ADTPWSSSSG AASVGLKKPF ALDTAIYTKG
201 GLEGKTIHST ARLSGSLKDV RAELAIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVKG FNI NPAAFPVSLP DAGLNFDLTA IPSFSDGIAL EGSLDLNLTN
301 AGFADRNGIP VRQVLGGFVI RQDGTVHIGN TSAALLGRGG IRLSGKIDTE
351 KDILDNLNIG NSVGAEDVLQ TAFKGRLDGS IGIGGTTASP KISWQLGIGT
401 ARTDGSIAIA SDPANGQRKL VLDTVNIAAG QGSLTAQGYL ELFKDRLLKL
451 DIRSRAFDPS RIDPQLPAGN INGSINLAGE LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIIK TDGGFGKKG DRLNLNITAPD
551 LSRFGFGLAG SLNVRGHL SG DLDGGIRTFE TDLSGAARNL HIGKAADIRS
601 LDFTLKGSPD TSRPIRADIK GSRLSLSGGA AVVDATDML DGTGVQHRIR
651 THAAMTLDGK PFKFDLDASG GINRELTRWK GSIGILDIGG AFNLKLQNRM
701 TLEAGAERVA ASANWQAMG GSNLQHFWS DKKTGISAKV GAHGLHIAEL
751 HNFFKPPFEH NLVLNGDWDV AYGRNARGYL NISRQSGDAV LPGGQALGLN
801 AFSLKTRFQN DRIGILLDGG ARFGRINADL GIANAFGGNM ANAPLGGRIT
851 ASLPDLGALK PFLPAAQNI TGSLNAAAI GGRVGSPPSVN AAVNGSSNYG
901 KINGNITVGQ SRSFDTAPLG GRNLNLTADA EVFRNFLPVG QTVKGSNLAA
951 VTLGGSIA DP HLGGSSINGDK LYRNQTQGI ILDNGLSLRSH IAGRKWIDS
1001 LKFRHEGTAE LSGTVGMENS GPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGDDVVVLG EVKKEAAAPL
1101 PVNMNLTLDL NDGIRFAGYG ADVTIGGKLT LTAQSGGSVR GVGTVRVIKG
1151 RYKAYGQDLD ITKGTVSFVG PLNDPNLNIR AERRLSPVGA GVEILGSLNS
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAG GALLAGQIND
1251 RIGLVDDLGF TSKRSRQAOT GELNPAEQVL TVGKQLTGKL YIGYEYSISS
1301 AEQSVKLIYR LTRAIQAVAR IGSRSSGGEL TYTIRFDRFS GSDKKDSAGN
1351 GKGK*

```

g285-1/m285-1 96.5% identity in 1354 aa overlap

10 20 30 40 50 60

662

	730	740	750	760	770	780
	790	800	810	820	830	840
g285-1.pep	NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLGIGNAFGGNM					
m285-1	NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLGIANAFGGNM					
	790	800	810	820	830	840
	850	860	870	880	890	900
g285-1.pep	ANTPLGGRITASLPDLGALKPFLPAAAQONITGSLNAAQIGGRVGSPSVNAAVNGSSNYG					
m285-1	ANAPLGGRITASLPDLGALKPFLPAAAQONITGSLNAAQIGGRVGSPSVNAAVNGSSNYG					
	850	860	870	880	890	900
	910	920	930	940	950	960
g285-1.pep	KINGNITVGQSRSFDTAPLGGRNLNLTVADAEAFRNFLPVGQTVKGSINAAVTLGGSIA DP					
m285-1	KINGNITVGQSRSFDTAPLGGRNLNLTVADAEVFRNFLPVGQTVKGSINAAVTLGGSIA DP					
	910	920	930	940	950	960
	970	980	990	1000	1010	1020
g285-1.pep	HLGGSINGDKLYYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVSMENS					
m285-1	HLGGSINGDKLYYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVSMENS					
	970	980	990	1000	1010	1020
	1030	1040	1050	1060	1070	1080
g285-1.pep	VPDVIDIGAVFDKYRILSRPNRRLTVSGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMP					
m285-1	GPDVIDIGAVFDKYRILSRPNRRLTVSGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMP					
	1030	1040	1050	1060	1070	1080
	1090	1100	1110	1120	1130	1140
g285-1.pep	SVGDDVVVLGEVKKEAAASLPVNMNLTLDLNDGIRFSGYGADVITIGGKLTTLTAQPGGNVR					
m285-1	SVGDDVVVLGEVKKEAAAPLPVNMNLTLDLNDGIRFAGYGADVITIGGKLTTLTAQSGGSVR					
	1090	1100	1110	1120	1130	1140
	1150	1160	1170	1180	1190	1200
g285-1.pep	GVGTVRVIKGRYKAYGQDLDTKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS					
m285-1	GVGTVRVIKGRYKAYGQDLDTKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS					
	1150	1160	1170	1180	1190	1200
	1210	1220	1230	1240	1250	1260
g285-1.pep	PRITLTANEPMSEKDKLSWLILNRAGSGSSGDNAALSAAGALLAGQINDRIGLVDDLGF					
m285-1	PRITLTANEPMSEKDKLSWLILNRAGSGSSGDNAALSAAGALLAGQINDRIGLVDDLGF					
	1210	1220	1230	1240	1250	1260
	1270	1280	1290	1300	1310	1320
g285-1.pep	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYGISSAEQSVKLIYRLTRAIQAVAR					
m285-1	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYSISSAEQSVKLIYRLTRAIQAVAR					
	1270	1280	1290	1300	1310	1320
	1330	1340	1350			
g285-1.pep	IGSRSSGGELTYTIRFDRLFSGSDKKDSAGNGKGK					
m285-1	IGSRSSGGELTYTIRFDRFSGSDKKDSAGNGKGKX					
	1330	1340	1350			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1191>:

a285-1.seq

```

1  CTGAAGCTGT  CGGCGGCACT  GCTGTCTGTT  CTGATTTTGG  CAGTATGTTT
51  CCTCGGCTGG  CTCGCCGCA  CGGAAGCGGG  TTTGCGCTTC  GGGCTGTACC
101  AAATCCCGTC  TTGGTTCGGC  GTAAACATTT  CCTCCCAAAA  CCTCAAAGGC
151  ACGCTGCTCG  ACGGCTTCGA  CGGCGACAAC  TGGTCGATAG  AAACCGAGGG
201  GGCAGACCTT  AAAATCAGCC  GCTTCCGCTT  CGCGTGGAAG  CCGTCCGAAC
251  TGATGCGCGC  CAGCCTGCAC  ATTACCGAAA  TTTCCGCGCG  CGACATCGCC
301  ATCGTTACCA  AACCGACTCC  GCCTAAAGAA  GAACGCGCCG  CGCTCAGCCT
351  TCCCGACAGC  ATAGACCTGC  CTGCCGCGGT  CTATCTCGAC  CGCTTCGAGA
401  CGGGCAAAAT  CAGCATGGGC  AAAGCCTTG  ACAAACAAAC  CGTCTATCTC
451  GAACGGCTGG  ATGCTTCATA  CCGTTACGAC  CGCAAAGGAC  ACCGCCTCGA

```

```

501 CCTGAAGGCT GCCGACACGC CGTGGAGCAG TTCGTCGGGG TCAGCCTCGG
551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGA CTGGAAG GCAAAACCAT ACACAGTACG GCTCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CGCGCCGAAC TGGCGATCGA CGGCGGCAAT ATCCGCCTCT
701 CGGGAAAATC CGTCATCCAC CCGTTTGCCG AATCATTGGA TAAAACATTG
751 GAAGAAGTAC TGGTCAAAGG GTTCAACATC AATCCGTCGG CCTTCGTGCC
801 TTCCCTGCCC GATGCCGGGC TGAATTTTCA CCTGACCGCC ATCCCGTCGT
851 TTTTCAGACGG CATCGCGCTG GAAGGCTCGC TCGATTGGA AAACACCAAA
901 GCCGGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTGAGG TTTTAGGCAG
951 CTTTGTGATC CGGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGTG
1001 CCCTGCTCGG ACGGGGCGGC ATCAGGCTGT CGGGCAAAAT CGACACCGAA
1051 AAAGACATCC TCGATTTAAA TATAGGCATC AACTCCGTG GCGCGGAAGA
1101 CGTACTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GTGGCAGCAC CGCCTCGCCC AAAATCTCTT GGCAACTCGG CATCGGCACG
1201 GCGCGCACGG ACGGCAGCCT CGCCATTGCA AGCGACCCCG CAAACGGACA
1251 GCGGAAACTG GTGCTCGACA CCGTCAACAT CGCCGCGGGG CAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCCGCGCATT CGACCCTTCG CGCATCGATC CGCAACTTCC
1401 GGCAGGCAAT ATCAACGGCT CAATAAACCT TGCCGGCGAA TGGCAAAAG
1451 AGAAATTAC AGGCAAAATG CGGTTTTTAC CCGGCACGTT CAACGGCGTA
1501 CCGATTGCGG CGAGTGCCGA CATTGTTTAC GAGTCCCGCC ACCTTCCGG
1551 TGCCGCGGTC GATTTGCGGC TGGGGCGGAA CATTATTAAA ACAGACGGCG
1601 GCTTCGGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGCACCCGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CCTTTCGGG GATTGGACG GTGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CGCGCGCGGC GCGCAACCTG CACATCGGCA AGCGGCGAGA CATCCGTTTCG
1801 CTGATTTC ACGTCAAAGG TTCGCGCGAC ACAAGCCGCC CGATACGCGC
1851 CGACATCAA GGCAGCCGCC TTTCGCTGTC GGGCGGAGCG GAGGTTGTTCG
1901 ATACCGCGGA CTTGATGCTG GACGGCACGG CGGTGCAGCA CCGCATCCGC
1951 ACACACGCCG CCATGACGCT GGATGGCAA CCGTTCAAAT TCGATTGGA
2001 CGCTTCAGGC GGCATCAACA GGAACCTTAC CCGATGGAAG GGCAGCATCG
2051 GCATCCTCGA CATCGGCGGC GCATTCAACC TCAAGTGC AACCCTATG
2101 ACGCTCGAAG CCGGTGCGGA ACGCGTGGCG GCAAGTGC CAAATTGGCA
2151 GGCAATGGGC GGCAGCCTCA ACCTGCAACA CTTTCTTGG GATAAAAAAA
2201 CCGGCATATC GGCAAAAGGC GGCACACAG GTCTGCATAT CGCCGAGTTG
2251 CACAATTCT TCAAACCGCC CTTCGAACAC AATCTGGTTT TAAACGGCGA
2301 CTGGGATGTC GCCTACGGGC GAAACGCGCG CGGCTACCTC AATATCAGCC
2351 GGCAAAAGCG CGATGCCGTA TTGCCCGGCG GGCAGGCTTT GGGTTTGAAC
2401 GCATTTTCCC TGAACACGCG CTTTCAAAC GACCGTATCG GAATCCTGCT
2451 TGACGGCGGC GCGCGTTTCG GCGGATTAA CGCGATTG GACATCGGCA
2501 ACGCCTTCGG CGGCAATATG GCAAATGCAC CGCTCGGCGG CAGGATTACC
2551 GCCTCCCTTC CCGACTTGGG CACATTGAAG CCCTTTCTGC CCGCCGCGCG
2601 GCAAAACATT ACCGGCAGCC TGAATGCCG CCGCAAAAT GCGGACGGG
2651 TCGGCTCTCC GTCCGTCAAT GCCCGCGTCA ACGGCAGCAG CAACTACGGG
2701 AAAATCAACG GCAACATCAC CGTCGGGCAA AGCCGCTCTT TCGATACCGC
2751 GCCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGTATTCC
2801 GCAACTTCCT ACCGGTCGGA CAAACCGTCA AAGGCAGCCT GAATGCCGCC
2851 GTAACCTCTG GCGGCAGCAT CGCCGATCCG CACTTGGGCG GCAGCATCAA
2901 CGGCGACAAA CTCTATTACC GCAACCAAA CCAAGGCATC ATCTTGGACA
2951 ACGGCTCGCT GCGTTTCGAT ATCGCGGCGA GGAATGGGT AATCGACAGC
3001 CTGAAATTCC GGCACGAAGG GACGGCGGAA CTCTCCGTA CGGTCGGTAT
3051 GGAAACAGC GGACCCGATG TCGATATCGG CGCGGTGTTC GACAAATACC
3101 GCATCCTGTC CCGCCCAAC CGCCGCTGA CGGTTTCGG CAACACCCGC
3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGGA TGATTAAAC
3201 GGATCAGGGG CTGTTTCGTT CGCAAAATC CTCGATGCCG TCCGTCGGCG
3251 ACGATGTCGT CGTATTAGG GAAGTCAAAA AAGAGGCGGC GGCACCGCTC
3301 CCCGTCAATA TGAACCTGAC TTAGACCTC AATGACGGCA TCCGCTTCG
3351 CGGCTACGGC GCGGACGTTA CCATAGGCGG CAAACTGACC CTGACCGCCC
3401 AATCGGGCGG AAGCGTGGG GCGGTGGGCA CGGTCCGCGT CATCAAAGGG
3451 CGTTATAAGG CATACGGGCA GGATTGGAC ATTACCAAAG GCACGGTCTC
3501 CTTTGTGCGC CGGCTCAACG ACCCAACCT CAACATCCGC GCCGAACGCC
3551 GCCTTTCCCC CGTCGGTGCG GCGGTGGAAA TATTGGGCG CCTCAACAGT
3601 CCGCGCATTG CGTGACGGC AAACGAACCG ATGAGTGAAG AAGACAAGCT
3651 CTCTTGCTC ATCTCAACC GCGCCGCGAG TGGCAGCAG GGCAGCAATG
3701 CCGCCCTGTC CGCAGCCGCC GCGCGCTGC TTGCCGGGCA AATCAACGAC
3751 CGCATCGGGG TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 CCGCAAAACC GCGCAACTCA ACCCGCCGGA ACAGGTGCTG ACCGTCGGCA
3851 AACAACCTGAC CGGCAAACTC TACATCGGCT ACGAATACAG CATCTCCAGC
3901 GCGGAACAGT CCGTCAAACT GATTTACCGG CTGACCCGCG CCATACAGGC
3951 GGTGCCCCGT ATCGGCAGCC GTTCGTGCGG CGGCGAGCTC ACATACACCA
4001 TACGTTTCGA CCGTTCTCC GGTTCGGACA AAAAAGACTC CGCCGGAAC
4051 AGCAAAGGAA AATAA

```

This corresponds to the amino acid sequence <SEQ ID 1192; ORF 285-1.a>:

664

a285-1.pep

```

1  LKLSAALLSV LILAVCFLGW LAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51  TLLDGFDDGN WSIETEGADL KISRFRFAWK PSELMRRSLH ITEISAGDIA
101 IVTKPTPPKE ERPPSLPDS IDLPAAYVLD RFETGKISMV KAFDKQTVYL
151 ERLDASYRYD RKGHRDLKA ADTPWSSSSG SASVGLKKPF ALDTAIYTKG
201 GLEGKTIHST ARLSGSLKDV RAELAIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP VRQVLGSFVI RQDGTVHIGN TSVALLGRGG IRLSGKIDTE
351 KDILDNLIGI NSVGAEDVLQ TAFKGRLDGS IGIGGTTASP KISWQLGIGT
401 ARTDGLAIA SDPANGQRKL VLDTVNIAAG QGSLTAQGYL ELFKDRLLKL
451 DIRSRAFDPS RIDPQLPAGN INGSINLAGE LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIIK TDGGFGKKGD RLNLNITAPD
551 LSRFGFGLAG SLNVRGHLGS DLDGGIRTFE TDLGAARNL HIGKAADIRS
601 LDFTLKGSPD TSRPIRADIK GSRLSLSGGA EVVDTADLML DGTGVQHRIR
651 THAAMTLDGK PFKFDLDASG GINRELTRWK GSIGILDIGG AFNLKLQNRM
701 TLEAGAERVA ASANWQAMG GSNLNLQHFSW DKKTGISAKG GAHGLHIAEL
751 HNFFKPPFEH NLVLNGDWDV AYGRNARGYL NISRQSGDAV LPGGQALGLN
801 AFSLKTRFQN DRIGILLDGG ARFGRINADL DIGNAFGGNM ANAPLGGRIT
851 ASLPDLGTLK PFLPAAQNI TGSNLAAQI GGRVGSPSVN AAVNGSSNYG
901 KINGNITVGQ SRSFDTAPLG GRNLTVADA EVFRNFLPVG QTVKGSLNAA
951 VTLGGSIAADP HLGGSINGDK LYRNRQTQGI ILDNGLSRSH IAGRKWVIDS
1001 LKFRHEGTAE LSGTVGMENS GPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGGDDVVVLG EVKKEAAAPL
1101 PVNMNLTLDL NDGIRFAGYG ADVTIGGKLT LTAQSGGSVR GVGTVRVIKG
1151 RYKAYQDLD ITKGTVSFVG PLNDPNLNIR AERRLSPVGA GVEILGSLNS
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAA GALLAGQIND
1251 RIGLVDDLGF TSKRSRNAQT GELNPAEQVL TVGKQLTGKL YIGYEYSISS
1301 AEQSVKLIYR LTRAIQAVAR IGSRSSGGEL TYTIRFDRFS GSDKKDSAGN
1351 SKGK*

```

a285-1/m285-1 99.3% identity in 1354 aa overlap

	10	20	30	40	50	60
a285-1.pep	LKLSAALLSVLILAVCFLGWLAGTEAGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGN					
m285-1	LKLSAALLSVLILAVCFLGWLAGTEAGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGN					
	10	20	30	40	50	60
a285-1.pep	WSIETEGADLKISRFRFAWKPSSELMRRSLHITEISAGDIAIVTKPTPPKEERPPSLPDS					
m285-1	WSIETEGADLKISRFRFAWKPSSELMRRSLHITEISAGDIAIVTKPTPPKEERPPSLPDS					
	70	80	90	100	110	120
a285-1.pep	IDLPAAYVLDRFETGKISMVKAQFQTVYLERLDASYRYDRKGRHLDLKAADTPWSSSSG					
m285-1	IDLPAAYVLDRFETGKISMVKAQFQTVYLERLDASYRYDRKGRHLDLKAADTPWSSSSG					
	130	140	150	160	170	180
a285-1.pep	SASVGLKKPFALDTAIYTKGGLEGKTIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIH					
m285-1	AASVGLKKPFALDTAIYTKGGLEGKTIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIH					
	190	200	210	220	230	240
a285-1.pep	PFAESLDKTL EEVLVKGFNI NPSAFVPSLPDAGLNFDLTAIPSFSDGIALEGSLENTK					
m285-1	PFAESLDKTL EEVLVKGFNI NPSAFVPSLPDAGLNFDLTAIPSFSDGIALEGSLENTK					
	250	260	270	280	290	300
a285-1.pep	AGFADRNGIPVRQVLGSFVIRQDGTVHIGNTSVALLGRGGIRLSGKIDTEKDILDNLIGI					
m285-1	AGFADRNGIPVRQVLGSFVIRQDGTVHIGNTSVALLGRGGIRLSGKIDTEKDILDNLIGI					
	310	320	330	340	350	360
a285-1.pep	NSVGAEDVLQTAFKGRLDGSIGIGGTTASPKISWQLGIGTARTDGLAIASDPANGQRKL					
m285-1	NSVGAEDVLQTAFKGRLDGSIGIGGTTASPKISWQLGIGTARTDGLAIASDPANGQRKL					
	370	380	390	400	410	420
a285-1.pep	AGFADRNGIPVRQVLGSFVIRQDGTVHIGNTSVALLGRGGIRLSGKIDTEKDILDNLIGI					
m285-1	AGFADRNGIPVRQVLGSFVIRQDGTVHIGNTSVALLGRGGIRLSGKIDTEKDILDNLIGI					
	430	440	450	460	470	480

665

a285-1.pep	VLDTVNIAAGQGS	LTAAQGYLELFKDRLLK	LDIRSR	AFDPSRIDPQLPAGNINGSIN	LAGE	
m285-1	VLDTVNIAAGQGS	LTAAQGYLELFKDRLLK	LDIRSR	AFDPSRIDPQLPAGNINGSIN	LAGE	
	430	440	450	460	470	480
a285-1.pep		490	500	510	520	530
		LAKEKFTGKMRFLPGTFNGVPIAGSADIVYESRHL	PRAAVDLRLGRNIIKTDGGFGKKG	D		
m285-1		LAKEKFTGKMRFLPGTFNGVPIAGSADIVYESRHL	PRAAVDLRLGRNIIKTDGGFGKKG	D		
	490	500	510	520	530	540
a285-1.pep		550	560	570	580	590
		RLNLNITAPDLSRFGFGLAGSLNVRGHL	SGDLGGIRT	FETDL	SGAARNLHIGKAADIR	S
m285-1		RLNLNITAPDLSRFGFGLAGSLNVRGHL	SGDLGGIRT	FETDL	SGAARNLHIGKAADIR	S
	550	560	570	580	590	600
a285-1.pep		610	620	630	640	650
		LDFTLKGS	PDTSRPIRADIKGSRLSLSGGAEVVD	TADLMLDGTGVQHRIR	THAAMTLDGK	
m285-1		LDFTLKGS	PDTSRPIRADIKGSRLSLSGGAEVVD	TADLMLDGTGVQHRIR	THAAMTLDGK	
	610	620	630	640	650	660
a285-1.pep		670	680	690	700	710
		PFKFDLDASGGINRELTRWKSGSIGILDIGGAFNLKLQNRMTLEAGAERVAASAANWQAMG				
m285-1		PFKFDLDASGGINRELTRWKSGSIGILDIGGAFNLKLQNRMTLEAGAERVAASAANWQAMG				
	670	680	690	700	710	720
a285-1.pep		730	740	750	760	770
		GSLNLQHFSWDKKTGISAKGGAHGLHIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYL				
m285-1		GSLNLQHFSWDKKTGISAKGGAHGLHIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYL				
	730	740	750	760	770	780
a285-1.pep		790	800	810	820	830
		NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLDIGNAFGGNM				
m285-1		NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLDIGNAFGGNM				
	790	800	810	820	830	840
a285-1.pep		850	860	870	880	890
		ANAPLGGRITASLPDLGLTKPFLPAAQAQITGSLNAAAQIGGRVGS	SPSVNAAVNGSSNYG			
m285-1		ANAPLGGRITASLPDLGLTKPFLPAAQAQITGSLNAAAQIGGRVGS	SPSVNAAVNGSSNYG			
	850	860	870	880	890	900
a285-1.pep		910	920	930	940	950
		KINGNITVQSRSFDTAPLGGRLNLTVADEAFRNFLPVGQTVKGS	LNAAVTLGGS	IAADP		
m285-1		KINGNITVQSRSFDTAPLGGRLNLTVADEAFRNFLPVGQTVKGS	LNAAVTLGGS	IAADP		
	910	920	930	940	950	960
a285-1.pep		970	980	990	1000	1010
		HLGGSINGDKLYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVGMENS				
m285-1		HLGGSINGDKLYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVGMENS				
	970	980	990	1000	1010	1020
a285-1.pep		1030	1040	1050	1060	1070
		GPDVDIGAVFDKYRILSRPNRRLTVSGNTRLRYS	PQKGISV	TGMIKTDQGLFGS	QKSSMP	
m285-1		GPDVDIGAVFDKYRILSRPNRRLTVSGNTRLRYS	PQKGISV	TGMIKTDQGLFGS	QKSSMP	
	1030	1040	1050	1060	1070	1080
a285-1.pep		1090	1100	1110	1120	1130
		SVGDDVVVLGEVKKEAAAPLPVNMNLTLDLNDGIRFAGYGADVTIGGKLT	LTAAQSGGS	SVR		
m285-1		SVGDDVVVLGEVKKEAAAPLPVNMNLTLDLNDGIRFAGYGADVTIGGKLT	LTAAQSGGS	SVR		
	1090	1100	1110	1120	1130	1140
a285-1.pep		1150	1160	1170	1180	1190
		GVGTVRVIKGRYKAYGQDLDTKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS				
m285-1		GVGTVRVIKGRYKAYGQDLDTKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS				

666

	1150	1160	1170	1180	1190	1200
	1210	1220	1230	1240	1250	1260
a285-1.pep	PRITLTANPEMSEKDKLSWLI	LNRRAGSGSSGDNAALSAAAGALLAGQ	INDRIGLVDDLGF			
m285-1	PRITLTANPEMSEKDKLSWLI	LNRRAGSGSSGDNAALSAAAGALLAGQ	INDRIGLVDDLGF			
	1210	1220	1230	1240	1250	1260
	1270	1280	1290	1300	1310	1320
a285-1.pep	TSKRSRNAQTGELNPAEQVLT	VGKQLTGKLYIGYEYSSISAEQSVKLI	YRLTRAIQAVAR			
m285-1	TSKRSRNAQTGELNPAEQVLT	VGKQLTGKLYIGYEYSSISAEQSVKLI	YRLTRAIQAVAR			
	1270	1280	1290	1300	1310	1320
	1330	1340	1350			
a285-1.pep	IGSRSSGGELTYTIRFDRFSG	SDKKDSAGNSKGKX				
m285-1	IGSRSSGGELTYTIRFDRFSG	SDKKDSAGNSKGKX				
	1330	1340	1350			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1193>:

g286.seq

1	atgcagaaca	ccggtaccat	gatgatcaaa	ccgaccgccc	tgctcctgcc
51	ggctttat	ttctttccgc	acgcatacgc	gcctgccgcc	gacctttccg
101	aaaacaagc	ggcgggtttc	gcattgttca	aaagcaaaag	ccccgacacc
151	gaatcagtc	aattaaaacc	caaattcccc	gtccgcacgc	acacgcagga
201	cagtgaatc	aaagatatgg	tcgaagaaca	cctgccgctc	atcacgcagc
251	agcaggaaga	ggttttggat	aaggaacaga	cgggattcct	tgccgaagaa
301	gcaccggaca	acgttaaaac	aatgctccgc	agcaaaggct	atttcagcag
351	caaggtcagc	ctgacggaaa	aagacggagc	ttatacgggtg	cacatcacac
401	cgggcccgcg	caccaaatac	gccaacgtcg	gcgtcgccat	cctcggcgac
451	atcctttcag	acggcaacct	cgccgaatac	taccgcaacg	cgctggaaaa
501	ctggcagcag	ccggtaggca	gcgatttcga	tcaggacagt	tgggaaaaaca
551	gcaaaacttc	cgctcctcggc	gcggtaacgc	gcaaaggcta	cccgcttgcc
601	aagctcggca	acaccggggc	ggccgtcaac	cccgcataccg	ccaccgcgca
651	tttgaacgtc	gtcgtggaca	gcggccgccc	cattgccttc	ggcgactttg
701	aatcacccgg	cacacagcgt	taccccgaaac	aaaccgtctc	cgccctggcg
751	cgcttccaac	cgggcacgcc	ctacgacctc	gacctgctgc	tcgacttcca
801	acaggcgctc	gaacaaaacg	ggcattat	cgccgcgtcc	gtacaagccg
851	acttcgaccg	cctcccaagg	ggaccgcgtc	cccgtcaaaag	tcagcgtaac
901	cgaggtcaaa	cgccacaaac	tcgaaaccgg	catccgcctc	gattcggaat
951	acggtttggg	cggcaaaatc	gcctacgact	attacaacct	cttcaacaaa
1001	ggctatatcg	gctcggtcgt	ctgggatatg	gacaaatacg	aaaccacgct
1051	tgccgccggc	atcagccagc	cgcgcaacta	tcggggcaac	tactggacaa
1101	gcaacgtttc	ctacaaccgt	tcgaccaccc	aaaacctcga	aaaacgcgcc
1151	ttctccggcg	gcatctggta	tgtgcgcgac	cgccggggca	tcgatgccag
1201	gctggggggc	gaatttctcg	cagaaggccg	gaaaatcccc	ggctcggtatg
1251	tcgatttggg	caacagccac	gccacgatgc	tgaccgcctc	ttggaaacgc
1301	cagctgctca	acaacgtgct	gcaccccgaa	aacggccatt	acctcgacgg
1351	caaaatcggg	acgactttgg	gcacattcct	gtcctccacc	gcgctaatec
1401	gcacctctgc	ccgcgcaggt	tatttcttca	cgcccgaata	caaaaaactc
1451	ggcacgttca	tcatacgcg	acaagcgggt	tacaccgttg	cacgcgacaa
1501	tgccgatgtc	ccctcggggc	tgatgttccg	cagcggcggc	gcgtcttccg
1551	tgccgggtta	cgaacttga			

This corresponds to the amino acid sequence <SEQ ID 1194; ORF 286.ng>:

g286.pep

1	MQNTGTMMIK	PTALLLPALF	FFPHAYAPAA	DLSENKAAGF	ALFKSKSPDT
51	ESVKLKPKFP	VRIDTQDSEI	KDMVEEHLPL	ITQQQEEVLD	KEQTGFLAEE
101	APDNVKTMLR	SKGYFSSKVS	LTEKDGAYTV	HITPGPRTKI	ANVGVAIIGD
151	ILSDGNLAAY	YRNALENWQQ	PVGSDFDQDS	WENSKTSVLG	AVTRKGYPLA
201	KLGNTRAAVN	PDTATADLNV	VVDSGRPIAF	GDFEITGTQR	YPEQTVSGLA
251	RFQPGTPYDL	DLLLDQQAL	EQNGHYSAS	VQADFRLPR	GPRPRQSQRN
301	RGQTPQTRNR	HPPRFGIRFG	RQNRLLRLQP	LQQRLYRLGR	LGYGQIRNHA
351	CRRHQPAQL	SGQLLDKQRF	LQPFDPKPR	KTRLLRRHLV	CARPRGHRQ
401	AGGGISRRRP	ENPRLGCRFG	QQPRHDADRL	LETPAAQORA	APKRRLPLRR

667

451 QNRDDFGHIP VLHRANPHLC PRRFLHARK QKTRHVHHTR TSGLHRCTRO
501 CRCPLGADV P QRRRVFRARL RT*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1195>:

m286.seq

```

1 ATGCACGACA CCCGTACCAT GATGATCAAA CCGACCGCCC TGCTCCTGCC
51 GGCTTTATTT TTCTTTCCGC ACGCATACGC GCCTGCCGCC GACCTTTCCG
101 AAAACAAGGC GCGGGTTTC GCATTGTTCA AAAACAAAAG CCCCAGACACC
151 GAATCAGTCA AATTAAACC CAAATTCCCC GTCCTCATCG ACACGCAGGA
201 CAGTGAATC AAAGATATGG TCGAAGAACA CCTGCCGCTC ATCAGCAGC
251 AGCAGGAAGA AGTATTGAC AAGGAACAGA CGGGTTTCCT CGCCGAAGAA
301 GCGCCGGACA ACGTTAAAC GATGCTCCGC AGCAAAGGCT ATTTACAGCAG
351 CAAAGTCAGC CTGACGGAAA AAGACGGAGC TTATACGGTA CACATCACAC
401 CGGGCCCGCG CACCAAAATC GCCAACGTCG GCGTCGCCAT CCTCGGCGAC
451 ATCCTTTCAG ACGGCAACCT CGCCGAATAC TACCGCAACG CGCTGGAAAA
501 CTGGCAGCAG CCGGTAGGCA GCGATTTCGA TCAGGACAGT TGGGAAAACA
551 GCAAAACTTC CGTCTCGGC GCGGTAACGC GCAAAGCCTA CCCGCTTGCC
601 AAGCTCGGCA ATACGCAGGC GGCCGTCAAC CCCGATACCG CCACCGCCGA
651 TTTGAACGTC GTCGTGGACA GCGGCCGCC CATCGCCTTC GCGCACTTTG
701 AAATCACCGG CACACAGCGT TACCCCGAAC AAATCGTCTC CGGCCTTGCG
751 CGTTCCAGC CCGGTATGCC GTACGACCTC GACCTGCTGC TCGACTTCCA
801 ACAGGCGCTC GAACAAAACG GGCATTATTC CGGCGCGTCC GTACAAGCCG
851 ACTTCGACCG CCTCCAAGC GACCGCGTCC CCGTCAAAGT CAGCGTAACC
901 GAGGTCAAAC GCCACAACT CGAAACCGGC ATCCGCTCG ATTCGGAATA
951 CGGTTTGGGC GGCAAAATCG CCTACGACTA TTACAACCTC TTCAACAAAG
1001 GCTATATCGG TTCGTCGTC TGGGATATGG ACAAATACGA AACCACGCTT
1051 GCCGCCGGCA TCAGCCAGCC GCCTCAACTAT CCGGGCAACT ACTGGACAAG
1101 CAACGTTTCC TACAACCGTT CGACCACCCA AAACCTCGAA AAACGCGCCT
1151 TCTCCGGCGG CGTCTGGTAT GTGCGCGACC GCGCGGGCAT CGATGCGCAGG
1201 CTGGGGGCGG AATTCTCGC AGAAGGCCGG AAAATCCCCG GCTCGGCTGT
1251 CGATTTGGGC AACAGCCACG CCACGATGCT GACCGCCTCT TGGAAACGCC
1301 AGCTGCTCAA CAACGTGCTG CATCCCGAAA ACGGCCATTA CCTCGACGGC
1351 AAAATCGGTA CGACTTTGGG CACATTCTTG TCCTCCACCG CGCTGATCCG
1401 CACCTCTGCC CGTGCAGGTT ATTTCTTAC GCCCGAAAAC AAAAACTCG
1451 GCACGTTTAT CATACGCGGA CAAGCGGGT ACACCGTTGC CCGCGACAAT
1501 GCGGACGTTT CTTCAGGGCT GATGTTCCGC AGCGGCGGCG CGTCTTCCGT
1551 GCGCGGTTAC GAACTCGACA GCATCGGACT TGCCGGCCCG AACGGATCGG
1601 TCCTGCCCCA ACGCGCCCTC CTGGTGGGCA GCCTGGAATA CCAACTGCCG
1651 TTTACGCGCA CCTTTCCGG CGCGGTGTT CACGATATGG GCGATGCCG
1701 CGCCAATTTC AAACGTATGA AGCTGAAACA CGGTTCCGGA CTGGGCGTGC
1751 GCTGGTTTCA CCGCTTGC GCGTTTTCT TCGACATCGC CTACGGGCAC
1801 AGCGATAAGA AAATCCGCTG GCACATCAGC TTGGGAACGC GCTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 1196; ORF 286>:

m286.pep

```

1 MHDTRTMMIK PTALLLPALF FFPHAYAPAA DLSENKAAGF ALFKNKSPDT
51 ESVKLPKFP VLIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFLAEE
101 APDNVKTMLR SKGYFSSKVS LTKDGDYTV HITPGPRTKI ANVGVAIGLD
151 ILSDGNLAEY YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKAYPLA
201 KLGNTQAAVN PDTATADLNV VVDSGRPIAF GDFEITGTQR YPEQIVSGLA
251 RFQPGMPYDL DLLLDFQAL EQNGHYS GAS VQADFDR LQG DRVPVKVSVT
301 EVKRHKLETG IRLDSEYGLG GKIAYDYNNL FNKGYSVSV WDMDKYETTL
351 AAGISQPRNY RGNYSWTSNV YNRSTTQNL KRAFSGGVWY VRDRAGIDAR
401 LGAEFLAEGR KIPGSAVDLG NSHATMLTAS WKRLNNVL HPENGHYLDG
451 KIGTTLTGFL SSTALIRTS RAGYFFTPEN KKLGTFIIR QAGYTVARDN
501 ADVPSGLMFR SGGASSVRGY ELDSIGLAGP NGSVLPERAL LVGSLEYQLP
551 FTRTLSGAVF HDMGDAAANF KRMKLKHGSG LGVRWFSPLA PFSFDIAYGH
601 SDKKIRWHIS LGTRF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m286/g286 95.9% identity in 293 aa overlap

668

	10	20	30	40	50	60
m286.pep	MHDTRTMMIKPTALLLPALFFFFPHAYAPAADLSENKAAGFALFKNKSPDTESVKLPKFP					
g286	MQNTGTMMIKPTALLLPALFFFFPHAYAPAADLSENKAAGFALFKSKSPDTESVKLPKFP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m286.pep	VLIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAEEAPDNVKTMLRSKGYFSSKVS					
g286	VRIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAEEAPDNVKTMLRSKGYFSSKVS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m286.pep	LTEKDGAYTVHITPGPRTKIANVGVAI LGDILSDGNLA EYYRNALENWQQPVGSDFDQDS					
g286	LTEKDGAYTVHITPGPRTKIANVGVAI LGDILSDGNLA EYYRNALENWQQPVGSDFDQDS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m286.pep	WENSKTSVLGAVTRKAYPLAKLGNTQAAVNPD TATADLNVVVD SGRPIAFGDFEITGTQR					
g286	WENSKTSVLGAVTRKGYPLAKLGNTRAAVNPD TATADLNVVVD SGRPIAFGDFEITGTQR					
	190	200	210	220	230	240
	250	260	270	280	290	299
m286.pep	YPEQIVSGLARFQPGMPYDL DLLDFQQA LEQNGHYS GASVQADFDRL-QGDRVPVKVSV					
g286	YPEQTVSGLARFQPGTPYDL DLLDFQQA LEQNGHYS GASVQADFDRLPRGPRPRQSQRN					
	250	260	270	280	290	300
	300	310	320	330	340	359
m286.pep	TEVKRHKLETGIRLDSEYGLGGKIAYDYNNLFNKG YIGSVVWMDKYETTIAAGISQPRN					
g286	RGQTPQTRNRHPPRFGRQNLRL LQPLQQR LYLRLG YGQIRNHACRRHQPA AQL					
	310	320	330	340	350	360

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1197>:

a286.seq

1	ATGCACGACA	CCCGTACCAT	GATGATTAAA	CCGACCGCCC	TGCTCCTGCC
51	GGCTTTATTT	TTCTTTCCGC	ACGCATACGC	GCCTGCCGCC	GACCTTTCCG
101	AAAACAAGGC	GGCGGGTTTC	GCATTGTTCA	AAAACAAAAG	CCCCGACACC
151	GAATCAGTTA	AATTAAACCC	CAAATTCCCC	GTCCGCATCG	ACACGCAGGA
201	TAGTGAAATC	AAAGATATGG	TCGAAGAACA	CCTGCCGCTC	ATCACGCAGC
251	AGCAGGAAGA	AGTATTGGAC	AAGGAACAGA	CGGGCTTCCT	CGCCGAAGAA
301	GCACCGGACA	ACGTTAAAAC	AATGCTCCGC	AGCAAAGGCT	ATTTCAGCAG
351	CAAAGTCAGC	CTGACGGAAA	AAGACGGAGC	TTATACGGTA	CACATCACAC
401	CGGGCCCGCG	CACCAAAATC	GCCAACGTCG	GCGTCGCCAT	CCTCGGCGAC
451	ATCCTTTCAG	ACGGCAACCT	CGCCGAATAC	TACCGCAACG	CGCTGGAAAA
501	CTGGCAGCAG	CCGGTAGGCA	GTGATTTCTG	TCAGGACAGT	TGGGAAAAACA
551	GCAAAACTTC	CGTCCTCGGC	GCGGTAACGC	GCAAAGCCTA	CCCGCTTGCC
601	AAGCTCGGCA	ACACCCGGGC	GGCCGTCAAC	CCCGATACCG	CCACCGCCGA
651	TTTGAACGTC	GTCTGTGGACA	GCGGCCGCCC	CATCGCCTTC	GGCGACTTTG
701	AAATTACCGG	CACGCAGCGT	TACCCCGAAC	AAATCGTCTC	CGGCTTGCGC
751	CGCTTCCAAC	CGGGCACGCC	CTACGACCTC	GACCTGCTGC	TCGACTTCCA
801	ACAGGCGCTC	GAACAAAACG	GGCATTATTC	CGGCGCGTCC	GTACAAGCCG
851	ACTTCGACCG	CCTCCAAGGC	GACCGCGTCC	CCGTCAAAGT	CAGCGTAACC
901	GAGGTCAAAC	GCCACAAGCT	CGAAACCGGC	ATCCGCCTCG	ATTCGGAATA
951	CGGTTTGGGC	GGCAAAATCG	CCTACGACTA	TTACAACCTC	TTCAACAAAG
1001	GCTATATCGG	TTCGGTCGTC	TGGGATATGG	ACAAATACGA	AACCACGCTT
1051	GCCGCCGGCA	TCAGCCAGCC	GCGCAACTAT	CGGGGCAACT	ACTGGACAAG
1101	CAACGTTTCC	TACAACCGTT	CGACCACCCA	AAACCTCGAA	AAACGCGCCT
1151	TCTCCGGCGG	CATCTGGTAT	GTGCGCGACC	GCGCGGGCAT	CGATGCCAGG
1201	CTGGGGGCGG	AGTTTCTCGC	AGAAGGCCGG	AAAATCCCCG	GCTCGGATAT
1251	CGATTTGGGC	AACAGCCACG	CCACGATGCT	GACCGCCTCT	TGGAAACGCC
1301	AGTGCTCAA	CAACGTGCTG	CATCCCGAAA	ACGGCCATTA	CCTCGACGGC

669

```

1351 AAAATCGGTA CGACTTTGGG CGCATTCTGT TCCTCCACCG CGCTGATCCG
1401 CACCTCTGCC CGCGCAGGTT ATTTCTTCAC GCCCGAAAAC AAAAACTCG
1451 GCACGTTTAT CACACGCGGA CAAGCGGGTT ACACCGTTGC CCGCGACAAT
1501 GCCAACGTTT CTTCAGGGCT GATGTTCCGC AGCGGCGGCG CGTCTTCCGT
1551 GCGCGGTTAC GAACTCGACA GCATCGGGCT TGCCGGCCCG AACGGATCGG
1601 TCCTGCCCCG ACGCGCCCTC TTGGTGGGCA GCCTGGAATA CCAACTGCCG
1651 TTTACGCGCA CCCTTTCCGG CGCGGTGTTC CACGATATGG GCGACGCCGC
1701 CGCCAATTTC AAACGTATGA AGCTGAAACA CGGTTCGGGA CTGGGCGTGC
1751 GCTGGTTCAG CCCGCTCGCG CCGTTTTCCT TCGACATCGC CTACGGGCAC
1801 AGCGACAAGA AAATCCGCTG GCACATCAGC TTGGGAACGC GCTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 1198; ORF 286.a>:

a286.pep

```

1 MHDTRTMMIK PTALLLPALF FFPHAYAPAA DLSENKAAGF ALFKNKSPDT
51 ESVKLKPKFP VRIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFLAEE
101 APDNVKTMLR SKGYFSSKVS LTKDGAYTV HITPGPRTKI ANVGVAI LGD
151 ILSDGNLA EY YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKAYPLA
201 KLGNTAAVN PDTATADLNV VVDSGRPIAF GDFEITGTOR YPEQIVSGLA
251 RFQPGTPYDL DLLLDFQQA LEQNGHYS GASVQADFRLQG DRVPVKVSVT
301 EVKRHKLETG IRLDSEYGLG GKIAYDYNNL FNKG YIGSVV WMDMKYETTL
351 AAGISQPRNY RGNWTSNVS YNRSTTQNL E KRAFSGGIWY VRDRAGIDAR
401 LGAEFLA EGR KIPGSDIDL G NSHATMLTAS WKRLNNVL HPENGHYLDG
451 KIGTTLGA FL SSTALIRTS A RAGYFPTEN KKLGTFIIRG QAGYTVARDN
501 ANVPSGLMFR SGGASSVRGY ELDSIGLAGP NGSVLPERAL LVGSLEYQLP
551 FTRTSLGAVF HDMGDAAANF KRMKLKHGSG LGVRWFSP LA PFSFDIAYGH
601 SDKKIRWHIS LGTRF*

```

m286/a286 98.7% identity in 615 aa overlap

	10	20	30	40	50	60
m286.pep	MHDTRTMMIKPTALLLPALFFFPHAYAPAADLSENKAAGFALFKNKSPDTESVKLKPKFP					
a286	MHDTRTMMIKPTALLLPALFFFPHAYAPAADLSENKAAGFALFKNKSPDTESVKLKPKFP					
	10	20	30	40	50	60
m286.pep	70	80	90	100	110	120
a286	70	80	90	100	110	120
m286.pep	VLIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAEEAPDNVKTMLRSKGYFSSKVS					
a286	VRIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAEEAPDNVKTMLRSKGYFSSKVS					
	70	80	90	100	110	120
m286.pep	130	140	150	160	170	180
a286	130	140	150	160	170	180
m286.pep	LTKDGAYTVHITPGPRTKIANVGVAI LGDILSDGNLA EY YRNALENWQQPVGSDFDQDS					
a286	LTKDGAYTVHITPGPRTKIANVGVAI LGDILSDGNLA EY YRNALENWQQPVGSDFDQDS					
	130	140	150	160	170	180
m286.pep	190	200	210	220	230	240
a286	190	200	210	220	230	240
m286.pep	WENSKTSVLGAVTRKAYPLAKLGNTQAAVNPDATADLNVVDSGRPIAFGDFEITGTOR					
a286	WENSKTSVLGAVTRKAYPLAKLGNTAAVNPDATADLNVVDSGRPIAFGDFEITGTOR					
	190	200	210	220	230	240
m286.pep	250	260	270	280	290	300
a286	250	260	270	280	290	300
m286.pep	YPEQIVSGLARFQPGMPYDL DLLLDFQQA LEQNGHYS GASVQADFRLQGDRVPVKVSVT					
a286	YPEQIVSGLARFQPGTPYDL DLLLDFQQA LEQNGHYS GASVQADFRLQGDRVPVKVSVT					
	250	260	270	280	290	300
m286.pep	310	320	330	340	350	360
a286	310	320	330	340	350	360
m286.pep	EVKRHKLETGIRLDSEYGLGGKIAYDYNNL FNKG YIGSVVWMDMKYETTLAAGISQPRNY					
a286	EVKRHKLETGIRLDSEYGLGGKIAYDYNNL FNKG YIGSVVWMDMKYETTLAAGISQPRNY					
	310	320	330	340	350	360
	370	380	390	400	410	420

670

m286.pep	RGNYWTSNVSYNRSTTQNLEKRAFSGGVWYVRDRAGIDARLGAEFLAEGRKIPGSAVDLG
a286	RGNYWTSNVSYNRSTTQNLEKRAFSGGIWIYVRDRAGIDARLGAEFLAEGRKIPGSDIDLG
	370 380 390 400 410 420
m286.pep	NSHATMLTASWKRQLLNVLHPENGHYLDGKIGTTLGTFLSSTALIRTSARAGYFFTPEN
a286	NSHATMLTASWKRQLLNVLHPENGHYLDGKIGTTLGAFLSSTALIRTSARAGYFFTPEN
	430 440 450 460 470 480
m286.pep	KKLGTFIIRGQAGYTVARDNADVPSGLMFRSGGASSVRGYELDSIGLAGPNGSVLPERAL
a286	KKLGTFIIRGQAGYTVARDNANVPSGLMFRSGGASSVRGYELDSIGLAGPNGSVLPERAL
	490 500 510 520 530 540
m286.pep	LVGSLEYQLPFFTRTLSGAVFHDMDAAANFKRMKLKHGSGLGVRWFSPPLAPFSFDIAYGH
a286	LVGSLEYQLPFFTRTLSGAVFHDMDAAANFKRMKLKHGSGLGVRWFSPPLAPFSFDIAYGH
	550 560 570 580 590 600
m286.pep	SDKKIRWHISLGTRFX
a286	SDKKIRWHISLGTRFX
	610

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1199>:

g287.seq

1	atgttttaaac	gcagtgat	tgcaatggct	tgtatttttc	ccctttcagc
51	ctgtgggggc	ggcgggtggcg	gatcgcccga	tgtcaagtcg	gcggacacgc
101	cgtcaaaaacc	ggccgcccc	gttgttgctg	aaaatgccgg	ggaaggggtg
151	ctgccgaaaag	aaaagaaaga	tgaggaggca	gcgggcgggtg	cgccgcaagc
201	cgatacgag	gacgcaaccg	ccggagaagg	cagccaagat	atggcggcag
251	tttcggcaga	aaatacaggc	aatggcggtg	cggcaacaac	ggacaacccc
301	aaaaatgaag	acgcgggggc	gcaaaatgat	atgccgcaaa	atgccgccga
351	atccgcaa	caaacaggga	acaaccaacc	cgccggttct	tcagattccg
401	cccccgctc	aaaccctgcc	cctgcgaatg	gcggtagcga	ttttggaagg
451	acgaacgtg	gcaattctgt	tgtgattgac	ggaccgtcgc	aaaaataaac
501	gttgaccac	tgtaaaggcg	attcttgtaa	tggtgataat	ttattggatg
551	aagaagcacc	gtcaaaatca	gaatttgaaa	aattaagtga	tgaagaaaaa
601	attaagcgat	ataaaaaaga	cgagcaacgg	gagaattttg	tcggtttggt
651	tgctgacagg	gtaaaaaagg	atggaactaa	caaatatata	atcttctata
701	cggacaaaacc	acctactcgt	tctgcacggg	cgaggagggtc	gcttccggcc
751	gagattccgc	tgattcccgt	caatcaggcc	gatacgtga	ttgtggatgg
801	ggaagcggtc	agcctgacgg	ggcattccgg	caatatcttc	gcgccgaag
851	ggaattaccg	gtatctgact	tacggggcgg	aaaaattgcc	cggcggtatcg
901	tatgccctcc	gtgtgcaagg	cgaaccggca	aaaggcgaaa	tgcttgttgg
951	cacggccgtg	tacaacggcg	aagtgtctga	tttccatatg	gaaaacggcc
1001	gtccgtaccc	gtccggaggc	aggtttgccg	caaaagtcga	tttcggcagc
1051	aatctgtgg	acggcattat	cgacagcggc	gatgatttgc	atatgggtac
1101	gcaaaaattc	aaagccgcca	tcgatggaaa	cggctttaag	gggacttgga
1151	cggaaaatgg	cggcggggat	gtttccggaa	ggttttacgg	cccggccggc
1201	gaggaaatgg	cgggaaaata	cagctatcgc	ccgacagatg	ctgaaaaggg
1251	cggattccgc	gtgtttgccg	gcaaaaaaga	tcgggattga	

This corresponds to the amino acid sequence <SEQ ID 1200; ORF 287.ng>:

g287.pep

1	MFKRSVIAMA	CIFPLSACGG	GGGGSPDVKS	ADTPSKPAAP	VVAENAGEGV
51	LPKEKKDEEA	AGGAPQADTQ	DATAGEGSQD	MAAVSAENTG	NGGAATTDNP
101	KNEDAGAQN	MPQNAAESAN	QTGNNQPAGS	SDSAPASNPA	PANGGSDFGR

671

```

151  TNVGNVVID  GPSQNITLTH  CKGDSCNGDN  LLDEEAPSKS  EFEKLSDEEK
201  IKRYKKDEQR  ENFVGLVADR  VKKDGTNKYI  IFYTDKPPTR  SARSRRSLPA
251  EIPLIPVNQA  DTLIVDGEAV  SLTGHSGNIF  APEGNYRYLT  YGAEKLPGGS
301  YALRVQGEPA  KGEMLVGTAV  YNGEVLHFHM  ENGRPYPSGG  RFAAKVDFGS
351  KSVDDGIIDSG  DDLHMGTOKF  KAAIDGNFGK  GTWTENGGGD  VSGRFYGPAG
401  EEVAGKYSYR  PTDAEKGGFG  VFAGKKDRD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1201>:

```

m287.seq
1   ATGTTTAAAC  GCAGCGTAAT  CGCAATGGCT  TGTATTTTGT  CCCTTTCAGC
51  CTGCGGGGGC  GGCGGTGGCG  GATCGCCCGA  TGTCAAGTCG  GCGGACACGC
101 TGTCAAAACC  TGCCGCCCTT  GTTGTCTTCT  AAAAAGAGAC  AGAGGCCAAG
151 GAAGATGCGC  CACAGGCAGG  TTCTCAAGGA  CAGGGCGCGC  CATCCGCACA
201 AGGCAGTCAA  GATATGGCGG  CGGTTTCGGA  AGAAAATACA  GGCAATGGCG
251 GTGCGGTAAC  AGCGGATAAT  CCCAAAAATG  AAGACGAGGT  GGCACAAAAT
301 GATATGCCGC  AAAATGCCGC  CGGTACAGAT  AGTTCGACAC  CGAATCACAC
351 CCCGGATCCG  AATATGCTTG  CCGGAAATAT  GGAATCAATC  GCAACGGATG
401 CCGGGGAATC  GTCTCAGCCG  GCAAACCAAC  CGGATATGGC  AAATGCGGCG
451 GACGGAATGC  AGGGGGACGA  TCCGTCGGCA  GGCGGGCAAA  ATGCCGGCAA
501 TACGGCTGCC  CAAGGTGCAA  ATCAAGCCGG  AAACAATCAA  GCCGCCGGTT
551 CTTGAGATCC  CATCCCCGCG  TCAAACCTTG  CACCTGCGAA  TGGCGGTAGC
601 AATTTTGGA  GGGTTGATTT  GGCTAATGGC  GTTTTGATTG  ACGGGCCGTC
651 GCAAAATATA  ACGTTGACCC  ACTGTAAAGG  CGATTCTTGT  AGTGCCAATA
701 ATTTCTTGGA  TGAAGAAGTA  CAGCTAAAAT  CAGAATTTGA  AAAATTAAGT
751 GATGCAGACA  AAATAAGTAA  TTACAAGAAA  GATGGGAAGA  ATGATAAATT
801 TGTGCGTTTG  GTTGCCGATA  GTGTGCAGAT  GAAGGGAATC  AATCAATATA
851 TTATCTTTTA  TAAACCTAAA  CCCACTTCAT  TTGCGCGATT  TAGGCGTTCT
901 GCACGGTCGA  GGCGGTCGCT  TCCGGCCGAG  ATGCCGCTGA  TTCCCGTCAA
951 TCAGGCGGAT  ACGCTGATTG  TCGATGGGGA  AGCGGTCAGC  CTGACGGGGC
1001 ATTCCGGCAA  TATCTTCGCG  CCCGAAGGGA  ATTACCGGTA  TCTGACTTAC
1051 GGGGCGGAAA  AATTGCCCGG  CGGATCGTAT  GCCCTTCGTG  TTCAAGGCCA
1101 ACCGGCAAAA  GCGGAAATGC  TTGCGGGCGC  GGCCGTGTAC  AACGGCGAAG
1151 TACTGCATTT  CCATACGGAA  AACGGCCGTC  CGTACCGGAC  CAGGGGCGAG
1201 TTTGCCGCAA  AAGTCGATTT  CGGCAGCAAA  TCTGTGGACG  GCATTATCGA
1251 CAGCGGCGAT  GATTTGCATA  TGGGTACGCA  AAAATTCAAA  GCCGCCATCG
1301 ATGGAAACGG  CTTTAAGGGG  ACTTGACGCG  AAAATGCGAG  CGGGGATGTT
1351 TCCGGAAGT  TTTACGGCCC  GGCCGGCGAG  GAAGTGGCGG  GAAAATACAG
1401 CTATCGCCCG  ACAGATGCGG  AAAAGGGCGG  ATTCGGCGTG  TTTGCCGGCA
1451 AAAAAGAGCA  GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1202; ORF 287>:

```

m287.pep
1   MFKRSVIAMA  CIFALSACGG  GGGGSPDVKS  ADTLSKPAAP  VVSEKETEAK
51  EDAPQAGSQ  QGAPSAQGSQ  DMAAVSEENT  GNNGAVTADN  PKNEDEVAQN
101 DMPQNAAGTD  SSTPNHTPDP  NMLAGNMENQ  ATDAGESSQP  ANQPDMANAA
151 DGMQDDPSA  GGQNAAGTAA  QGANQAGNNQ  AAGSSDPIPA  SNPAPANGGS
201 NFRVVDLANG  VLIDGPSQNI  TLTHCKGDSC  SGNNFLDEEV  QLKSEFEKLS
251 DADKISNYKK  DGKNDKFVGL  VADSVQMKGI  NQYIIFYKPK  PTSFARFRRS
301 ARSRRSLPAE  MPLIPVNQAD  TLIVDGEAVS  LTGHSGNIFA  PEGNYRYLTY
351 GAEKLPGGSY  ALRVQGEPAK  GEMLAGAAVY  NGEVLHFHTE  NGRPYPTRGR
401 FAAKVDFGSK  SVDGIIDSGD  DLHMGTOKF  KAAIDGNFGK  GTWTENGGGD
451 SGKFYGPAGE  EVAGKYSYRP  TDAEKGGFGV  FAGKKEQD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m287/g287 70.1% identity in 499 aa overlap

```

          10      20      30      40      49
m287.pep  MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVVSE-----KETE
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g287       MFKRSVIAMACIFPLSACGGGGGGSPDVKSADTSPKPAAPVVAENAGEGVLPKEKKDEEA
          10      20      30      40      50      60

```

	50	60	70	80	90	100	109
m287.pep	KEDAPQAGSQGQ	GAPSAQGSQDMA	AVSEENTGNGG	AVTADNP	KNEDEVAQND	MFPQNAAGT	
	:	:::			:		
g287	AGGAPQADTQD	--ATAGEGSQDMA	AVSAENTGNGG	AATTDNPKNE	DAGAQNDMPQNA	AA--	
	70	80	90	100	110		
m287.pep	110	120	130	140	150	160	169
	DSSTPNHTPDPN	MLAGNMENQAT	DAGESSQPANQ	PDMANAADGM	QGGDDPSAGG	QONAGNTA	
g287	-----						
m287.pep	170	180	190	200	210	220	229
	AQGANQAGNNQA	AGSSDPIPASNP	PAPANGGSNFG	RVDLANGVLID	GPSQNITLTH	CKKGDS	
	: : :				:	:	
g287	-ESANQTGNNP	AGSSDSAPASNP	PAPANGGSDFG	RTNVGNSSVID	GPSQNITLTH	CKKGDS	
	120	130	140	150	160	170	
m287.pep	230	240	250	260	270	280	289
	CSGNNFLDEEV	QLKSEFEKLS	DADKISNYKK	DGKNDKFVGL	VADSVQMKGI	NYIIFYKP	
	: :		: :	:	: :	:	
g287	CNGDNLLEEAP	SKSEFEKLS	DEEKIKRYKK	DEQRENFVGL	VADRVKKDG	TNKYIIFYTD	
	180	190	200	210	220	230	
m287.pep	290	300	310	320	330	340	349
	KPTSFAFRFRS	ARSRRSLPAE	EMPLIPVNQAD	TLIVDGEAVS	LTGHSGNIFA	PEGNYRYLT	
	:						
g287	KPPT-----	RSARSRRSLPA	EIPLIPVNQAD	TLIVDGEAVS	LTGHSGNIFA	PEGNYRYLT	
	240	250	260	270	280	290	
m287.pep	350	360	370	380	390	400	409
	YGAEKLPGGSY	ALRVQGEPAK	GEMLAGAAVY	NGEVLHFHT	ENGRPYPTR	RGRFAAKVD	FGS
			: :			: :	
g287	YGAEKLPGGSY	ALRVQGEPAK	GEMLVGTAVY	NGEVLHFH	ENGRPYPSG	GRFAAKVD	FGS
	300	310	320	330	340	350	
m287.pep	410	420	430	440	450	460	469
	KSVDGIIDS	GDDLHMG	TQKFKA	AIDGNGFKGT	WTENGSGDV	SGKFYGPAGE	EVAGKYSYR
					: :		
g287	KSVDGIIDS	GDDLHMG	TQKFKA	AIDGNGFKGT	WTENGSGDV	SGRFGPAGE	EVAGKYSYR
	360	370	380	390	400	410	
m287.pep	470	480	489				
	PTDAEKG	GGGVFAGK	KEQDX				
			: :				
g287	PTDAEKG	GGGVFAGK	KDRDX				
	420	430					

a287.seq

1	ATGTTTAAAC	GCAGTGTGAT	TGCAATGGCT	TGTATTGTTG	CCCTTTCAGC
51	CTGTGGGGGC	GGCGGTGGCG	GATCGCCCGA	TGTTAAGTCG	GCGGACACGC
101	TGTCAAAAAC	TGCCGCCCTT	GTTGTTACTG	AAGATGTCGG	GGAAGAGGTG
151	CTGCCAAAAG	AAAAGAAAGA	TGAGGAGCG	GTGAGTGGT	CGCCGCAAGC
201	CGATACGCAG	GACGCAACCG	CCGGA AAAAG	CGGTCAAGAT	ATGGCGGCAG
251	TTTCGGCAGA	AAATACAGGC	AATGGCGGTG	CGGCAACAAC	GGATAATCCC
301	GAAAATAAAG	ACGAGGGACC	GCAAAATGAT	ATGCCGCAA	ATGCCGCCGA
351	TACAGATAGT	TCGACACCGA	ATCACACCCC	TGCACCGAAT	ATGCCAACCA
401	GAGATATGGG	AAACCAAGCA	CCGGATGCCG	GGGAATCGGC	ACAACCGGCA
451	AACCAACCGG	ATATGGCAAA	TGCGGCGGAC	AGGAATGCAGG	GGGACGATCC
501	GTCGGCAGGG	GAAAAATGCCG	GCAATACGGC	AGATCAAGCT	GCAAATCAAG
551	CTGAAAACAA	TCAAGTCGGC	GGCTCTCAAA	ATCCTGCCTC	TTCAACCAAT
601	CCTAACGCCA	CGAATGGCGG	CAGCGATTTT	GGAAGGATAA	ATGTAGCTAA
651	TGGCATCAAG	CTTGACAGCG	GTTTCGGAAAA	TGTAACGTTG	ACACATTGTA
701	AAGACAAAGT	ATGCGATAGA	GATTTCCTAG	ATGAAGAGTG	ACCACCAAAA
751	TCAGAATTTG	AAAAATTAAG	TGATGAAGAA	AAAATTAATA	AATATAAAAA

801	AGACGAGCAA	CGAGAGAATT	TTGTCGGTTT	GGTTGCTGAC	AGGGTAGAAA
851	AGAATTGGAAC	TAACAAATAT	GTCAATCATTT	ATAAAGACAA	GTCCGCTTCA
901	TCTTTCATCTG	CGCGAATTAC	CGGTTCTGCA	CGGTCTGAGG	GGTCGCTTCC
951	GGCCGAGATG	CGCTGATTCC	CCGTCAATCA	GGCGGATACG	CTGATTGTCTG
1001	ATGGGGAAGC	GGTCAGCCTG	ACGGGGCATT	CCGGCAATAT	CTTCGCGCCC
1051	GAAGGGAATT	ACCGGTATCT	GACTTACGGG	GCGGAAAAAT	TGTCGGGCGG
1101	ATCGTATGCC	CTCAGTGTGC	AAGCGCAACC	GGCAAAGGC	GAATGTCTTG
1151	CGGGCACGGC	CGTGTACAAC	GGCGAAGTGC	TGCATTTTCCA	TATGGAAATC
1201	GGCCGTCCGT	CCCGTCCGG	AGCGAGGTTT	GCGCAAAAG	TCGATTTCTGG
1251	CAGCAAATCT	GTGGACGGCA	TTATCGACAG	CGGCGATGAT	TTGCATATGG
1301	GTACGCAAAA	ATTCAAAGCC	GTTATCGATG	GAACAGGCTT	TAAGGGGACT
1351	TGGACGGAAA	ATGGCCGGCG	GGATGTTTCA	GGAAGGTTTT	ACGGCCCGGC
1401	CGGCGAAGAA	GTGGCGGGAA	AATACAGTCC	TGCGCCGACA	GATCGGAAA
1451	AGGGCGGATT	CGGCGTGTTT	GCCGGCAAAA	AAGAGCAGGA	TTGA

a287.pep

1	<u>MFKRSVIAMA</u>	<u>CIVALSACGG</u>	GGGGSPDVKS	ADTLSPAAP	VVTEVDGEEV
51	LPKEKKDEEA	VSGAPQADTQ	DATAGKGGQD	MAAVSAENTG	NGGAATTDNP
101	ENKDEGPQND	MPQNAADTDS	STPNHTPAPN	MPTRDMNQVA	PDAGESAQPA
151	NQPDMANAAD	GMQGDDPSAG	ENAGNTADQA	ANQAENNQVG	GSQNPASSTN
201	PNATNGGSDF	GRINVANGIK	LDSGSENVTL	THCKDKVCDR	DFLDEEAPPK
251	SEFEKLSDEE	KINKYKKDEQ	RENFVGLVAD	RVEKNGTNKY	VIIYKDKSAS
301	SSSRFRFSA	RSRRSLPAEM	PLIPVNQADT	LIVDGEAVSL	TGHSNFIAP
351	EGNYRYLTYG	AAKLSGGSYA	LSVQGEPAKG	EMLAGTAVYN	GEVLHFHFMN
401	GRPSPSGGRF	AAKVDFGSKS	VDGIIDSGDD	LHMGTQKFFA	VIDGNFGKGT
451	WTENGGGDVS	GRFYGPAGEE	VAGKYSYRPT	DAEKGFGVF	AGKKEQD*

	10	20	30	40	49
m287.pep	MFKRSVIAMACIFALSACGGGGGGSPDVK	SADTL	SKPAA	PV	VS-----KETEA
a287	MFKRSVIAMACIVALSACGGGGGGSPDVK	SADTL	SKPAA	PVV	TEDVGEEVLPKEKKDEEA
	10	20	30	40	50
m287.pep	50	60	70	80	90
a287	50	60	70	80	90
	100	109			
m287.pep	KEDAPQAGSQGGAPSAQGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQN	DMPQNAAGT			
a287	VSGAPQADTQ--DATAGKGGQDMAAVSAENTGNGGAATTDNPENKDEGPQNDMPQNAADT				
	70	80	90	100	110
m287.pep	110	120	130	140	150
a287	110	120	130	140	150
	160	169			
m287.pep	DSSTPNHTPDPNMLAGNMENQATDAGESSQFANQPDMANAADGMQGGDDPSAGGQNA	GN			
a287	DSSTPNHTPAPNMPTRDMGNQAPDAGESAQFANQPDMANAADGMQGGDDPSAG-ENAG	NTA			
	120	130	140	150	160
m287.pep	170	180	190	200	210
a287	170	180	190	200	210
	220	229			
m287.pep	AQGANQAGNNQAAGSSDPIPASNPAPANGGSNFRGVDLANGVLIDGPSQ	NITLTHCKGDS			
a287	DQAANQAENNQVGGSQNPASSTNPNATNGGSDFRINANGIKLDSGSENVTLTHCKDKV				
	180	190	200	210	220
m287.pep	230	240	250	260	270
a287	230	240	250	260	270
	280	289			
m287.pep	CSGNNFLDEEVQLKSEFEKLSADAKISNYKKDGKNDKFVGLVADSVQMKGINQYII	IFYKP			
a287	CD-RDFLDEEAPPKSEFEKLSDEEKINKYKKDEQRENFVGLVADRVEKNGTNKYVII	YKD			
	240	250	260	270	280
m287.pep	290	300	310	320	330
a287	290	300	310	320	330
	340	350			
m287.pep	KP--TSFARFRRSARSRRLPAEMPLIPVNQADTLIVDGEAVSLTGHS	GNIFAPEGNYRY			
a287	KSASSSSARFRRSARSRRLPAEMPLIPVNQADTLIVDGEAVSLTGHS	GNIFAPEGNYRY			
	300	310	320	330	340

674

	350	360	370	380	390	400
m287.pep	LTYGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDF					
a287	LTYGAEKLSGGSYALSVQGEPAKGEMLAGTAVYNGEVLHFHMENGRPSPSGGRFAAKVDF					
	360	370	380	390	400	410
	410	420	430	440	450	460
m287.pep	GSKSVVDGIIDSGDDLHMGTKQFKAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYS					
a287	GSKSVVDGIIDSGDDLHMGTKQFKAAIDGNGFKGTWTENGSGDVSGRFGYPAGEEVAGKYS					
	420	430	440	450	460	470
	470	480	489			
m287.pep	YRPTDAEKGGFGVFAGKKEQDX					
a287	YRPTDAEKGGFGVFAGKKEQDX					
	480	490				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1205>:

```

g288.seq
1   atgcacaccg gacaggcggg aagccggggt ctgtctcgga cagtcattcc
51  tctaggcata ccgttgccgg tatgctcaag caacctacc gaacgctcgg
101 cgggcagcgt cattgcgttc tgtttggtct tgctccgaat ggggtttggc
151 ctgccgcata ttgttaccaa atgcgcgggt cgcccttacc gcaccttttc
201 acccttgccg gtgctgccaa agcagccatc ggccggtttg ctttctgttc
251 cactttccgt cgcgttaccg cgcccgccg ttaaccggca ttctaccctg
301 cggagcccgg actttcctcc ccgtatgcct tacgcgatac gcggcgactg
351 tctgcccgtc ccgtgtgcgg cgcggattat aacacgaaac gcaaaaatgc
401 cgtctgaaac ggtacaggtt tcagacggca tacagcctaa actacacacc
451 ctgtttcagg ctggcttcga tgaagccgtc caagtcgccg tccaatacgg
501 ctttgtggtt gccgacttcg tagcctgtac gcaagtcctt gatgcgtga

```

This corresponds to the amino acid sequence <SEQ ID 1206; ORF 288.ng>:

```

g288.pep
1   MHTGQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPLP VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPFRMP YAIRGDCLPV PCAARIITRN AKMPSETVQV SDGIQPKLHT
151 LFQAGFDEAV QVAVQYGFVV ADFVACTQVF DA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1207>:

```

m288.seq
1   ATGCACACCG GACAGGCGGT AAGCCGGGTT CTGTCTCGGA CAGTCATTCC
51  TCTAGGCATA CCGTTACCGG TATGCTCAAG CAACCTACCC GAACGCTCGG
101 CGGGCAGCGT CATTGCGTTC TGTTTGGTCT TGCTCCGAAT GGGGTTTGCC
151 CTGCCGCATA TTGTACCAA ATGCGCGGTG CGCCCTTACC GCACCTTTTC
201 ACCCTTACCT GTGCTGCCAA AGCAGCCATC GGCGGTTTTG CTTTCTGTTC
251 CACTTTCCGT CGCGTTACCG CGCCCGGCCG TTAACCGGCA TTCTACCCTG
301 CGGAGCCCGG ACTTTCCTCC CCGTATGCCT TACGCGATAC GCGGCGACTG
351 TCTGCCCGTC CCGTGTGCGG CGCGGATTAT AACACGAAAC ACAAAAATGC
401 CGTCTGAAAC GGTACAGGTT TCAGACGGCA TACAGCCTAA ACTACAGGCC
451 CTGTTTCAGG CTGGCTTCGA TGAAGCCGTC CAAGTCGCCA TCCAATACGG
501 CTTTGGTGTT GCCGACTTCG TAGCCTGTAC GCAAGTCTTT GATACGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1208; ORF 288>:

```

m288.pep
1   MHTGQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPLP VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPFRMP YAIRGDCLPV PCAARIITRN TKMPSETVQV SDGIQPKLHA
151 LFQAGFDEAV QVAIQYGFVV ADFVACTQVF DT*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m288/g288 97.8% identity in 181 aa overlap

	10	20	30	40	50	60
m288.pep	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGPLPHIVTKCAV					
g288	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGPLPHIVTKCAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m288.pep	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
g288	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m288.pep	PCAARIITRNTKMPSETVQVSDGIQPKLHALFQAGFDEAVQVAIQYGFVADFVACTQVF					
	: : :					
g288	PCAARIITRNAKMPSETVQVSDGIQPKLHTLFQAGFDEAVQVAVQYGFVADFVACTQVF					
	130	140	150	160	170	180
m288.pep	DTX					
	:					
g288	DAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1209>:

a288.seq

1	ATGCACACCG	GACAGGCGGT	AAGCCGGGTT	CTGTCTCGGA	CAGTCATTCC
51	TCTAGGCATA	CCGTTGCCGG	TATGCTCAAG	CAACCTACCC	GAACGCTCGG
101	CGGGCAGCGT	CATTGCGTTC	TGTTTGGTCT	TGCTCCGAAT	GGGGTTTGGC
151	CTGCCGCATA	TTGTTACCAA	ATGCGCGGTG	CGCCCTTACC	GCACCTTTTC
201	ACCCTTGCCCT	GTGCTGCCAA	AGCAGCCATC	GGCGGTTTTC	CTTTCTGTTC
251	CACTTTCCGT	CGCGTTACCG	CGCCCGGCCG	TTAACCGGCA	TTCTACCCTG
301	CGGAGCCCGG	ACTTTCCTCC	CCGTATGCCT	TACGCGATAC	GCGGCGACTG
351	TCTGCCCGTC	CCGTGTGCGG	CGCGGATTAT	AACACGAAAC	GCAAAAATGC
401	CGTCTGAAAC	GGTACAGGTT	TCAGACGGCA	TACAGCCTAA	ACTACAGGCC
451	CTGTTTCAGG	CTGGCTTCGA	TAAAGCCGTC	CAAGTCGCCG	TCCAATACGG
501	CTTTGGTGTT	GCCGACTTCG	TAGCCTGTGC	GCAAGTCTTT	AATGCGTGA

This corresponds to the amino acid sequence <SEQ ID 1210; ORF 288.a>:

a288.pep

1	MHTGQAVSRV	LSRTVIPLGI	PLPVCSSNLP	ERSAGSVIAF	CLVLLRMGFG
51	LPHIVTKCAV	RPYRTFSPLP	VLPKQPSAVL	LSVPLSVALP	RPAVNRHSTL
101	RSPDFPPRMP	YAIRGDCLPV	PCAARIITRN	AKMPSETVQV	SDGIQPKLHA
151	LFQAGFDKAV	QVAVQYGFV	ADFVACAQVF	NA*	

m288/a288 97.2% identity in 181 aa overlap

	10	20	30	40	50	60
m288.pep	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGPLPHIVTKCAV					
a288	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGPLPHIVTKCAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m288.pep	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
a288	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m288.pep	PCAARIITRNTKMPSETVQVSDGIQPKLHALFQAGFDEAVQVAIQYGFVADFVACTQVF					
	: : :					

676

```

a288      PCAARIITRNAKMPSETVQVSDGIQPKLHALFQAGFDKAVQVAVQYGFVADVFVACAQVF
              130      140      150      160      170      180

m288.pep   DTX
            ::
a288      NAX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1211>:

```

g290.seq
1   atggcaaaaa tgatgaaatg ggcggctggt ggcggcggtcg cgcggcgacgc
51  ggtttggggc ggatggtctt atctgaagcc cgaaccgcag gctgcttata
101 ttacggaagc ggtcaggcgc ggcgatatca gccggacggt ttccgcgacg
151 ggcgagattt cgccgtccaa cctggtatcg gtcggcgcgcg aggtctcggg
201 gcagattaaa aagctttatg tcaaaactcg gcaacaggtc aaaaaggcg
251 atttgattgc ggaaatcaat tcgaccacgc agaccaacac gatcgatatg
301 gaaaaatcca aattggaaac gtatcaggcg aagctggtgt ccgcacagat
351 tgcattgggc agcgcgga aaatataaa gcgtcaggcg gcgttgtgga
401 aggatgatgc gacctctaaa gaagatttgg aaagcgcgca ggatgcgctt
451 gccgccgcca aagccaatgt tgccgagttg aaggctttta tcagacagag
501 caaaatttcc atcaataccg ccgagtcgga tttgggctac acgcgcatta
551 ccgcgacgat ggacggcagc gtggtggcga ttcccgtgga agaggggcag
601 actgtgaacg cggcgcgagc tacgccgacg attgtccaat tggcgaatct
651 ggatatgatg ttgaacaaaa tgcagattgc cgagggcgat attaccaagg
701 tgaaggcggg gcaggatatt tcgtttacga ttttgtccga accggatacg
751 ccgattaagg cgaagctcga cagcgtcgac cccgggctga ccacgatgtc
801 gtcgggcggc tacaacagca gtacggatac ggcttccaat gcggtctatt
851 attatgcccg ttcgtttgtg ccgaatccgg acggcaaaact cgccacgggg
901 atgacgacgc agaatacggg tgaaatcgac ggtgtgaaaa atgtgttgct
951 tattccgtcg ctgaccgtga aaaatcgcgg cggcaaggcg ttcgtacgcg
1001 tgttgggtgc ggacggcaag gcagtggaaac gcgaaatccg gaccggtatg
1051 aaagacagta tgaataccga agtgaaaagc ggggtgaaag agggggacaa
1101 agtggcatc tccgaaataa ccgccgccga gcagcaggaa agcggcgaa
1151 gcgccctagg cggcccgccg cgccgataa

```

This corresponds to the amino acid sequence <SEQ ID 1212; ORF 290.ng>:

```

g290.pep
1   MAKMMKWA AV AAVAAAAVWG GWSYLKPEPQ AAYITEAVRR GDISRTVSAT
51  GEISPSNLVS VGAQASGQIK KLYVKLGQOV KKGDLIAEIN STTQTNTIDM
101 EKSLETYQA KLVSAQIALG SAEKKYKRQA ALWKDDATSK EDLESAQDAL
151 AAAKANVAEL KALIRQSKIS INTAESDLGY TRITATMDGT VVAIPVEEQG
201 TVNAAQSTPT IVQLANLDM LNKMQIAEGD ITKVKAGQDI SFTILSEPD
251 PIKAKLDSVD PGLTMSGGG YNSSTDASN AVYYYARFV PNPDGKLTATG
301 MTTQNTVEID GVKNVLLIPS LTVKNRGGKA FVRVLGADGK AVEREIRTGM
351 KDSMNTEVKS GLKEGDKVVI SEITAAEQQE SGERALGGPP RR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1213>:

```

m290.seq (partial)
1   ..GTATCGGTCG GCGCGCAGGC ATCGGGGCAG ATTAAGATAC TTTATGTCAA
51  ACTCGGGCAA CAGGTTAAAA AGGCGGATTT GATTGCGGAA ATCAATTCTGA
101 CCTCGCAGAC CAATACGCTC AATACGGAAA AATCCAAGTT GGAAACGTAT
151 CAGGCGAAGC TGGTGTCTGC ACAGATTGCA TTGGGCAGCG CGGAGAAGAA
201 ATATAAGCGT CAGGCGGCGT TATGGAAGGA AAACGCGACT TCCAAAGAGG
251 ATTTGGAAAG CGCGCAGGAT GCGTTTGCCG CCGCCAAAGC CAATGTTGCC
301 GAGCTGAAGG CTTTAATCAG ACAGAGCAA ATTTCCATCA ATACCGCCGA
351 GTCGGAATTG GGCTACACGC GCATTACCGC AACGATGGAC GGCACGGTGG
401 TGGCGATTCT CGTGAAGAG GGGCAGACTG TGAACGCGGC GCAGTCTACG
451 CCGACGATTG TCCAATTGGC GAATCTGGAT ATGATGTTGA ACAAATGCA
501 GATTGCCGAG GGCGATATTA CCAAGGTGAA GGCGGGGCAG GATATTTCTG
551 TTACGATTTT GTCCGAACCG GATACGCCGA TTAAGGCGAA GCTCGACAGC
601 GTCGACCCCG GGCTGACCAC GATGTCGTCG GGCGGTTACA ACAGCAGTAC
651 GGATACGGCT TCCAATGCGG TCTACTATTA TGCCCGTTTCG TTTGTGCCGA

```

677

```

701   ATCCGGACGG CAAACTCGCC ACGGGGATGA CGACGCAGAA TACGGTTGAA
751   ATCGACGGCG TGAAAAATGT GCTGATTATT CCGTCGCTGA CCGTGAAAAA
801   TCGCGGCGGC AAGGCGTTTG TGCGCGTGTT GGGTGCGGAC GGCAAGGCGG
851   CGGAACGCGA AATCCGGACC GGTATGAGAG ACAGTATGAA TACCGAAGTA
901   AAAAGCGGGT TGAAAGAGGG GGACAAAGTG GTCATCTCCG AAATAACCGC
951   CGCCGAGCAA CAGGAAAGCG GCGAACGCGC CCTAGGCGGC CCGCCGCGCC
1001  GATAA

```

This corresponds to the amino acid sequence <SEQ ID 1214; ORF 290>:

```

m290.pep (partial)
1   ..VSVGAQASGQ IKILYVKLGQ QVKKGDLIAE INSTSQNTNL NTEKSKLETY
51  QAKLVSAQIA LGSAEKYKQR QAALWKENAT SKEDLESAQD AFAAAKANVA
101 ELKALIRQSK ISINTAESEL GYTRITATMD GTVVAILVEE GQTVNAAQST
151 PTIVQLANLD MMLNKMQIAE GDITKVKAGQ DISFTILSEP DTPIKAKLDS
201 VDPGLTTMSS GGYNSSTDTA SNAVYYYARS FVPNPDGKLA TGMTTQNTVE
251 IDGVKNVLI I PSLTVKNRGG KAFVRVLGAD GKAAEREIRT GMRDSMNTEV
301 KSGLKEGDKV VISEITAAEQ QESGERALGG PPRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m290/g290 96.1% identity in 334 aa overlap

```

                                10      20      30
m290.pep                      VSVGAQASGQIKILYVKLGQQVKKGDLIAE
                                |||
g290      PQAAYITEAVRRGDISRTVSATGEISPSNLVSVGAQASGQIKKLYVKLGQQVKKGDLIAE
          30      40      50      60      70      80

                                40      50      60      70      80      90
m290.pep  INSTSQNTLNTEKSKLETYQAKLVSAQIALGSAEKYKQRQAALWKENATSKEDLESAQD
          |||:|||||:| |||
g290      INSTTQTNTIDMEKSKLETYQAKLVSAQIALGSAEKYKQRQAALWKDDATSKEDLESAQD
          90      100     110     120     130     140

                                100     110     120     130     140     150
m290.pep  AFAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST
          |:|||||:| |||
g290      ALAAAKANVAELKALIRQSKISINTAESDLGYTRITATMDGTVVVAIPVEEGQTVNAAQST
          150     160     170     180     190     200

                                160     170     180     190     200     210
m290.pep  PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
          |||
g290      PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
          210     220     230     240     250     260

                                220     230     240     250     260     270
m290.pep  GGYNSSTDASNAVYYYARSFVPNPDGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
          |||
g290      GGYNSSTDASNAVYYYARSFVPNPDGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
          270     280     290     300     310     320

                                280     290     300     310     320     330
m290.pep  KAFVRVLGADGKAAEREIRTGMRDSMNTEVKSGLKEGDKVVISEITAAEQQESGERALGG
          |||
g290      KAFVRVLGADGKAVEREIRTGMKDSMNTEVKSGLKEGDKVVISEITAAEQQESGERALGG
          330     340     350     360     370     380

m290.pep  PPRRX
          |||
g290      PPRRX
          390

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1215>:

```
a290.seq
1  ATGGCAAAAA TGATGAAATG GCGCGCTGTT GCGGCGGTCG CCGCGGCAGC
51  GGTTTGGGGC GGATGGTCTT ATCTGAAGCC CGAGCCGCAG GCTGCTTATA
101 TTACGGAAAC GGTCAAGCGC GCGCATCA GCGGACGGT TTCTGCAACA
151 GGGGAGATTT CGCCGTCAA CCTGGTATCG GTCGCGCGC AGGCATCGGG
201 GCAGATTAAG AAACCTTATG TCAAACTCGG GCAACAGGTT AAAAAGGGCG
251 ATTTGATTGC GGAAATCAAT TCGACCTCGC AGACCAATAC GCTCAATACG
301 GAAAAATCCA AATTGGAAAC GTATCAGGCG AAGCTGGTGT CGGCACAGAT
351 TGCATTGGGC AGCGCGGAGA AGAAATATAA GCGTCAGGCG GCGTTGTGGA
401 AGGATGATGC GACCGCTAAA GAAGATTTGG AAAGCGCACA GGATGCGCTT
451 GCCGCCGCCA AAGCCAATGT TGCCGAGCTG AAGGCTCTAA TCAGACAGAG
501 CAAAATTTCC ATCAATACCG CCGAGTCGGA ATTGGGCTAC ACGCGCATTA
551 CCGCAACGAT GGACGGCAGC GTGGTGCGCA TTCTCGTGGA AGAGGGGCAG
601 ACTGTGAACG CGGCGCAGTC TACGCCGACG ATTGTCCAAT TGGCGAATCT
651 GGATATGATG TTGAACAAAA TGCAGATTGC CGAGGGCGAT ATTACCAAGG
701 TGAAGGCGGG GCAGGATATT TCGTTACGA TTTGTCCGA ACCGGATACG
751 CCGATTAAGG CGAAGCTCGA CAGCGTCGAC CCCGGGCTGA CCACGATGTC
801 GTCGGGCGGC TACAACAGCA GTACGGATAC GGCTTCCAAT GCGGTCTACT
851 ATTATGCCCG TTCGTTTGTG CCGAATCCGG ACGGCAAACT CGCCACGGGG
901 ATGACGACGC AGAATACGGT TGAAATCGAC GGTGTGAAAA ATGTGCTGAT
951 TATTCCGTCG CTGACCGTGA AAAATCGCGG CCGCAGGGCG TTTGTGCGCG
1001 TGTGGGTGTC AGACGGCAAG GCGGCGGAAC GCGAAATCCG GACCGGTATG
1051 AGAGACAGTA TGAATACCGA AGTAAAAAGC GGGTTGAAAG AGGGGACAA
1101 AGTGGTCATC TCCGAAATAA CCGCCGCCGA GCAGCAGGAA AGCGGCGAAC
1151 GCGCCCTAGG CGGCCGCCG CGCCGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1216; ORF 290.a>:

```
a290.pep
1  MAKMMKWA AV AAVAAA VWG GWSYLKPEPQ AAYITETVRR GDISRTVSAT
51  GEISPSNLVS VQAQASGQIK KLYVKLGQOV KKGDILAEIN STSQTNTLNT
101 ESKKLETYQA KLVSAQIALG SAEKKYKRQA ALWKDDATAK EDLESAQDAL
151 AAANKANVAEL KALIRQSKIS INTAESELGY TRITATMDGT VVAILVEEGQ
201 TVNAAQSTPT IVQLANLDM LNMQIAEGD ITKVKAGQDI SFTILSEPDT
251 PIKAKLDSVD PGLTTMSSGG YNSSTDASN AVYYYARSFV PNPDGKLATG
301 MTTQNTVEID GVKNVLIIPS LTVKNRGGRA FVRVLGADGK AAEREIRTGM
351 RDSMNTEVKS GLKEGDKVVI SEITAEQQE SGERALGGPP RR*

m290/a290 98.2% identity in 334 aa overlap

m290.pep
10 20 30
VSVGAQASGQIKILYVKLGQOVKKGDILAE
|||||

a290
30 40 50 60 70 80
PQAAYITETVRRGDISRTVSATGEISPSNLVS VQAQASGQIKKLYVKLGQOVKKGDILAE

m290.pep
40 50 60 70 80 90
INSTSQTNTLNTEKSKLETYQAKLVSAQIALGSAEKKYKRQAALWKENATSKEDLESAQD
|||||

a290
90 100 110 120 130 140
INSTSQTNTLNTEKSKLETYQAKLVSAQIALGSAEKKYKRQAALWKDDATAKEDLESAQD

m290.pep
100 110 120 130 140 150
AFAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST
|:|||||

a290
150 160 170 180 190 200
ALAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST

m290.pep
160 170 180 190 200 210
PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVD PGLTTMSS
|||||

a290
210 220 230 240 250 260
PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVD PGLTTMSS

220 230 240 250 260 270
```

679

```

m290.pep      GGYNSSTDASNAVYYYARSFVNPDPGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a290          GGYNSSTDASNAVYYYARSFVNPDPGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
               270      280      290      300      310      320

               280      290      300      310      320      330
m290.pep      KAFVRVLGADGKAAEREIRTGMRDSMNTVEKSGLKEGDKVVI SEITAAEQQESGERALGG
               :||||||||||||||||||||||||||||||||||||||||||||||||||||||
a290          RAFVRVLGADGKAAEREIRTGMRDSMNTVEKSGLKEGDKVVI SEITAAEQQESGERALGG
               330      340      350      360      370      380

m290.pep      PPRRX
               |||||
a290          PPRRX
               390

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1217>:

```

g292.seq
1   atgaaaacca agttaatcaa aatcttgacc ccctttaccg tcctgccgct
51  gctggcttgc gggcaaacgc ccgtttccaa tgccaacgcc gaatccgccg
101 tcaaagccga atccgccggc aaatccgttg ccgcttcttt gaaagcgcg
151 ttggaaaaaa cctattccgc ccaagatttg aaagtgttga gcgtcagcga
201 aacaccggtc aaaggcattt acgaagtcgt cgtcagcggc aggcagatta
251 tctacaccga tgccgaaggc ggctatatgt tcgtcggcga actcatcaac
301 atcgacacgc gcaaaaacct gaccgaagaa cgcgccgccg atttgaacaa
351 aatcgacttc gcctccctgc ctttggacaa agccatcaaa gaagtacgcg
401 gcaacggcaa gctgaaagtc gccgtcttct ccgaccccca ttgtccgttc
451 tgcaaacgct tggaacatga gtttgaaaaa atgaccgacg tgacggttta
501 cagctttatg atgcccattg ccggcctgca cccagatgcc gcgcgcaagg
551 cgcaaactct atggtgtcag cccgaccgtg ccaaagcgtg gacggattgg
601 atgcgtaaag gcaaattccc ggtcggcggc agcatctgcg acaatcccgt
651 cgcggaacc acttccttgg gcgaacagtt cggcttcaac ggcacgccga
701 cccttcgtct tcccaacggc gcgcacccaa agcggttaca gcccgatgcc
751 ccaactggag gaaatcatcc gcaaaaacca gcagtaaacc cgcaatga

```

This corresponds to the amino acid sequence <SEQ ID 1218; ORF 292.ng>:

```

g292.pep
1   MKTKLIKILT PFTVLPLLAC GQTPVSNANA ESAVKAESAG KSAVASLKAR
51  LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYTDAGG GYMFGVGLIN
101 IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLV AVFSDPDCPF
151 CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201 MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLRLPQR AHPKRLQPPA
251 PTGGNHPQKP AVNPQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1219>:

```

m292.seq
1   ATGAAAACCA AGTTAATCAA AATCTTGACC CCCTTTACCG TCCTCCCGCT
51  GCTGGCTTGC GGGCAAACGC CCGTTTCCAA TGCCAACGCC GAACCCGCCG
101 TCAAAGCCGA GTCCGCCGGC AAATCCGTTG CCGCTCTTTT GAAAGCCCGT
151 TTGGAAAAAA CCTATTCCGC CCAAGATTTG AAAGTGTGTA GCGTCAGCGA
201 AACACCGGTC AAAGGCATTG ACGAAGTCGT CGTCAGCGGC AGGCAGATTA
251 TCTACACCGA TGCCGAAGGC GGCTATATGT TCGTCGGCGA ACTCATCAAC
301 ATCGACACGC GCAAAAACCT GACCGAAGAA CGCGCCGCCG ATTTGAACAA
351 AATCGACTTC GCCTCCCTGC CTTTGGACAA AGCCATCAAA GAAGTGC CGC
401 GCAACGGCAA GCTGAAAGTC GCCGTCTTCT CCGACCCCGA TTGTCCGTTC
451 TGCAAACGCT TGGAACACGA GTTTGAAAAA ATGACCGACG TGACGGTTTA
501 CAGCTTTATG ATGCCCATTG CCGGCCTGCA CCCCAGTGCC GCGCGCAAGG
551 CGCAAATCTT ATGGTGTGAG CCCGACCGCG CCAAAGCGTG GACGGATTGG
601 ATGCGTAAAG GCAAATTCCC GGTCCGCCGC AGCATCTGCG ACAATCCCGT
651 CGCGGAAACC ACTTCCTTGG GCGAACAATT CCGCTTCAAC GGCACGCCGA
701 CCCTCGTCTT CCCCAACGGG CGCAGCCAAA GCGGCTACAG CCCGATGCC

```

680

751 CAACTGGAGG AAATCATCCG CAAAAATCAA TAA

This corresponds to the amino acid sequence <SEQ ID 1220; ORF 292>:

```

m292.pep
  1 MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSVASLTKAR
 51 LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYTDAEG GYMFVGELIN
101 IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLV AVFSDPDCPF
151 CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201 MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG RSQSGYSPMP
251 QLEEIIRKNQ *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m292/g292 98.7% identity in 238 aa overlap

	10	20	30	40	50	60
m292.pep	MKTKLIKILTPFTVLPLLACGQTPVSNANAEPKAVKAESAGKSVASLTKARLEKTYSAQDL					
g292	MKTKLIKILTPFTVLPLLACGQTPVSNANAESAVKAESAGKSVASLTKARLEKTYSAQDL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m292.pep	KVLVSSETPVKGIYEVVVSQRQIIYTDAEGGYMFVGELINIDTRKNLTEERAADLNKIDF					
g292	KVLVSSETPVKGIYEVVVSQRQIIYTDAEGGYMFVGELINIDTRKNLTEERAADLNKIDF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m292.pep	ASLPLDKAIKEVRGNGKLVAVFSDPDCPFCKRLEHEFEKMTDVTVYSFMMPIAGLHPDA					
g292	ASLPLDKAIKEVRGNGKLVAVFSDPDCPFCKRLEHEFEKMTDVTVYSFMMPIAGLHPDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m292.pep	ARKAQILWCQPDRAKAWTDWMRKGFVPVGSICDNPVAETTSLSGEQFGFNGTPTLVFPNG					
g292	ARKAQILWCQPDRAKAWTDWMRKGFVPVGSICDNPVAETTSLSGEQFGFNGTPTLRPQR					
	190	200	210	220	230	240
	250	260				
m292.pep	RSQSGYSPMPQLEEIIRKNQX					
g292	AHPKRLQPDAPTGGNHPQKPAVNPOX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1221>:

```

a292.seq
  1 ATGAAAACCA AGTTAATCAA AATCTTGACC CCCTTTACCG TCCTCCCGCT
 51 GCTGGCTTGC GGGCAAACGC CCGTTTCCAA TGCCAACGCC GAACCCGCCG
101 TCAAAGCCGA GTCCGCCGGC AAATCCGTTG CCGCCTCTTT GAAAGCGCGT
151 TTGGAAAAAA CCTATTCCGC CCAAGATTG AAAGTGTTGA GCGTCAGCGA
201 AACACCGGTC AAAGGCATTT ACGAAGTCGT CGTCAGCGGC AGGCAGATTA
251 TCTACACCGA TGCCGAAGGC GGCTATATGT TCGTCGGCGA ACTCATCAAC
301 ATCGACACGC GCAAAAACCT GACCGAAGAA CGCGCCGCCG ATTTGAACAA
351 AATCGACTTC GCCTCCCTGC CTTTGGACAA AGCCATCAA GAAGTGCGCG
401 GCAACGCAA GCTGAAAGTC GCCGTCTTCT CCGACCCCGA TTGTCCGTT
451 TGCAAACGCT TGGAACACGA GTTTGAAAAA ATGACCGACG TGACGGTTTA
501 CAGCTTTATG ATGCCCATG CCGGCCGCA CCCCAGTGCC GCGCGCAAGG
551 CGCAAATCTT ATGGTGTCAG CCCGACCGCG CCAAAGCGTG GACGGATTGG
601 ATGCGTAAAG GCAAATCCG GGTGCGCGGC AGCATCTGCG ACAATCCCGT
651 CGCGGAAACC ACTTCCTGG GCGAACATT CGGCTTCAAC GGCACGCCGA
701 CCCTCGTCTT CCCCACGGG CGCAGCCAAA GCGGCTACAG CCCGATGCCC
751 CAACTGGAGG AAATCATCCG CAAAAATCAA TAA

```


This corresponds to the amino acid sequence <SEQ ID 1222; ORF 292.a>:

```

a292.pep
  1  MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSPAASLKAR
 51  LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYTDAGG GYMFVGELIN
101  IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLK AVFSDPDCPF
151  CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201  MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG RSQSGYSPMP
251  QLEEIIRKNQ *

m292/a292    100.0% identity in 260 aa overlap

      10      20      30      40      50      60
m292.pep    MKTKLIKILTPFTVLPLLACGQTPVSNANAEPVKAESAGKSPAASLKARLEKTYSAQDL
a292         MKTKLIKILTPFTVLPLLACGQTPVSNANAEPVKAESAGKSPAASLKARLEKTYSAQDL
      10      20      30      40      50      60

      70      80      90     100     110     120
m292.pep    KVLVSSETPVKGIYEVVVSQRQIIYTDAGGGMFVGELINIDTRKNLTEERAADLNKIDF
a292         KVLVSSETPVKGIYEVVVSQRQIIYTDAGGGMFVGELINIDTRKNLTEERAADLNKIDF
      70      80      90     100     110     120

      130     140     150     160     170     180
m292.pep    ASLPLDKAIKEVRGNGKLKAVFSDPDCPFCKRLEHEFEKMTDVTYVSFMMPIAGLHPDA
a292         ASLPLDKAIKEVRGNGKLKAVFSDPDCPFCKRLEHEFEKMTDVTYVSFMMPIAGLHPDA
      130     140     150     160     170     180

      190     200     210     220     230     240
m292.pep    ARKAQILWCQPDRAKAWTDWMRKGKFPVGGSSICDNPVAETTSLSGEQFGFNGTPTLVFPNG
a292         ARKAQILWCQPDRAKAWTDWMRKGKFPVGGSSICDNPVAETTSLSGEQFGFNGTPTLVFPNG
      190     200     210     220     230     240

      250     260
m292.pep    RSQSGYSPMPQLEEIIRKNQX
a292         RSQSGYSPMPQLEEIIRKNQX
      250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1223>:

```

g294.seq (partial)
  1  atgcgtatta cctgtgcgcc gatgtcgctt ttgtcggcgg cagtctggtc
 51  ggttcgggct gtcagaacat catcgaaccg ctttcctgcg gcgttacgac
101  gatattcggc ttttcgacct acaatttttc cgaagcctgc cggcacgcct
151  tggcatcggg tgcggcgggt caagtcgaat cggcggacgc gtggcgtgaa
201  gccgttgaaa aaaccttata tggcgagggg ggcggaatgc agatgcaggc
251  gcgcgtggac ggctttatcg cacaacatcg cggagcgggc gcgagaatcg
301  ccgaggcggt gcgggaagcg gtatgcggac atcgggggcg atagtatac
351  aatccgtatc cgagttttcc ggttgagca tcgtatgagt atttatgccg
401  tcgcgcacat catccacctg tattgcgcca ccgcctttgt cggcggcgtg
451  ttttttgaag tgctggtttt gtccgtccct catacgggac ggggtgcgcg
501  cgaggcgagg cggaagtgg aaaaggcaat gtcttaccgc gccgtcaggg
551  tgatgccgtt tgcgtcggg ctgctgttcg ccagggggaa tctagagtcg
601  actgcagcag catgccctc...

```

This corresponds to the amino acid sequence <SEQ ID 1224; ORF 294.ng>:

```

g294.pep (partial)
  1  MRITCAPMSL LSAAVWSVRA VRTSSNRFPA ALRRYSAFRP TIFPKPAGTP
 51  WHRVRRFKSN RRTRGVKPLK KPYLARGAEC RCRRRAWTALS HNIAERARES
101  PRRCGKRYAD IGGDSDTIRI RVFRLEHRMS IYAVAHIIHL YCATAFVGGV
151  FFEVLVLSVL HTGRVSREAR REVEKAMSYR AVRVMPPFAVG LLFARGTLES
201  TAAACP....

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1225>:

682

m294.seq
 1 ATGCGTATTA CCTGTGCGCC GATGTCGCTT TTGTCGGCGG CAGTCTGGTC
 51 GATTCGGGTT GTCAGAACAT CATCGAACCG CTTTCCTGCG GCGTTCCGAC
 101 GATATTCGGC TTTTCAACCT ACAATTTTTC CGAAGCCTGC CGACACGCCT
 151 TGGCATCGGG TCGGCGGGT CAAGTCGAAT CGGCGGATGC GTGGCGGGAA
 201 GCCGTTGAAA AAACCTTATC GTCCGAGGGG GGGGGGATGC AGATGCAGGC
 251 GCGCGTGGAC GGCTTTATCG CACAACATCG CGGAGCGGGC GCGAGAATCG
 301 CCGAGGCGGT GCGGGAAGCG GTATGCGGAT ATCGGGGGCG ATAGTGATAC
 351 AATCCGTATC CGAGTTTTC GTTTGGAGCA TCGTATGAGT ATTTATGCCG
 401 TCGCGCACAT CGTTCATCTG TATTGCGCTA TTGCCTTTGT CGGCGGCGTG
 451 TTTTTTGAAG TGCTGGTTTT GTCCGTCCTG CATACGGGAC GGGTGTCGCG
 501 CGAGGCGCGG CGCGAAGTGG AAAAGGCAAT GTCTTACCGC GCCGTCAGGG
 551 TGATGCCGTT TGTGGTCGGA CTGCTGTTCG CCAGCGGCAT CGTGATGGCG
 601 GCAAACCGCT ATCTTTCTAT ATTGGGCGAA CCGTTTGCCA CTTCTTCGG
 651 TACGATGCTG ACGCTGAAAA TCCTGTTGGC GTTCAGCGTA TTGGCGCACT
 701 TCGCCATCGC CGTCGTCAAA ATGGCGCGTT CCACACTGAC GGTGCGTTGG
 751 TCGAAATACA TACACGCCGT CGTCTTACC CATATGcTGC TGATTGTCTT
 801 TTTGGCAAAA GCGATGTTTT ATATCAGCTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1226; ORF 294>:

m294.pep
 1 MRITCAPMSL LSAAVWSIRV VRTSSNRFP AFRRYSAFQP TIFPKPADTP
 51 WHRVRREFSN RMRGGKPLK KPYRPRGGC RCRRRAWTALS HNIAERARES
 101 PRRCGKRYAD IGGDSDTIRI RVERLEHRMS IYAVAHIVHL YCAIAFVGGV
 151 FFEVLVLSVL HTGRVSREAR REVEKAMSYR AVRVMFVVG LFFASGIVMA
 201 ANRYSILGE PFATSFGTML TLKILLAFSV LAHFIAVVK MARSTLTVGW
 251 SKYIHAVVFT HMLLIVFLAK AMFYISW*

g294/m294 92.3% identity in 196 aa overlap

	10	20	30	40	50	60
g294.pep	MRITCAPMSLLSAAVWSVRAVRTSSNRFPALRRYSAFRPTIFPKPAGTPWHRVRREFSN					
m294	: : : : :					
	10	20	30	40	50	60
	70	80	90	100	110	120
g294.pep	RRTRGVKPLKKPYLARGAECRCRRRAWTALSHNIAERARESPRRCGKRYADIGGDSDTIRI					
m294	:					
	70	80	90	100	110	120
	130	140	150	160	170	180
g294.pep	RVERLEHRMSIYAVAHIIHLYCATAFVGGVFFEVLVLSVLHTGRVSREARREVEKAMSYR					
m294	: : : : : : : : : :					
	130	140	150	160	170	180
	190	200				
g294.pep	AVRVMFVAVGLLFARGTLESTAAACP					
m294	:					
	190	200	210	220	230	240
	AVRVMFVVGGLLFASGIVMAANRYSILGEPFATSFGTMLTLKILLAFSVLAHFIAVVK					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1227>:

a294.seq
 1 ATGCGTATTA CCTGTGCGCC GATGTCGCTT TTGTCGGCGG CAGTCTGGTC
 51 GATTCGGGCT GTCAGAACAT CATCGAACCG CTTTCCTGCG GCGTTCCGAC
 101 GATATTCGGC TTTTCGACCT ACAATTTTTC CGAAGCCTGC CGGACACGCCT
 151 TGGCATCGGG TCGGCGGGT CAAGTCGAAT CGGCGGACGC GTGGCGGGAA
 201 GCCGTTGAAA AAAACTTATC GTCCGAGGAG GCGGGAATGC AGATGCAGGC
 251 GCGCGCGGAC GGCTTTATCG CACAACATCG CGGAGCGGGC GCGAGAATCG
 301 CCGAGGCGGT ACGGGAAGCG GTATGCGGAC ATCGGGGACG ATAGTGATAC
 351 AATCCGTATC CGAGTTTTC GGTGAGTA CCGTATGAGT ATTTATGCCG
 401 TCGCGCACAT CGTCCACCTG TATTGCGCCA TCGCCTTTGT CGGCGGCGTG
 451 TTTTTTGAAG TGCTGGTTTT GTCCGTCCTG CATACGGGAC GGGTGTCGCG
 501 CGAGGCGCGG CGCGAAGTGG AAAAGGCAAT GTCTTACCGC GCCGTCAGGG
 551 TGATGCCGTT TGTGGTCGGA CTGCTGTTCG CCAGCGGCAT CGTGATGGCG
 601 GCAAACCGCT ATCTTTCTAT ATTGGGCGAA CCGTTTGCCA CTTCTTCGG
 651 TACGATGCTG ACGCTGAAAA TCCTGTTGGC GTTCAGCGTG TTGGCGCACT

683

701 TCGCCATCGC CGTCGTCAAA ATGGCGCGTT CCACACTGAC CGTCGGCTGG
 751 TCGAAATACA TACACACCGT CGTCTTACC CATATGCTGC TGATTGTCTT
 801 TTTGGCAAAA GCGATGTTTT ATATCAGCTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1228; ORF 294.a>:

a294.pep
 1 MRITCAPMSL LSAAVWSIRA VRTSSNRFP AFRYSAPFR TIFPKPAGTP
 51 WHRVRFRKSN RTRGGKPLK KTYRPRRAEC RCRRARTALS HNIAERARES
 101 PRRYGKRYAD IGDDSDTIRI RVFRLEYRMS IYAVAHIVHL YCAIAFVGGV
 151 FFEVLVLSVL HTGRVSCEAR REVEKAMSYR AVRVMFVVG LLFASGIVMA
 201 ANRYLSILGE PFATSFGTML TLKILLAFSV LAHFAIAVVK MARSTLTVGW
 251 SKYIHTVVFT HMLLIVFLAK AMFYISW*

m294/a294 94.9% identity in 277 aa overlap

	10	20	30	40	50	60
m294.pep	MRITCAPMSLLSAAVWSIRVVRTSSNRFPAAFRYSAPFQPTIFPKPADTPWHRVRFRKSN					
a294	MRITCAPMSLLSAAVWSIRAVRTSSNRFPAAFRYSAPFRPTIFPKPAGTPWHRVRFRKSN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m294.pep	RRMRGGKPLKKPYRPRGGGCRRAWTALSHNIAERARESPRRCGKRYADIGGDSDTIRI					
a294	RRTRGGKPLKKTYRPRRAECRCRRARTALSHNIAERARESPRRYGKRYADIGGDSDTIRI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m294.pep	RVFRLEHRMSIYAVAHIVHLYCAIAFVGGVFEVLVLSVLHTGRVSREARREVEKAMSYR					
a294	RVFRLEYRMSIYAVAHIVHLYCAIAFVGGVFEVLVLSVLHTGRVSCEARREVEKAMSYR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m294.pep	AVRVMFVVGLLFASGIVMAANRYLSILGEPFATSFGTMLTLKILLAFSVLAHFAIAVVK					
a294	AVRVMFVVGLLFASGIVMAANRYLSILGEPFATSFGTMLTLKILLAFSVLAHFAIAVVK					
	190	200	210	220	230	240
	250	260	270			
m294.pep	MARSTLTVGWSKYIHAVVFTHMLLIVFLAKAMFYISWX					
a294	MARSTLTVGWSKYIHTVVVFTHMLLIVFLAKAMFYISWX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1229>:

g295.seq
 1 atgctcggga tggcgcggca cgacggccag cagggcatcg ccgcgatatt
 51 gttgccacgc cgccagcagt ttttcgcct cgtcttcgcc ccgataaacg
 101 cgcgtgctgc cgacacggc aaccggccgg cctccgatgc gtttttcaa
 151 ctgccccgcc agcgttttca tgtcttcaga cggcatcagg tcgtatttgg
 201 tattgccgca cacctgcacg gatgccgcgc ccaatttcgc caaccgcgcc
 251 gcatccgcct ccgtctgcgc cagacagccc gtcagcgaag cggtctgcgg
 301 acggatcagg cggcgactt tcagataacc gttcagcgat ttttcgaca
 351 gccgcgcatt cgccaaaaac agcggcacac ccgtctgcgc gcattccttc
 401 atcagattgg gccagatttc ggtttccatc aaaatgccga acatcggcg
 451 gtgttcgcgc aaaaactgcc gtaccacgt tttttgtca tacggaagat
 501 agcggcattg cgcattcagg aacagaactt gcgcgggttc ccgtcccgtc
 551 ggggtcatct gcgtcatcag cagcggcgca tcgggaaaac gccgcgcaa
 601 ctgcgctatc aagggctggg cggcacgcgt ttctccgacc gaaacggcgt
 651 gtatccaaac cgcgccggta acgggattcg gatgcggctt gccgaaacgc
 701 tcgtccctat gcgcccggta tgccggggca cttccggagc gtttgtccaa
 751 ataacgccgt atccatatcg gcgcaagcag ccacaatata tcataaagcc
 801 attggaacat ctttctattt cctgcaaaac aaatgccgtc cgaacggttc
 851 ggacggcatt tcggcaacgg aatcaaatat cgtag

This corresponds to the amino acid sequence <SEQ ID 1230; ORF 295.ng>:

684

g295.pep

```

1  MLGMARHDDQ QGIAAILLPR RQOFFRLVFA PINARAAAHG NRPASDAFFK
51  LPRQRHVLFR RHQVVFGIAA HLHGCRAQFR QPRRIRLRLR QTARQSRGCG
101 TDQAADFQIT VQRFFRQPRI RQKQRHTRSP AFLHQIGPDF GFHQAETHRA
151 VFAQKLPYPR FFVIRKIAAL RIGKQNLRGF PSRRGHLRHQ QRRIGKTPPQ
201 LAYQGLGGTR FSDRNGVYPN RAGNGIRMLR AETLVPMRPV CRGTSGAFVQ
251 ITPYPYRRKQ PQYIIKPLEH LSISCKTNAV RTVRTAFRQR NQIS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1231>:

m295.seq

```

1  ATGCTCGGGA TGGCGCGGCA CGACGACCAG CAGCGCATCG CCGCGATATT
51  GTTGCCACGC CGCCAGCAGT TTTTCCGCTT CGTCTTCACC CCGATAAACG
101 CGCGTGCTGC CGCACACGGC AACCGGCCGG CCTCCGATGC GTTTTCAAAA
151 CTGCCCCGCC AGCGTTTTCA TCTGTTCCGA CGGTATGATG TCGTATTGCG
201 TATTGCCGCA CACCTGCACG GATGCCGCGC CCAATTTTCG CAACCGCGCC
251 GCATCCGCTT CTGTCTGCGC CAGACACCCC GTCAGCGAAG CGGCGGCAGG
301 ACGGATCAGG CGGCGGACTT TCAGATAACC GTTCAACGAT TTTTCCGACA
351 GCCGCGCATT CGCCAAAAAC AGCGGCACAC CCGCGCGCCG GCATTCCCTC
401 ATCAGGTTGG GCCAGATTTC GGTTTCCATC AAAATGCCGA ACATCGGGCG
451 GTGTTCCGCG AAAAAGTGGC GTACCCACGT TTTTGTGTC TACGGAAGAT
501 AGCGGCATTG CGCATCGGGA AACAGAACTT GCGCGGTTTC CCGCCCCGTC
551 GGGGTGATCT GCGTATCAG CAGCGGCGCA TCGGGAAGAC GCCGCGCGCA
601 CTCGCGTATC AAGGACTGGG CGGCACGCGT TTCTCCGACC GAAACGGCGT
651 GTATCCAAAC CGCGCCGGTA ACGGGATTTC GATACGGCTT GCCGAAACGC
701 TCGTCCCGAT GCGCCCGATA TGCCGGGGCA CTTCGGGAGC GTTGTGTCGA
751 ATAACGCCGT ATCCATATCG GCGCAAGCAG CCACAATACA TCATAAAGCC
801 ATTGGAACAT CTTTCTATTT CTGCAAAAC AAATGCCGTC TGAACGGTTC
851 AGACGGCATT TCGGCAACGG AATCAATAT CGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1232; ORF 295>:

m295.pep

```

1  MLGMARHDDQ QRIAAILLPR RQOFFRLVFT PINARAAAHG NRPASDAFFK
51  LPRQRHVLFR RYDVVFGIAA HLHGCRAQFR QPRRIRLCLR QTARQSRGGR
101 TDQAADFQIT VQRFFRQPRI RQKQRHTRAP AFPHQVGPDP GFHQAETHRA
151 VFAQKLPYPR FFVIRKIAAL RIGKQNLRGF PRRRGLRHQ QRRIGKTPPQ
201 LAYQGLGGTR FSDRNGVYPN RAGNGIRIRL AETLVPMRPI CRGTSGAFVQ
251 ITPYPYRRKQ PQYIIKPLEH LSISCKTNAV XTVQTAFRQR NQIS*

```

m295/g295 93.9% identity in 294 aa overlap

	10	20	30	40	50	60
m295.pep	MLGMARHDDQRIAAILLPRRQOFFRLVFTPINARAAAHGNRPASDAFFKLPRQRHVLFR					
g295	MLGMARHDDQRIAAILLPRRQOFFRLVFPINARAAAHGNRPASDAFFKLPRQRHVLFR					
	10	20	30	40	50	60
m295.pep	RYDVVFGIAAHLHGCRAQFRQPRRIRLCLRQTARQSRGGRTDQAADFQITVQRFFRQPRI					
g295	RHQVVFGIAAHLHGCRAQFRQPRRIRLRLRQTARQSRGGRTDQAADFQITVQRFFRQPRI					
	70	80	90	100	110	120
m295.pep	RQKQRHTRAPAFPHQVGPDPGFHQAETHRAVFAQKLPYPRFFVIRKIAALRIGKQNLRGF					
g295	RQKQRHTRSPAFPHQVGPDPGFHQAETHRAVFAQKLPYPRFFVIRKIAALRIGKQNLRGF					
	130	140	150	160	170	180
m295.pep	RQKQRHTRAPAFPHQVGPDPGFHQAETHRAVFAQKLPYPRFFVIRKIAALRIGKQNLRGF					
g295	RQKQRHTRSPAFPHQVGPDPGFHQAETHRAVFAQKLPYPRFFVIRKIAALRIGKQNLRGF					
	190	200	210	220	230	240
m295.pep	PSRRGHLRHQRRIGKTPPQLAYQGLGGTRFSDRNGVYPNRAGNGIRIRLAETLVPMRPI					
g295	PSRRGHLRHQRRIGKTPPQLAYQGLGGTRFSDRNGVYPNRAGNGIRIRLAETLVPMRPI					
	250	260	270	280	290	
m295.pep	CRGTSGAFVQITPYPYRRKQPQYIIKPLEHLSISCKTNAVXTVQTAFRQRNQISX					
g295	CRGTSGAFVQITPYPYRRKQPQYIIKPLEHLSISCKTNAVXTVQTAFRQRNQIS					

685

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1233>:

```
a295.seq
1  ATGCTCGGGA TGGCGCGGCA CGACGACCAG CAGGGCATCG CCGCGATATT
51  GTTGCCACGC CGCCAGCAGT TTTTCCGCCT CGTCTTCACC CCGATAAACG
101 CGCGTGCTGC CGCACACGGC AACCTGCCGG TCTCCGATGC GTTTTTCAAA
151 CTGCCCCGCC AGCGTTTTCA TCTGTTCCGA CGGCATCAGG TCGTATTTGG
201 TATTGCCGCA CACCTGCACG GATGCCGCGC CCAATTTCGC CAACCGCGCC
251 GCATCCGCCT CCGTCTGTGC CAGACAGCCC GTCAGCGAAG CGGCGGCAGG
301 ACGGATCAGG CTGCGGACTT TCAGATAACC GTTTAGCGAT TTTTCCGACA
351 GCCGCGCATT CGCCAAAAAC AGCGGCACAC CCGTGCGCCG GCATTCTTTC
401 ATCAGATTGG GCCAGATTTC GGTTCCTATC AAAATGCCGA ACATCGGGCG
451 GTGTTTCGCG AAAAAGTCCG GTACCCACGT TTTTGTGTC TACGGAAGAT
501 AGCGGCATTG TGCATCAGGA AACAGAACTT GCGCGGTTTC CCGTCCCGTC
551 GGGGTCATCT GCGTCATCAG CAGCGGCGCA TCGGGAAGAA GCTGCCGCAA
601 CTCGCGTATC AAAGGTTGGG CGGCACGCGT TCCCCGACC GAAACGGCGT
651 GTATCCAAAC CGCGCCGGTA ACGGGATTTC GATACGGCTT GCCGAAACGC
701 TCGCCCCGAT GCGCCCGATA TGCAGGGGCA CTTCCGGAGC GTTTGTCCAA
751 ATAACGCCGT ATCCATATCG GCGCAAGCAG CCACAATACA TCATAAAGCC
801 ATTGGAACAT CTTTCTATTT CCTGCAAAAC AAATGCCGTC CGAACGGTTC
851 GGACGGCATT TCGGCAACGG AATCAAATAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 1234; ORF 295.a>:

```
a295.pep
1  MLGMARHDDQ QGIAAILLPR RQOFFRLVFT PINARAAAHG NLPVSDAFFK
51  LPRQRFHLFR RHQVVFGLIA HLHGCRAQFR QPRRIRLRLC QTARQSRGGR
101 TDQAADFQIT V*FFRQPRI RQKQRHTRAP AFLHQIGPDF GFHQNAEHRA
151 VFAQKLPYPR FVIRKIAAL CIRKQNLRGF PSRRGHLRHQ QRRIGKTLPLQ
201 LAYQRLGGTR FPDNRGVYPN RAGNGIRIRL AETLAPMRPI CRGTSGAFVQ
251 ITPYPYRRKQ PQYIIKPLEH LSISCKTNAV RTVRTAFRQR NQIS*
```

m295/a295 93.2% identity in 294 aa overlap

	10	20	30	40	50	60
m295.pep	MLGMARHDDQ	RIAAILLPR	RQOFFRLVFT	PINARAAAHG	NRNPASDAFFK	LPRQRFHLFR
a295	MLGMARHDDQ	QGIAAILLPR	RQOFFRLVFT	PINARAAAHG	NLPVSDAFFK	LPRQRFHLFR
	10	20	30	40	50	60
m295.pep	RYDVVFGLIA	HLHGCRAQFR	QPRRIRLRLC	QTPRQSRGGR	TDQAADFQIT	VQRFRRQPRI
a295	RHQVVFGLIA	HLHGCRAQFR	QPRRIRLRLC	QTARQSRGGR	TDQAADFQIT	VXRFFRQPRI
	70	80	90	100	110	120
m295.pep	RQKQRHTRAP	AFPHQVGP	DFGFHQNAE	HRAVFAQKLP	YPRFFVIRK	IAALRIGKQNL
a295	RQKQRHTRAP	AFPHQVGP	DFGFHQNAE	HRAVFAQKLP	YPRFFVIRK	IAALRIGKQNL
	130	140	150	160	170	180
m295.pep	PPRRGHLRHQ	QRRIGKTP	PQLAYQGL	GGTRFSDR	NGVYPN	RAGNGIRIRL
a295	PSRRGHLRHQ	QRRIGKTL	PQLAYQGL	GGTRFSDR	NGVYPN	RAGNGIRIRL
	190	200	210	220	230	240
m295.pep	CRGTSGAFVQ	ITPYPYRR	KQPQYIIK	PLEHLSIS	CKTNAVXT	VQTAFRQRNQ
a295	CRGTSGAFVQ	ITPYPYRR	KQPQYIIK	PLEHLSIS	CKTNAVXT	VQTAFRQRNQ
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1235>:

```
g297.seq
1  ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAAATACG CGCTGCGCGC
```

```

51  GCTTGCCGTT TCGATTATTC TGGTgtcgGC GGCATACATT Gcttcgacag
101 aggggaccga ggcggtcaga ccgcAGCGCG TggaacaaAA ACTGCCGCCG
151 CTGTCTtGGg gcggaacagg CGTtcagacg gcaTATTGGG TGCAGGAGGC
201 GGTGCagccg ggggactcgC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
251 CGCGGGacga gattgCCcga ATcacGGAAA aataTggcgG CGAAGCCGAT
301 TTGCGgcatt tGCGTGCCGA CCAGTCGGTT CATGTTTTGG TCGCGGCGCA
351 CGGCAGTGCG CGCGAAGTGC AGTTTTttaC CGACGAAGAC GGCAGCGCA
401 aTctGGTCGC TTTGGAAAAA AAAGGCGGCA TATGGCGCGG GTCGGCTTCT
451 GATGCGGATA TGAAGGTTTT GCCGACACTG CGTTCGGTCG TGGTCAAAAC
501 GTCGGCGCGC GGTTCGCTGG CGCGGGCGGA AGTGCCCGTC GAAATCCGCG
551 AATCCTTAAG CGGGATTTTT GCCGGCCGCT TCAGCCTTGA CGGTTTGAAG
601 GAAGGCGATG CCGTGCGCCT GCTTTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTTTGGCGGC GGAAGTTGTC AAGGGCGGCA
701 CAACCATCA GCGCTTCTAT TACCGTTCGG ACAAGGAAG CGGAGGGGCG
751 GGCAATTATT ACGATGAAGA CGGCAGGTG TGCAGGAAA AAGGCGGCTT
801 CAACATCgaG CCGCTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
851 GTATGCACCC CATCCTGCAC ACATGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTcAGGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGCG GATACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAACGCTG TACGCGCACT TGAGCGCGTT TTCGcAGGCA
1051 CAAGGCAATG TGCGCGGCGG CGAGGTCATC GGTTTTGTG GTTCGACAGG
1101 CGTTTCGACG GGGCCGCACC TGCATTACGA GGCGCGCATC AACGGGCAGC
1151 CCGTCAATCC TGTTTCGGTC GCATTGCCGA CACCCGAATT GACGCAGGCG
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1236; ORF 297.ng>:

g297.pep

```

1  MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTEGTERVR PORVEQKLPP
51  LSWGGNGVQT AYWVQEAQVP GDSLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGDGSA REVQFFTDDE GERNLVALEK KGGIWRRSAS
151 DADMKVLPPL RSVVVKTSAR GSLARAEVPV EIRESLSGIF AGRFSLDGLK
201 EGDVRLLYD SLYFHGQOVA AGDILAAEVV KGGTTHQAFY YRSDKEGGGG
251 GNYDEEDGRV LOEKGGFNIE PLVYTRISSP FGyRMHPILH TWRLHTGIDY
301 AAPQGTpVRA SADGVITFKG RKGGYGNAMV IRHANGVETL YAHLSAFSQA
351 QGNVRGGEVI GFVGSSTGRST GPHLYEARI NGQPVNPVSV ALPTPELTQA
401 DKAFAAQKQ KADALLARLR GIPVTVSQSD *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1237>:

m297.seq

```

1  ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAAATACG CGCTGCGTGC
51  GCTTGCCGTT TCGATTATTT TGGTGTcGGC GGCATACATT GCTTCGACAG
101 AGAGGACGGA GCGCGTCAGA CCGCAGCGCG TGGAAACAAA TCTGCCGCCG
151 CTGTCTTGGG GCGCGAGCGG CGTTCAGACG GCATATTGGG TGCAGGAGGC
201 GGTGCAGCCG GCGACTCGC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
251 CGCGGGACGA GATTGCCCCG ATCACGGAAA AATATGGCGG CGAAGCCGAT
301 TTGCGGCATT TGCGTGCCGA CCAGTCGGTT CATGTTTTGG TCGCGGCGCA
351 CGGCGGCGCG CGCGAAGTGC AGTTTTTTAC CGACGAAGAC GGCAGCGCA
401 ATCTGTTCGC TTTGGAAAAA AAAGGCGGCA TATGGCGCGG GTCGGCTTCT
451 GAGGCGGATA TGAAGGTTTT GCCGACGCTG CGTTCGGTCG TGGTCAAAAC
501 GTCGGCGCGC GGTTCGCTGG CGCGGGCGGA AGTGCCCGTC GAAATCCGCG
551 AATCCTTAAG CGGGATTTTC GCCGGCCGCT TCAGCCTTGA CGGTTTGAAG
601 GAAGGCGATG CCGTGCGCCT GATGTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTTTGGCGGC TGAAGTCGTT AAGGGCGGCA
701 CAAGGCATCA GCGCTTCTAT TACCGTTCGG ACAAGGAAGG CGGAGGGGCG
751 GGCAATTATT ATGATGAAGA CGGCAAGGTG TTGCAGGAAA AAGGCGGCTT
801 CAACATCGAG CCGCTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
851 GTATGCACCC CATCCTGCAC ACATGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTcAGGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGCG GATACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAACGCTG TACGCGCACT TGAGCGCGTT TTCGcAGGCG
1051 GAAGGCAATG TGCGCGGCGG CGAGGTCATC GGTTTTGTG GTTCGACCGG
1101 GCGTTTCGAC GGGCCGCACC TGCATTACGA GGCGCGCATC AACGGGCAGC
1151 CCGTCAATCC TGTTTCGGTC GCATTGCCGA CACCCGAATT GACGCAGGCG
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1238; ORF 297>:

m297.pep

```

1  MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTERTERV PORVEQNLPP
51  LSWGGSGVQT AYWVQEAQVP GDSLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGDGGA REVQFFTDDE GERNLVALEK KGGIWRRSAS
151 EADMKVLPPL RSVVVKTSAR GSLARAEVPV EIRESLSGIF AGRFSLDGLK

```

```

201 EGDVRLMYD SLYFHGQOVA AGDILAAEVV KGGTRHQAFY YRSDKEGGGG
251 GNYDEDEGKV LQEKGGFNIE PLVYTRISSP FGyRMHPILH TWRLHTGIDY
301 AAPQGTPVRA SADGVITFKG RKGyGNAVM IRHANGVETL YAHLSAFSQA
351 EGNVRGGEVI GFVGSTGRST GPHLHYEAR NGQPNPVS ALPTPELTQA
401 DKAFAAQKQ KADALLARLR GIPVTVSQSD *

```

m297/g297 97.9% identity in 430 aa overlap

	10	20	30	40	50	60
m297.pep	MAVFPLSAKHKYALRALAVSIILVSAAYIASTERTERVRPQORVEQNLPPLSWGGSGVQT					
g297	MAVFPLSAKHKYALRALAVSIILVSAAYIASTEGTERVRPQORVEQKLPPLSWGGNGVQT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m297.pep	AYWVQEAQPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGDGGA					
g297	AYWVQEAQPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGDGSA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m297.pep	REVQFFTTDEDGERNLVALEKKGGIWRRSASEADMKVLPTLRSVVVKTSARGSLARAEVPV					
g297	REVQFFTTDEDGERNLVALEKKGGIWRRSASDADMKVLPTLRSVVVKTSARGSLARAEVPV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m297.pep	EIRELSGIFAGRFSLDGLKEGDAVRLMYDSLYFHGQOVAAGDILAAEVVKGGTRHQAFY					
g297	EIRELSGIFAGRFSLDGLKEGDAVRLLYDSLYFHGQOVAAGDILAAEVVKGGTTHQAFY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m297.pep	YRSDKEGGGGGNYDEDEGKVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY					
g297	YRSDKEGGGGGNYDEDEGRVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY					
	250	260	270	280	290	300
	310	320	330	340	350	360
m297.pep	AAPQGTPVRASADGVITFKGRKGGYGNVAMIRHANGVETLYAHLSAFSQAEGNVRGGEVI					
g297	AAPQGTPVRASADGVITFKGRKGGYGNVAMIRHANGVETLYAHLSAFSQAQGNVRGGEVI					
	310	320	330	340	350	360
	370	380	390	400	410	420
m297.pep	GFVGSTGRSTGPHLHYEARINGQPNPVSVALPTPELTQADKAFAAQKQKADALLARLR					
g297	GFVGSTGRSTGPHLHYEARINGQPNPVSVALPTPELTQADKAFAAQKQKADALLARLR					
	370	380	390	400	410	420
	430					
m297.pep	GIPVTVSQSDX					
g297	GIPVTVSQSDX					
	430					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1239>:

```

a297.seq
1   ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAAATACG CGCTGCGCGC
51  GCTTGCCGTT TCGATTATTT TGGTGTCGGC GGCATACATT GCTTCGACAG
101 AGAGGACGGA GCGCGTCAGA CCGCAGCGCG TGGAAACAAA ACTGCCGCCG
151 CTGTCTTGGG GCGGCAGCGG TGTCAGACG GCATATTGGG TGCAGGAGGC
201 GGTGCAGCCA GCGCACTCGC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
251 CGCGGGACGA AATTGCCCGA ATAACGGAAA AATATGGCGG CGAAGCCGAT
301 TTGCGGCATT TGCGTGCCGA CCAGTCGGTT CATGTTTTGG TCGGCGGCGA
351 CGGCGGCGCG CGCGAAGTGC AGTTTTTTAC CGACGAAGAC GGCGAGCGCA
401 ATCTGGTCGC TTTGGAAAAA AAAGGCGGCA TATGGCGGCG GTCGGCTTCT
451 GAGGCGGATA TGAAGGTTTT GCCGACGCTG CGTTCGGTCG TGGTCAAAAC
501 GTCGGCGCGC GGTTCGCTGG CGCGGGCGGA AGTGCCCGTC GAAATTCGCG

```

688

```

551 AATCCTTAAG CGGGATTTTC GCCGGCCGCT TCAGCCTTGA TGGTTTGAAG
601 GAAGGCGATG CCGTGCGCCT GATTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTCTGGCGGC GGAAGTCGTT AAGGGCGGCA
701 CAAGGCATCA GCGTTTCTAT TACCGTTCGG ACAAGGAAGG AGGAGGGGGC
751 GGCAATTATT ACGATGAAGA CGGCAGGGTG TTGCAGGAAA AAGGCGGCTT
801 CAACATCGAG CCACTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
851 GTATGCACCC CATCCTGCAC ACTTGGCGGC TGACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTACGGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGTG GCTACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAAACGCTG TATGCGCACT TGAGCGCGTT TTCTCAGGCA
1051 GAAGGCAATG TGC GCGGCGG CGAGGTCATC GGTTTGTGCG GTTCGACCGG
1101 GCGTTCGACG GGGCCGCACC TGCATTACGA GGCGCGCATC AATGGGCAGC
1151 CCGTCAATCC TGTTTCGGTC GCATTGCCGA CACCCGAATT GACGCAGGCG
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTG GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1240; ORF 297.a>:

```

a297.pep
1  MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTERTERV R PQRVEQKLPP
51  LSWGGSGVQT AYWVQEA VQP GDSLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGD GGA REVQFFTD DED GERNLVALEK KGGIWRRSAS
151 EADMKVLP TL RSVVVKTSAR GSLARAEV PV EIRESLSGIF AGRFSLDGLK
201 EGDVRLIYD SLYFHGQ QVA AGDILAAEVV KGGTRHQAFY YRSDKEGGGG
251 GNYDDE DGRV LQEKGGFNIE PLVYTRISSP FG YRMHPILH TWRLHTGIDY
301 AAPQGT PVR A SADGVITFKG RKG YGNVAVM IRHANGVETL YAHLSAFSQA
351 EGNVRG GEVI GFV GSTGRST GPHLHYEAR I NGQPVNPVSV ALPTPELTQA
401 DKAFAAQKQ KADALLARLR GIPVTVSQSD *

```

m297/a297 99.3% identity in 430 aa overlap

```

              10      20      30      40      50      60
m297.pep      MAVFPLSAKH RKYALRALAVSIILVSAAYIASTERTERV R PQRVEQNL PPLSWGGSGVQT
              |||
a297           MAVFPLSAKH RKYALRALAVSIILVSAAYIASTERTERV R PQRVEQKL PPLSWGGSGVQT
              10      20      30      40      50      60

              70      80      90      100     110     120
m297.pep      AYWVQEA VQP GDSLADVLAR SGMARDEIAR ITEKYGGEAD LRHLRADQSV HVLVGGD GGA
              |||
a297           AYWVQEA VQP GDSLADVLAR SGMARDEIAR ITEKYGGEAD LRHLRADQSV HVLVGGD GGA
              70      80      90      100     110     120

              130     140     150     160     170     180
m297.pep      REVQFFTD DEDGERNLVALEK KGGIWRRSASEADMKVLP TL RSVVVKTSARGSLARAEV PV
              |||
a297           REVQFFTD DEDGERNLVALEK KGGIWRRSASEADMKVLP TL RSVVVKTSARGSLARAEV PV
              130     140     150     160     170     180

              190     200     210     220     230     240
m297.pep      EIRESLSGIFAGRFSLDGLKEGDAVRLMYDSL YFHGQQAAGDILAAEVV KGGTRHQAFY
              |||
a297           EIRESLSGIFAGRFSLDGLKEGDAVRLIYDSL YFHGQQAAGDILAAEVV KGGTRHQAFY
              190     200     210     220     230     240

              250     260     270     280     290     300
m297.pep      YRSDKEGGGGGNYDDE GKV LQEKGGFNIEPLVYTRISSPFG YRMHPILHTWRLHTGIDY
              |||
a297           YRSDKEGGGGGNYDDE GKV LQEKGGFNIEPLVYTRISSPFG YRMHPILHTWRLHTGIDY
              250     260     270     280     290     300

              310     320     330     340     350     360
m297.pep      AAPQGT PVRASADGVITFKGRKG YGNVAVMIRHANGVETLYAHLSAFSQAEGNVRGGEVI
              |||
a297           AAPQGT PVRASADGVITFKGRKG YGNVAVMIRHANGVETLYAHLSAFSQAEGNVRGGEVI
              310     320     330     340     350     360

```


689

	370	380	390	400	410	420
m297.pep	GFVVGSTGRSTGPHLHYEARINGQPVNPVSVALPTPELTQADKAAFAAQKQKADALLARLR					
a297	GFVVGSTGRSTGPHLHYEARINGQPVNPVSVALPTPELTQADKAAFAAQKQKADALLARLR					
	370	380	390	400	410	420
	430					
m297.pep	GIPVTVSQSDX					
a297	GIPVTVSQSDX					
	430					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1241>:

g298.seq

```

1  ATGAAAAACT TTCTTTCCCT TTTCTCCTCC ATACTGATGT CTGCCCTGAT
51  TGCCGTGTGG TTCAGCCAAA ACCCCATCAA CGCCTACTGG CAGCAGACCT
101 ACCACCGCAA CAGCCCGCTC GAACCGCTTG CCGCTACGG ATGGTGGCGG
151 AGCGGAGCGG CGTTGCAAGA AAACGCCTAC GCCCTTTCAG ACGGCATCAA
201 AACCTTCCTG TCCGGCGAAA cgcceccac ggCTCAAGAC GGCGGTTCGG
251 CAGATATGCC GCCTGAAGCC GCCGCATCCG AAGCCGCCCC GCCGGCCGGC
301 GGAACAGAAT GGAAACAAGG CACCGAAGCC GCCGCCGTCC GCAGCGGCGA
351 CAAAGTCTTT TTCGCCGAG ATTCTGCTGAT GCAGGGCGTT GCGCCTTTCG
401 TGCAAAAAAG CCTGAAACAG CAATACGGCA TCGAATCCGC CAACCTCAGC
451 AAACAAAGCA CGGGGCTTTC CTATCCCTCA TTCTTCGACT GGCCGAAAAC
501 GATTGAAGAA ACCTTGAAAA AACATCCCGA AATCAGCGTA CTCGCCGTCT
551 TCCTCGGCCC GAACGACCCG TGGGATTTCC CCGTCGGCAA ACGCTACCTC
601 AAATTCGCTT CCGACGAATG GCGCAAGAA TACCTGAAAC GCGTCGACCG
651 CATCCTTGAA GCCGCACACA CGCACCGBT CCAAGTCGTC TGGCTCGGCA
701 TCCCTACAT GAAAAAGTC AAGCTCGACG GTCAGATGCG CTACCTCGAC
751 AAATGCTTT CGGAACACTT GAAAGGCAAA ATCATCCTGA TTCCACCGC
801 GCAAACTAG AGCGGCGGGA AAGgcccGTA CACCGATTCC GTCAACGTCA
851 ACGGCAAAAC CGTCCGCTAC CGCAGTAAGG ACGGCATACA CTTACCGCC
901 GAAGGACAAA AACTGCTGGC GGAAAAATA ATGGAAAAAA TCGTTTTTGA
951 ACCGAGTACG CAACCATCAA GTACACAGCC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1242; ORF 298.ng>:

g298.pep

```

1  MKNFLSLFAS ILSALIAVW FSQNPINAYW QQTYHRNSPL EPLAAYGWWR
51  SGAALQENAY ALSDGIKTFL SGETPPTAQD GGSADMPPEA AASEAAPAG
101 GTEWKQGTGA AAVRSGDKVF FAGDSLMOGV APFVQKSLKQ QYGIESANLS
151 KSTGLSYPS FFDWPKTIEE TLKKHPEISV LAVFLGPNDP WDFPVGKRYL
201 KFASDEWAQE YLKRVDRILE AAHTRVQVW WLGIPLYMKKV KLDGQMRYL
251 KLLSEHLKGI IILIPTAQLT SGGKGRYTDS VNVNGKPVRY RSKDGIHFTA
301 EGQKLLAEKI MEKIVFEPST QPSSTQP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1243>:

m298.seq

```

1  ATGAAAAACT TTCTTTCCCT TTTCTCCTCC ATACTGATGT CTGCCCTGAT
51  TGCCGTGTGG TTCAGCCAAA ACCCCATCAA CGCCTACTGG CAGCAGACCT
101 ACCACCGCAA CAGCCCGCTC GAACCGCTTG CCGCTACGG ATGGTGGCGG
151 AGCGGTGCGG CGTTGCAAGA AAACGCCTAC GCCCTTTCAG ACGGCATCAA
201 AGCCTTCCTG TCCGGCGAAA CGCCGCCGAC GGCTCAAGAC GGCGGTTCGG
251 CAGATATGCC GTCTGAAGCC GCCGCATCCG AAGCCGTCCC TCAAACCGGT
301 GAAACAGAAT GGAAACAAGA CACCGAAGCC GCCGCCGTCC GCAGCGGCGA
351 CAAAGTCTTT TTTGTCGGCG ACTCGCTGAT GCAGGGCGTT GCCCTTTCG
401 TGCAAAAAAG CCTGAAACAG CAATACGGCA TCGAATCCGT CAACCTCAGC
451 AAACAAAGCA CGGGGCTGTC CTACCCCTCA TTCTTCGACT GGCCGAAAAC
501 GATTGAAGAA ACCCTGCAAA AACATCCCGA AATCAGCGTA CTCGCCGTCT
551 TCCTCGGACC GAACGACCCG TGGGATTTCC CCGTCGGCAA ACTCTATCTC
601 AAATTCGCTT CCGACGAATG GCGCAAGAA TACCTGAAAC GTGTCGACCG
651 CATCCTTGAA GCCGCACACA CGCACCGBT CCAAGTCGTC TGGCTCGGCA
701 TCCCTACAT GAAAAAGCC AAGCTCGACG GACAGATGCG CTACCTAGAC
751 AAATCGCTTT CGGAACATTT GAAAGGCAAA ATCATCCTGA TTCCACAC
801 GCACACCTAG AGCGGCGGGA AAGACCGCTA CACCGACTCC GTCAACGTCA
851 ACGGCAAAAC CGTCCGCTAC CGCAGCAAGG ACGGCATACA CTTACCGCC
901 GAAGGACAAA AACTGCTGGC GGAAAAATA ATGGAAAAAA TCGTTTTTGA
951 ACCAAGTACG CAACCATCAA GTACACAGCC ATGA

```

m298/g298 94.8% identity in 327 aa overlap

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1245>:

a298.seq							
1	ATGAAAAACT	TTCTTTCCCT	TTTCGCCTCC	ATACTGATGT	CTGCCCTGAT		
51	TGCCGTGTGG	TTCAGCCAAA	ACCCCATCAA	CGCCTACTGG	CAGCAGACCT		
101	ACCACCCGAA	CACCCCGCTC	GAACCGCTTG	CGCCTACGG	ATGCTGGCGG		
151	AGCGGTGCGG	CATTGCAAGA	AAACGCCTAC	GCCCTTTCAG	ACGGCATCAA		
201	AGCCTTCCTG	TCCGGCGAAA	CGCCGCCGAC	GGCTCAAGAC	GGCGGTTCTGG		
251	CAGATATGCC	GTCTGAAGCC	GCCGCACCCG	AAACCGCCCC	TCAAACCTGGC		
301	GAACAGAAAT	GACAAACAAA	CACCGAAGCC	GCCGCCGTCC	GAACAGGGGA		
351	CAAAGTCTTT	TTCGCCGGCG	ACTCGCTGAT	GCAGGGCGTT	GCACCCCTTCG		
401	TGCAAAAAAG	CCTGAAACAG	CAATACGGCA	TCGAATCCGT	CAACCTCAGC		
451	AAACAAAGCA	CGGGGCTGTC	CATACCCCTCA	TCTTTCGACT	GGCCGAAAAAC		
501	GATTGAAGAA	ACCCTGAAAA	AACATCCCGA	AATCAGCGTG	CTCGCCGTCT		
551	TCCTCGGTCC	GAACGACCCG	TGGGATTTCC	CCGTTGGCAA	ACGCTACCTC		
601	AAATTCGCTT	CCGACGAATG	GGCGCAAGAA	TACCTGAAAC	GCGTCGACCG		
651	CATCCTTGAA	GCCGCACACA	CGCACCTACG	CCAAGTCGTC	TGGCTCGGCA		
701	TCCCTTACAT	GAAAAAAGCC	AGACTCGACG	GACAGATGCG	CTACCTAGAA		

691

```

751  AAAGTCTTT  CGGAATATTT  GAAAGGCAAA  ATCATCCTGA  TTCCCACCGC
801  GCACACCTTG  AGCGGCGGGA  AAGACCGCTA  CACCGACTCC  GTCAACGTCA
851  ACGGCAAACC  CGTCCGCTAC  CGCAGCAAGG  ACGGCATACA  CTTTACCGCC
901  GAAGGACAAA  AACTGCTGGC  GGCAAAAATA  ATGGAAAAAA  TCGTTTTTGA
951  ACCAAGTACG  CAACCATCAA  GTACACAGCC  ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1246; ORF 298.a>:

```

a298.pep
1   MKNFLSLFAS  ILMSALIAVW  FSQNPINAYW  QQTYHRNSPL  EPLAAYGWWR
51  SGAAALQENAY  ALSDGIKAFI  SGETPPTAQD  GGSADMPSEA  AAPETAPQTG
101 ETEWKQNTTEA  AAVRTGDKVF  FAGDSLMOGV  APFVQKSLKQ  QYGIESVNLS
151 KQSTGLSYPS  FFDWPKTIEE  TLKKHPEISV  LAVFLGPNDP  WDFPVGKRYL
201 KFASDEWAQE  YLKRVDRILE  AAHTHYVQVV  WLGIPYMKKA  KLDGQMRYLD
251 KLLSEYLGK  IILIPHTAHL  SGGKDRYTD  VNVNGKPVRY  RSKDGIHFTA
301 EGQKLLAAKI  MEKIVFEPST  QPSSTQP*

```

m298/a298 96.3% identity in 327 aa overlap

	10	20	30	40	50	60
m298.pep	MKNFLSLFSSILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
a298	MKNFLSLFASILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m298.pep	ALSDGIKAFISGETPPTAQDGGADMPSEAAASEAVPQTGETEWKQDTEAAAVRSGDKVF					
a298	ALSDGIKAFISGETPPTAQDGGADMPSEAAAPETAPQTGETEWKQNTTEAAAVRTGDKVF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m298.pep	FVGDSLMOGVAPFVQKSLKQQYGIESVNLSKQSTGLSYPSFFDWPKTIEETLQKHPEISV					
a298	FAGDSLMOGVAPFVQKSLKQQYGIESVNLSKQSTGLSYPSFFDWPKTIEETLKKHPEISV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m298.pep	LAVFLGPNDPWDFPVGKLYLKFADEWAQEYLYKRVDRILEAAHTHRVQVWLGIPYMKKA					
a298	LAVFLGPNDPWDFPVGKRYLKFADEWAQEYLYKRVDRILEAAHTHYVQVWLGIPYMKKA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m298.pep	KLDGQMRYLDKLLSEHLKGKIIILIPHTHTLSGGKDRYTDVNVNGKPVRYRSKDGIHFTA					
a298	KLDGQMRYLDKLLSEYLGKIIILIPHTHTLSGGKDRYTDVNVNGKPVRYRSKDGIHFTA					
	250	260	270	280	290	300
	310	320				
m298.pep	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
a298	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1247>:

```

g299.seq
1   ATGAACCCCA  AACACTTCAT  CGCATTTTCC  GCCCTGTTCC  CCGCCACGCA
51  GGCAGAAGCC  CTGCCCCGTC  CCTCCGTCAG  CCCCGACACC  GTTACCGTTT
101 CCCCCTCCGC  CCCCTACACC  GATACAAACG  GCGTGTGAC  CGACTACGGC
151 AACGCCCGCG  CCTCGCCTTG  GATGAAAAAA  CTCCGATCCG  TCGCACAAAG
201 CAGCGGCGAG  GCCTTCCGCA  TCCTGCAAAT  CGGCGACTCG  CATACCGCCG
251 GCGACTTCTT  TACCGACGCC  CTGCGCAAAC  GCCTGCAAAA  AACATGGGGC
301 GACGGCGGCA  TAGGCTGGGT  TTACCCCGCC  AACGTCAAAG  GGCAGCGCAT
351 GGCGGCGGTC  CGTCACAGCG  GCAACTGGCA  AAGCTTCACC  AGCAGGAACA
401 ATACCGGAGA  TTTCCCGCTC  GCGGCATCC  TCGCCCAAAC  CGGCAGCGGC
451 GGCGGCATGA  CCCTGACCGC  GTCTGACGGC  AAAACCGGCA  AACAGCGCGT

```

g299.pcp

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1249>:

m299.seq

m299.pgp

1	<u>MNP</u> <u>KHL</u> <u>IAF</u> <u>S</u>	<u>ALFA</u> <u>ATO</u> <u>QAE</u> <u>A</u>	LPVASVSLDT	VTVSPSAPYT	DTNGLLLTDYG
51	NASASPWMKK	LQSVAGQSGE	TFRILQIGDS	HTAGDFFTDS	LRKRLQKTFWG
101	DGGIGWVYP	NVKGQRMAS	RHNGNWQSLT	SRNNTGDFPL	GGGIAHTGSG
151	GSMTLTASDG	IASKQRVSLF	AKPLLAEQTL	TVNGNTVSAN	CGGQVQLDTG
201	AALPLTIHTE	MPWDIGFINI	ENPAGGITVS	AMGINGAQLT	QWSKWRADRM
251	NDLAQPTGADL	VILSYGTNEA	FNNNIIDIAT	EQKVALQVTQ	IRDSLPAAGI
301	LIGAPESLK	NGLVCGGTRP	VRLTEVQQQ	RKRVARQGTQ	FWSWQNAIMG
351	ICSMKNWLNQ	GWAAKDGVHF	SAKGYRRAE	MLADSLEELV	RSAAIRO*

m299/g299 95.5% identity in 397 aa overlap

m299.pep MNPKHLIAFSALFAATQAEALPVASVSLDTVTVSPSPAPYTDNGLLTDYGNASASPWMKK

693

g299	MNPKEHFIASFALFAATQAEALPVASVSPDVTVSPSAPYTDNGLLTDYGNAAASPWMKK
	10 20 30 40 50 60
m299.pep	LQSVAGSGSETFRILQIGDSHTAGDFFTDLSLRKRLQKTWGDGGIGWVYPANVKGQORMAAV
	70 80 90 100 110 120
g299	LRSLVAGSGEAFRILQIGDSHTAGDFFTDALRKRLQKTWGDGGIGWVYPANVKGQORMAAV
	70 80 90 100 110 120
m299.pep	RHNGNWQSLTSRNNTGDFPLGGILAHTGSGGSMTLTASDGIASKQRVSLFAKPLLAEQTL
	130 140 150 160 170 180
g299	RHSGNWQSFSTRNNTGDFPLGGILAQTGSGGSMTLTASDGKTGQRVSLFAKPLLAEQTL
	130 140 150 160 170 180
m299.pep	TVNGNTVSANGGGWQVLDTGAAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT
	190 200 210 220 230 240
g299	TVNGNTVSANGGGWQVLDTGAAALPLAIQTTEMPWDIGFINIENPAGGITVSAMGINGAQLT
	190 200 210 220 230 240
m299.pep	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDSLPAAGI
	250 260 270 280 290 300
g299	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDSLPAAGI
	250 260 270 280 290 300
m299.pep	LIIGAPESLKNLTGVCGRPVRLTEVQQMQRRVARQGQTMFWSWQNAMGGICSMKNWLNQ
	310 320 330 340 350 360
g299	LIIGAPESLKNLTGVCGRPVLLTEVQQMQRRVARQGQTMFWSWQNAMGGICSMKNWLNQ
	310 320 330 340 350 360
m299.pep	GWAAKDGVHFSAGGYRRAAEMLADSLEELVRSAAIRQX
	370 380 390
g299	GWAAKDGVHFSAGGYRRAAEMLADSLEELVRAAAIRQX
	370 380 390

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1251>:

```

a299.seq
1  ATGAACCCCA AACACCTCAT CGCATTTTCC GCCCTATTTCG CCGCCACGCA
51  GGCAGAAGCC CTACCTGTCG CCTCAGTCAG CCTCGACACC GTTACCGTTT
101 CCCCGTCCGC CCCCTACACC GATACAAACG GGCTGCTGAC CGACTACGGC
151 AACGCCTCCG CCTCGCCTTG GATGAAAAAA CTCCAATCCG TCGCACAAAG
201 CAGCGGCGAG ACCTTCCGTA TCCTGCAAAAT CGGCGACTCG CATACCGCCG
251 GCGACTTCTT TACCGACAGC CTGCGCAAAC GCCTACAAAA AACTTGGGGC
301 GACGGCGGCA TAGGCTGGGT TTACCCCGCC AACGTCAAAG GGCAGCGCAT
351 GGCAGCCGTC CGGCACAACG GTAACCTGGA AAGCCTCACC AGCAGGAACA
401 ACACCGGAGA CTTCCTCGCTC GGCAGCATCC TCGCCACAC CCGCAGCGGC
451 GGCAGCATGA CCCTGACCGC ATCGGACGGC ATAGCAAGCA AGCAGCGCGT
501 TTCCCTGTTT GCCAAACCCC TGCTTGCCGA ACAAACCCTG ACCGTCAACG
551 GCAACACCGT CTCCGCCAAC GGCAGCGGCT GGCAGGTACT GGATACGGGC
601 GCGGCACTGC CCCTGACCAT ACACACCGAA ATGCCGTGGG ACATCGGCTT
651 CATCAACATC GAAAATCCCG CCGGCGGCAT TACCGTTTCC GCGATGGGCA
701 TCAACGGCGC ACAATTAACC CAGTGGTCGA AATGGCGTGC CGACCGTATG
751 AACGACCTTG CCCAAACCGG CGCCGATCTA GTCATCCTTG CCTACGGTAC
801 CAACGAAGCC TTCGGCGACA ACATCGACAT TGCCGATACC GAACAGAAAT
851 GGCTGGATAC CGTCCGCCAA ATCCGCGACA GCCTACCTGC CGCCGGCATC
901 CTCATCATCG GCGCGCCCGA ATCCCTGAAA AACACGCTCG GCGTATGCGG
951 CACACGCCCC GTCCGCCTGA CCGAAGTCCA ACAGATGCAG CGGCGCATCG
1001 CCCGTGAGGG GCAGACGATG TTCTGGTCTT GGCAAAACGC GATGGGCGGC
1051 GTTTGCAGCA TGAAAACTG GCTCAACCAC GGATGGGCGG CCAAAGACGG
1101 CGTACACTTT TCCGCCAAAG GCTACCAACG GTCGGCGGAA ATGCTCGCCG
1151 ACAGCCTCGA AGAAGTCGTC CGCTCCGCTG CAATCAGGCA ATAA

```

694

This corresponds to the amino acid sequence <SEQ ID 1252; ORF 299.a>:

```
a299.pep
1  MNPKHIAFS ALFAATQAEA LPVASVSLDT VTVSPSAPYT DTNGLLTDYG
51  NASASPWMKK LQVAQGSGE TFRILQIGDS HTAGDFFTD LKRRLQKTWG
101 DGGIGWVYPA NVKGQRMMAV RHNGNWQSLT SRNNTGDFPL GGILAHTGSG
151 GSMTLTASDG IASKQRVSLF AKPLLAEQTL TVNGNTVSAN GGGWQVLDTG
201 AALPLTIHTE MPWDIGFINI ENPAGGITVS AMGINGAQLT QWSKWRADRM
251 NDLAQTGADL VILAYGTNEA FGDNIDIADT EQKWLDTVRQ IRDSLPAAGI
301 LIIGAPESLK NTLGVCGRTP VRLTEVQQMQ RRIARQGQTM FWSWQNAMGG
351 VCSMKNWLNH GWAAKDGVHF SAKGYQRSAE MLADSLEELV RSAAIRQ*
```

m299/a299 98.0% identity in 397 aa overlap

	10	20	30	40	50	60
m299.pep	MNPKHIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTDNGLLTDYGNASASPWMKK					
a299	MNPKHIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTDNGLLTDYGNASASPWMKK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m299.pep	LQVAQGSGETFTRILQIGDSHTAGDFFDLSLRKRLQKTWGDGGIGWVYPANVKGQRMMAV					
a299	LQVAQGSGETFTRILQIGDSHTAGDFFDLSLRKRLQKTWGDGGIGWVYPANVKGQRMMAV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m299.pep	RHNGNWQSLTSRNNTGDFPLGGILAHTGSGGSMTLTASDGIASKQRVSLFAKPLLAEQTL					
a299	RHNGNWQSLTSRNNTGDFPLGGILAHTGSGGSMTLTASDGIASKQRVSLFAKPLLAEQTL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m299.pep	TVNGNTVSANGGGWQVLDTGAAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT					
a299	TVNGNTVSANGGGWQVLDTGAAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m299.pep	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDSLPAAGI					
a299	QWSKWRADRMNDLAQTGADLVILAYGTNEAFGDNIDIADTEQKWLDTVRQIRDSLPAAGI					
	250	260	270	280	290	300
	310	320	330	340	350	360
m299.pep	LIIGAPESLKNTLGVCGRTPVRLTEVQQMQRRVARQGQTMFWSWQNAMGGICSMKNWLNQ					
a299	LIIGAPESLKNTLGVCGRTPVRLTEVQQMQRRRIARQGQTMFWSWQNAMGGVCSMKNWLNH					
	310	320	330	340	350	360
	370	380	390			
m299.pep	GWAAKDGVHFSAGGYRRAEMLADSLEELVRSAAIRQX					
a299	GWAAKDGVHFSAGGYQRSAEMLADSLEELVRSAAIRQX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1253>:

```
g302.seq
1  ATGCACTCAA TATATTTTTT TAAGGAGAAG CAGATGAGTC AAACCGACGC
51  GCGTCGTAGC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101 TGCCGCACCC GGTACGCTT TTTATTATTT TCATTGTGTT ATTGCTGATT
151 GCCTCTGCCG TCGGTGCGTA TTTCGGACTA TCCGTCCCCG ATCCGCGTCC
201 TGTGGGGCG AAAGGACGTG CCGATGACGG TTTGATTACG GTTGTACGCC
251 TGCTCGATGC CGACGGTTTG ATCAAAATCC TGACGCATAC CGTTAAAAAT
301 TTCACCGGTT TCGCGCCGTT GGAACGGTG TTGGTTCTTT TATTGGGCGT
```

```

351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAATG CGCTTATTGC
401 TCACAAAATC CCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCCA ATACGGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCGGTC ATCTTTCATT CGCTCGGCCG CCATCCGCTT GCCGGTTTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 GGCACAATCG ATCCGCTCTT GGCAGGCATC ACCCAACAGG CGGCGCAAAAT
651 CATCCATCCC GACTACGTCT TAGGCCCTGA AGCCAACTGG TTTTATATGG
701 CAGCCAGTAC GTTTGTGATT GCTTTGATTG GTTATTTTGT TACTGAAAAA
751 ATCGTCGAAC CGCAATTGGG CCCTTATCAA TCAGATTTGT CACAAGAAGA
801 AAAAGACATT CGGCATTCCA ATGAAATCAC GCCTTTGGAA TATAAAGGAT
851 TAATTGGGGC AGGCGTGGTG TTTGTTGCCT TATCCGCCCT ATTGGCTTGG
901 AGCATCGTCC CTGCCGACGG TATTTTTCGT CATCCTGAAA CAGGATTGGT
951 TGCCGGTTCG CCGTTTTTAA AATCGATTGT TGTTTTTATT TTCTTGTGTG
1001 TTGCGCTGCC GGCATTGTAT TATGGCCGGA TAACCCGAAG TTTGCGCGGC
1051 GAACGGGAAG TCGTTAATGC GATGGCCGAA TCGATGAGTA CTTTGGGACT
1101 TTATTTGGTC ATCATCTTTT TTGCCGCACA GTTTGTGCGA TTTTAAATT
1151 GGACGAATAT TGGGCAATAT ATTGCCGTTA AAGGGGCGGT GTTCTTAAAA
1201 GAAGTCGGCT TGGGCGGCAG TGTGTTGTTT ATCGGTTTTA TTTTAATTTG
1251 TGCTTTTATC AATCTGATGA TAGGCTCCGC CTCCGCGCAA TGGGCGGTAA
1301 CTGCGCCGAT TTTCGTCCCT ATGCTGATGT TGGCCGGCTA CGCGCCCCAA
1351 GTCATTCAAG CCGCTTACCG CATCGGTGAT TCCGTTACCA ATATTATTAC
1401 GCCGATGATG AGTTATTTTC GGCTGATTAT GGCGACGGTA ATCAAATACA
1451 AAAAAGATGC GGGCGTAGGC ACGCTGATTT CTATGATGTT GCCGTATTCC
1501 GCTTCTTCT TAATTGCATG GATCGCCTTA TCTGCATTT GGGTATTTGT
1551 TTTGGGTCTG CCCGTCGGTC CCGGCACACC CACATTCTAT CCGGTGCCTT
1601 AA

```

This corresponds to the amino acid sequence <SEQ ID 1254; ORF 302.ng>:

g302.pep

```

1 MHSIYFFKEK QMSQTDARRS GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51 ASAVGAYFGL SVPDPRPVGA KGRADDGLIH VVSLLDADGL IKILTHTVKN
101 FTGFAPLGTV LVSLLGVGIA EKSLGISALM RLLLTSPRK LTFMVVFTG
151 ILSNTASELG YVVLIPLSAV IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 GTIDPLLAGI TQQAQIIHP DYVVGPEANW FFMAASTFVI ALIGYFVTEK
251 IVEPQLGPYQ SDLSQEEKDI RHSNEITPLE YKGLIWAGVV FVALSALLAW
301 SIVPADGILR HPETGLVAGS PFLKSIVVFI FLLFALPGIV YGRITRSLRG
351 EREVVNAMAE SMSTLGLYLV IIFFAAQFVA FFWNTNIGQY IAVKGAFLK
401 EVGLGGSVLF IGFILICAFI NLMIGSASAQ WAVTAPIFVP MLMLAGYAPQ
451 VIQAAYRIGD SVTNIITPMM SYFGLIMATV IKYKKDAGVG TLISMMLPYS
501 AFFLIAWIAL FCIWVFLGL PVGPGTPTFY PVP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1255>:

m302.seq

```

1 ATGCACTCAA TATATTTTTT TAAGGAGAAG CAGATGAGTC AAACCGATAC
51 GCAACGGGAC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101 TGCCGCATCC GGTACGCTT TTTATTATTT TCATTGTGTT ATTGCTGATT
151 GCCTCTGCCG TCGGTGCGTA TTTCGGACTA TCCGTCCCCG ATCCGCGCCC
201 TGTTGGTGCG AAAGGACGTG CCGATGACGG TTTGATTTAC ATTGTCAGCC
251 TGCTCAATGC CGACGGTTTT ATCAAAATCC TGACGCATAC CGTTAAAAAT
301 TTCACCGGTT TCGCGCCGTT GGGAACGGTG TTGGTTTCTT TATTGGGCGT
351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAATG CGCTTATTGC
401 TCACAAAATC GCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCTA ATACCGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCCATC ATCTTTCATT CCCTCGGCCG CCATCCGCTT GCCGGTCTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 AGCACAATCG ATCCGCTCTT GGCATGCATC ACCCATCAGG CGGCGGTCGT
651 AGGCCCTGAA GCCAACTGGT TTTTATGGT AGCCAGTACG TTTGTGATTG
701 CTTTGATTGG TTATTTTGTG ACTGAAAAAA TCGTCGAACC GCAATTGGGC
751 CTTTATCAAT CAGATTTGTC ACAAGAAGAA AAAGACATTC GCATTCCAA
801 TGAAATCACG CCTTTGGAAT ATAAAGGATT AATTTGGGCT GGCGTGGTGT
851 TTGTTGCCTT ATCCGCCCTA TTGGCTTGGA GCATCGTCCC TGCCGACGGT
901 ATTTTGCCTC ATCTGAAAC AGGATTGGTT TCCGGTTCGC CGTTTTTAA
951 ATCGATTGTT GTTTTTATTT TCTTGTGTTT TGCATGyCG GGCmTTGTTT
1001 ATGGMCGGGT AACCCGAAGT TTGCGCGGCG AACAGGAAGT CGTTAATGCG

```

1051	ATGGCCGAAT	CGATGAGTAC	TCTGGsGCTT	TmTTTGswCA	KcATCTTTTT
1101	TGCCGCACAG	TTTGTGCGAT	TTTTTAATTG	GACGAATATT	GGGCAATATA
1151	TTGCCGTAA	AGGGGCGACG	TTCTTAAAG	AAGTCGGCTT	GGGCGGCAGC
1201	GTGTTGTTTA	TCGGTTTTAT	TTTAATTTGT	GCTTTTATCA	ATCTGATGAT
1251	AGGCTCCGCC	TCCGCGCAAT	GGGCGGTAAC	TGCGCCGATT	TTCGTCCCTA
1301	TGCTGATGTT	GGCCGGCTAC	GCGCCCGAAG	TCATTCAAGC	CGCTTACCGC
1351	ATCGGTGATT	CCGTATACCA	TATTATTACG	CCGATGATGA	GTTATTTTCGG
1401	GCTGATTATG	GCACGGTGA	TCAAATACAA	AAAAGATGCG	GGCGTGGGTA
1451	CGCTGATTTT	TATGATGTTG	CCGATTTCCG	CTTTCTTCTT	GATTGCGTGG
1501	ATTGCCTTAT	TCTGCATTTG	GGTATTTGTT	TTGGGCCTGC	CCGTGCGTCC
1551	CGGCGCGCCC	ACATTCTATC	CCGCACCTTA	A	

m302.ppt

1	MHSIYFFKEK	QMSQTDTRD	GRFLRTVEWL	GNMLPHPVTL	FIIFIVLLLI
51	<u>ASAVGAYFGL</u>	SVPDRPVGA	KGRADDGLIY	IVSLLNADGF	IKILTHTVKN
101	<u>FTGFAPLGTU</u>	LVSLLGVGIA	EKSGLISALM	RLLLTSPRK	LTTFMVFTG
151	<u>ILSNTASELG</u>	YVVLIPLSAI	IFHSLGRHPL	AGLAAAFAGV	SGGYSANLFL
201	<u>STIDPELLACI</u>	THQAAVVGPE	ANWFFMVAST	FVIALIGYFV	TEKIVEPQLG
251	PYQSDLSQEE	KDIRHSNEIT	PLEYKGLIWA	GVVFVLSAL	LAWSIVPADG
301	ILRHPETGLV	SGSPFLKSIV	VFIFLLFALX	GXVYGRVTRS	LRGEQEVVNA
351	MAESMSTLXL	XLXXIFFAAQ	FVAFFWNWTNI	GQYIAVKGAT	FLKEVGLGGS
401	<u>VLFIGILICL</u>	AFINLMIGSA	SAQWAVTAPI	FVPMLMLAGY	APEVIAQAYR
451	IGDSVTNIIT	PMSYFGLMI	ATVIKYKDA	GVGTLISMML	PYSAFFLIWA
501	IALFCIWVVFV	LGLPVGPGAP	TFYPAP*		

Homology with a predicted ORF from *N. gonorrhoeae*

m302/g302

	10	20	30	40	50	60
m302.pep	MHSIYFFKEKQMSQTD	TQRDGRFLRTVEWL	GNMLPHPVTLFII	FIVLLLLIASAV	GAYFGL	
g302	MHSIYFFKEKQMSQTD	ARRSGRFLRTVEWL	GNMLPHPVTLFII	FIVLLLLIASAV	GAYFGL	
	10	20	30	40	50	60
m302.pep	70	80	90	100	110	120
m302.pep	SVPDPRPVGAKGRADD	GLIYIVSLLNADGFI	KILTHTVKNFTGF	APLGTVLVSL	LGVGIA	
g302	SVPDPRPVGAKGRADD	GLIHVVSLLDADGLI	KILTHTVKNFTGF	APLGTVLVSL	LGVGIA	
	70	80	90	100	110	120
m302.pep	130	140	150	160	170	180
m302.pep	EKSGLISALMRLLL	TKSPRKLTTFMVFT	GILSNTASELGY	VVLIPLSAII	FHSLGRHPL	
g302	EKSGLISALMRLLL	TKSPRKLTTFMVFT	GILSNTASELGY	VVLIPLSAVI	FHSLGRHPL	
	130	140	150	160	170	180
m302.pep	190	200	210	220	230	
m302.pep	AGLAAAFAGVSGGYS	ANLFLSTIDPLL	ACITHQAA-----	VVGPEANWFF	MVASTFVI	
g302	AGLAAAFAGVSGGYS	ANLFLGTIDPLL	AGITQQAQII	HPDYVVGPEAN	WFFMAASTFVI	
	190	200	210	220	230	240
m302.pep	240	250	260	270	280	290
m302.pep	ALIGYFVTEKIVEP	QLGPYQSDLSQEEK	DIRHSNEITPLEY	KGLIWAGVVF	VALSALLAW	
g302	ALIGYFVTEKIVEP	QLGPYQSDLSQEEK	DIRHSNEITPLEY	KGLIWAGVVF	VALSALLAW	
	250	260	270	280	290	300
	300	310	320	330	340	350

697

m302.pep	SIVPADGILRHPETGLVSGSPFLKSI	VVFIFLLFALXGXVYGRVTRSLRGEQEVVNAMAE
g302	SIVPADGILRHPETGLVAGSPFLKSI	VVFIFLLFALPGIVYGRITRSLRGEREVVNAMAE
	310 320 330 340 350 360	
m302.pep	SMSTLXLXLXIIFFAAQFVAFFNWTNIGQYIAVKGATFLKEVGLGGSVLFIFIGFILICAFI	
g302	SMSTLGLYLVIIFFAAQFVAFFNWTNIGQYIAVKGAVFLKEVGLGGSVLFIFIGFILICAFI	
	360 370 380 390 400 410	
m302.pep	NLMIGSASAQWAVTAPIFVPMLMLAGYAPEVIQAAYRIGDSVTNIIITPMMSYFGLIMATV	
g302	NLMIGSASAQWAVTAPIFVPMLMLAGYAPQVIQAAYRIGDSVTNIIITPMMSYFGLIMATV	
	420 430 440 450 460 470	
m302.pep	IKYKKDAGVGTLSMMLPYSAFFLIAWIALFCIWVFLGLPVGPGAPTFFYPAPX	
g302	IKYKKDAGVGTLSMMLPYSAFFLIAWIALFCIWVFLGLPVGPGTPTFFYPVPX	
	480 490 500 510 520	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1257>:

```

a302.seq
1  ATGCACTCAA TATATTTTTT TAAGGAGAAG CAGATGAGTC AAACCGATAC
51  GCAACGGGAC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101 TGCCGCACCC GGTACGCTT TTTATTATTT TCATTGTGTT ATTGCTGATT
151 GCCTCTGCCG CCGGTGCGTA TTTTCGACTA TCCGTCCCCG ATCCGCGCCC
201 TGTTGGTGCG AAAGGACGTG CCGATGACGG TTTGATTACG GTTGTCAGCC
251 TGCTCGATGC TGACGTTTGT ATCAAAATCC TGACGCATAC CGTTAAAAAT
301 TTCACCGGTT TCGCGCCGTT GGGAACGGTG TTGGTTTCTT TATTGGGCGT
351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAATG CGCTTATTGC
401 TCACAAATC TCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCTA ATACCGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCCATC ATCTTTCATT CCCTCGGCCG CCATCCGCTT GCCGGTCTGG
551 CTGCGGCTTT CGCGGCGGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 GGCACAATCG ATCCGCTCTT GGCAGGCATC ACCCAACAGG CGGCGCAAT
651 CATCCATCCC GACTACGTCG TAGGCCCTGA AGCCAACTGG TTTTATATGG
701 TAGCCAGTAC GTTTGTGATT GCTTTGATTG GTTATTTTGT TACTGAAAAA
751 ATCGTCGAAC CGCAATTGGG CCCTTATCAA TCAGATTGTG CACAAGAAGA
801 AAAAGACATT CGACATTCCA ATGAAATCAC GCCTTTGGAA TATAAAGGAT
851 TAATTTGGGC TGGCGTGGTG TTTGTTGCCT TATCCGCCCT ATTGGCTTGG
901 AGCATCGTCC CTGCCGACGG TATTTTGCCT CATCTGAAA CAGGATTGGT
951 TTCCGGTTCT CCGTTTTTAA AATCAATTGT TGTTTTTATT TTCTTGTGT
1001 TTGCACTGCC GGGCATTGTT TATGGCCGGG TAACCCGAAG TTTGCGCGGC
1051 GAACAGGAAG TCGTTAATGC GATGGCCGAA TCGATGAGTA CTCTGGGGCT
1101 TTATTTGGTC ATCATCTTTT TTGCCGCACA GTTTGTCGCA TTTTAAATT
1151 GGACGAATAT TGGGCAATAT ATTGCCGTTA AAGGGCGGAC GTTCTTAAAA
1201 GAAGTCGGCT TGGGCGGCAG CGTGTGTGTT ATCGGTTTTA TTTTAATTTG
1251 TGCTTTTATC AATCTGATGA TAGGCTCCGC CTCCGCGCAA TGGGCGGTAA
1301 CTGCGCCGAT TTTCTGCCCT ATGCTGATGT TGGCCGGCTA CGCGCCCGAA
1351 GTCATTCAAG CCGTTACCG CATCGGTGAT TCCGTACCA ATATTATTAC
1401 GCCGATGATG AGTTATTTCT GGCTGATTAT GGCGACGGTG ATCAAATACA
1451 AAAAAGATGC GGGCGTGGGT ACGCTGATTT CTATGATGTT GCCGTATTCC
1501 GCTTTCTTCT TGATTGCGTG GATTGCCTTA TTCTGCATT GGGTATTGT
1551 TTTGGGCTG CCCGTCGGTC CCGGCGCGCC CACATTCTAT CCCGCACCTT
1601 AA

```

This corresponds to the amino acid sequence <SEQ ID 1258; ORF 302.a>:

```

a302.pep
1  MHSIYFFKEK QMSQTDQTD GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51  ASAAGAYFGL SVPDPRPVGA KGRADDGLIH VVSLLDADGL IKILHTVKN
101 FTGFAPLGTV LVSLLGVGIA EKSGLISALM RLLLTSPRK LTTFMVFTG

```

698

```

151 ILSNTASELG YVVLIPLSAI IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 GTIDPLLAGI TQAAQIIHP DYVVGPEANW FFMVASTFVI ALIGYFVTEK
251 IVEPQLGPYQ SDLSQEEKDI RHSNEITPLE YKGLIWAGVV FVALSALLAW
301 SIVPADGILR HPETGLVSGS PFLKSIVVFI FLLFALPGIV YGRVTRSLRG
351 EQEVVNAMAE SMSTLGLYLV IIFFAAQFVA FFNWTNIGQY IAVKGATFLK
401 EVGLGGSVLF IGFILICAFI NLMIGSASAQ WAVTAPIFVP MLMLAGYAPE
451 VIQAAYRIGD SVTNIITPMM SYFGLIMATV IKYKKGAGVG TLISMMLPYS
501 AFFLIAWIAL FCIWVFLGL PVGPGAPTFY PAP*

```

m302/a302 96.1% identity in 533 aa overlap

	10	20	30	40	50	60
m302.pep	MHSIYFFKEKQMSQTD	QDRGRFLRTVEWLG	NMLPHPVTLFII	FIVLLLIASAVG	AYFGL	
a302	MHSIYFFKEKQMSQTD	QDRGRFLRTVEWLG	NMLPHPVTLFII	FIVLLLIASAAG	AYFGL	
	70	80	90	100	110	120
m302.pep	SVPDPRPVGAKGRADD	GLIYIVSLLNADG	FIKILHTVKNFT	GFAPLGTVLVS	LLGVGIA	
a302	SVPDPRPVGAKGRADD	GLIHVVSLLDAD	GLIKILHTVKNFT	GFAPLGTVLVS	LLGVGIA	
	130	140	150	160	170	180
m302.pep	EKSGLISALMRLLLT	KSPRKLTFMVVFT	GILSNTASELGY	VVLIPLSAIIF	HSLGRHPL	
a302	EKSGLISALMRLLLT	KSPRKLTFMVVFT	GILSNTASELGY	VVLIPLSAIIF	HSLGRHPL	
	190	200	210	220	230	
m302.pep	AGLAAAFAGVSGGYS	ANLFLSTIDPL	LACITHQAA-----	VVGPEANWFF	FMVASTFVI	
a302	AGLAAAFAGVSGGYS	ANLFLGTIDPL	LAGITQAAQIIHP	DYVVGPEANW	FFMVASTFVI	
	240	250	260	270	280	290
m302.pep	ALIGYFVTEKIVEP	QLGYPQSDLSQ	EEDIRHSNEIT	PLEYKGLIWAG	VVFVALSALL	AW
a302	ALIGYFVTEKIVEP	QLGYPQSDLSQ	EEDIRHSNEIT	PLEYKGLIWAG	VVFVALSALL	AW
	300	310	320	330	340	350
m302.pep	SIVPADGILRHPET	GLVSGSPFLKS	IVVFIFLLFAL	GXVYGRVTR	SLRGEQEV	VNAMAE
a302	SIVPADGILRHPET	GLVSGSPFLKS	IVVFIFLLFAL	PGIVYGRVTR	SLRGEQEV	VNAMAE
	360	370	380	390	400	410
m302.pep	SMSTLXLXLXII	FFAAQFVAFF	FNWTNIGQYIA	VKGATFLKE	VGLGGSVLF	IGFILICAFI
a302	SMSTLGLYLVII	FFAAQFVAFF	FNWTNIGQYIA	VKGATFLKE	VGLGGSVLF	IGFILICAFI
	420	430	440	450	460	470
m302.pep	NLMIGSASAQWAV	TAPIFVPMML	LAGYAPEVIQ	AAYRIGDS	SVTNIITP	MMSYFGLIMATV
a302	NLMIGSASAQWAV	TAPIFVPMML	LAGYAPEVIQ	AAYRIGDS	SVTNIITP	MMSYFGLIMATV
	480	490	500	510	520	
m302.pep	IKYKKGAGVGT	LISMMLPYSA	FFLIAWIALFC	IWVFLGLP	VGPGAPTFY	PAPX
a302	IKYKKGAGVGT	LISMMLPYSA	FFLIAWIALFC	IWVFLGLP	VGPGAPTFY	PAPX
	490	500	510	520	530	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1259>:

699

g305.seq

```

1 ATGGATTTTT TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
51 TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTCCG
101 GCAATCTGAT TGGTTTTCAC AGCAATCACA AGGTTTTTGA AATTGCCATC
151 CAGCTCGGTG CGGTTTGGC GGTAGTGTTT GAATACCGGC AGCGTTTCAG
201 CAATGTGTTG CATGGCGTGG GAAAAGACCG GAAAGCCAAC CGTTTCGTCC
251 TCAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTC
301 GACAAACAAA TCAAAGAGTA TCTGTTTAAAC CCCTTGAGTG TTGCAGTCAT
351 GCTGGTTTTG GCGGTTTTT TATTTTGTG GGTGGAGAAA CGCCAAAGCC
401 GAGCAGAGCC TAAAATTGCC GATGTTGATG CATTGCGTCC GATTGATGCG
451 TTGATGATCG GTGTGCCCCA AGTGTGTGCA CTGGTTCCCG GTACGTCCCG
501 TTCGGGCAGT ACGGTTATGG GCGGGATGCT TTGGGGAAATC GAGCGGAAAA
551 CGGCAACGGA GTTTTCATTT TTCTTGCCCG TTCCGATGAT GGTTGCAGCA
601 ACGGCTTATG ATGTCCTGAA ACATTACCGA TTTTTCACCC TGCATGATGT
651 CGGTTTGATT TTGATAGGCT TTATTGCCGC TTTTGTTCCT GGTTTGGTAG
701 CGGTTAAAGC ACTGCTGAAG TTTGTTTCCA AGAAAACTA TATCCCGTTT
751 GCCTATTACC GCATTGTTTT CGGCATTGTC ATCATAATAT TGTGGTTGTC
801 GGGCTGGATA AGTTGGGAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 1260; ORF 305.ng>:

g305.pep

```

1 MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIGFH SNHKVFEIAI
51 QLGAVLAVVF EYRQRFSNVL HGVGKDRKAN RFVLNLIAIAF IPAAMVGLLF
101 DKQIKEYLFN PLSVAVMLVL GGFILWVEK RQSRAPKIA DVDALRPIDA
151 LMIGVAQVFA LVPGTSRSGS TVMGGMLWGI ERKTATEFSF FLAVPMMVAA
201 TAYDVLKHYR FFTLHDVGLI LIGFIAAFVS GLVAVKALLK FVSKKNYIPF
251 AYYRIVFGIV IILWLSGWI SWE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1261>:

m305.seq (partial)

```

1 AtGGATTTTC TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
51 TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTCCG
101 GCAATCTGAT TGGTTTTCAC AGCAATCACA AGGTTTTTGA AATTGCCATC
151 CAGCTCGGTG CAGTTTGGC GGTAGTGTTT GAATACCGGC AACGTTTCAG
201 CAATGTGTTG CACGGCTTGG GAAAAGACCG GAAAGCCAAC CGCTTCGTCC
251 TTAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTC
301 GGCAWACAAA TCAAAGAGyA TCTGTTTAAAC CCCTTGAGTG TTGCAGTCAT
351 GCTGGTTyTG GrCGGTTTTT yTATTTTGTG GGTGGAGAAA CGCCAAAGCC
401 GAGCAGAGCC TAAAATTGCC GATGTTGATG CATTGCGTCC GATTGATGCC
451 TTGATGATCG GCGTTGCCCA AGTGTGTGCA CTGGTTCCCG GTACGTCCCG
501 TTCGGGCAGT ACGATTATGG GCGGGATGCT TTGGGGCATC GAACGGAAAA
551 CTGCGACAGA ATTCTCGTTT TTCTTGGCTG TGCCGATGAT GGTTGCCGCA
601 ACGGCTTATG ATGTCCTGAA ACATTACCGA TTTTTCACCC TGCATGATGT
651 CGGTTTGATT CTGATAGGCT TTATTGCTGC CTTTGTTCCTA GGCTTGGTAG
701 CGGTAAGAGC GTTGCTGAGG TTTGTTTCGG GTAC...

```

This corresponds to the amino acid sequence <SEQ ID 1262; ORF 305>:

m305.pep (partial)

```

1 MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIGFH SNHKVFEIAI
51 QLGAVLAVVF EYRQRFSNVL HGLGKDRKAN RFVLNLIAIAF IPAAMVGLLF
101 GXQIKEXLFN PLSVAVMLVL XGFXILWVEK RQSRAPKIA DVDALRPIDA
151 LMIGVAQVFA LVPGTSRSGS TIMGGMLWGI ERKTATEFSF FLAVPMMVAA
201 TAYDVLKHYR FFTLHDVGLI LIGFIAAFVS GLVAVKALLR FVSG...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 305 shows 96.7% identity over a 243 aa overlap with a predicted ORF (ORF 305.ng) from *N. gonorrhoeae*:

g305/m305

```

          10      20      30      40      50      60
g305.pep  MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHKVFEIAIQLGAVLAVVF
          |||||
m305      MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHKVFEIAIQLGAVLAVVF
          10      20      30      40      50      60

```

700

	70	80	90	100	110	120
g305.pep	EYRQRFNSVLHGVGKDRKANRFVNLAIAFIPAAVMGLLFDKQIKEYLFNPLSVAVMLVL					
	:					
m305	EYRQRFNSVLHGLGKDRKANRFVNLAIAFIPAAVMGLLFGXQIKEXLFNPLSVAVMLVL					
	70	80	90	100	110	120
	130	140	150	160	170	180
g305.pep	GGFFILWVEKQRSRAEPKIADVDALRPIDALMIGVAQVFALVPGTSRSGSTVMGGMLWGI					
	:					
m305	XGFXILWVEKQRSRAEPKIADVDALRPIDALMIGVAQVFALVPGTSRSGSTIMGGMLWGI					
	130	140	150	160	170	180
	190	200	210	220	230	240
g305.pep	ERKTATEFSFFLAVPMMVAATAYDVLKHRYFFTLHDVGLILIGFIAAFVSGLVAVKALLK					
	:					
m305	ERKTATEFSFFLAVPMMVAATAYDVLKHRYFFTLHDVGLILIGFIAAFVSGLVAVKALLR					
	190	200	210	220	230	240
	250	260	270			
g305.pep	FVSKKNYIPFAYYRIVFGIVIIILWLSGWISWEX					
m305	FVSG					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1263>:

```

a305.seq
1  ATGGATTTTC TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
51  TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTTCG
101 GCAATCTGAT TGATTTTCAC AGCAATCACA AGGTTTTTGA AATTACCATC
151 CAGCTCGGTG CGGTTTTGGC GGTAGTGTTC GAATACCGGC AGCGTTTCAG
201 CAATGTGTTC CATGGCGTGG GAAAAGACCG GAAAGCCAAC CGTTCGTCC
251 TTAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTC
301 GGCAACAAA TCAAAGAGTA TCTGTTTAA CCCTTGAGTG TTGCAGTCAT
351 GCTGGTTTG GCGGTTTTT TTATTTTGTG GGTGGAGAAA CGCCAAAGCC
401 GAGCAGAGCC TAAAATTGTC GATGTTGATG CATTGCGTCC GATTGATGCG
451 TTGATGATCG GCGTTGCCA AGTGTGTTG CACTGGTCCAG GTACGTCCCG
501 TTCGGGCAGT ACGATTATGG GCGGGATGCT TTGGGGAATC GAGCGGAAAA
551 CGGCAACGGA GTTTTCATTT TTCTTGSCCG TTCCGATGAT GGTGACGAG
601 ACGGCTTATG ATGTCCTGAA GCATTACCGG TTTTTCACCC TGCATGATGT
651 CGGTTTGATT TTGATTGGCT TTGTTGCTGC CTTTGTTCCT GGCTTGGTGG
701 CGGTCAAAGC GTTGCTGAGG TTGTTTCCA AGAAAAATTA TATTCCTTTT
751 GCCTATTACC GCATTGTTTT TGGTATTGCC ATCATTATAT TGTGGCTGTC
801 AGGCTGGATA AGTTGGGAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 1264; ORF 305.a>:

```

a305.pep
1  MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIDFH SNHKVFEITI
51  QLGAVLAVVF EYRQRFNSVL HGVGKDRKAN RFVNLAIAG IPAAVMGLLF
101 GKQIKEYLFN PLSVAVMLVL GGFILWVEK QRSRAEPKIV DVDALRPIDA
151 LMIGVAQVFA LVPGTSRSGS TIMGGMLWGI ERKTATEFSF FLAVPMMVAA
201 TAYDVLKHRY FFFTLHDVGLI LIGFVAAFVS GLVAVKALLR FVSKKNYIPF
251 AYYRIVFGIA IILWLSGWI SWE*

```

m305/a305 96.3% identity in 243 aa overlap

	10	20	30	40	50	60
m305.pep	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHNKVFEITAIQLGAVLAVVF					
	:					
a305	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIDFHSNHNKVFEITAIQLGAVLAVVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m305.pep	EYRQRFNSVLHGLGKDRKANRFVNLAIAGIPAAVMGLLFGXQIKEXLFNPLSVAVMLVL					
	:					
a305	EYRQRFNSVLHGVGKDRKANRFVNLAIAGIPAAVMGLLFGKQIKEYLFNPLSVAVMLVL					

701

	70	80	90	100	110	120
m305.pep	130	140	150	160	170	180
	XGFXILWVEKRQSRAPKIDVDALRPIDALMIGVAQVFALVPGTSRSGSTIMGGMLWGI					
a305	130	140	150	160	170	180
	GGFFILWVEKRQSRAPKIDVDALRPIDALMIGVAQVFALVPGTSRSGSTIMGGMLWGI					
m305.pep	190	200	210	220	230	240
	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFIAAFVSGLVAVKALLR					
a305	190	200	210	220	230	240
	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFVAAAFVSGLVAVKALLR					
m305.pep						
	FVSG					
a305						
	FVSKKNYIPFAYYRIVFGIAIIILWLSGWISWEX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1265>:

```

g306.seq
1   ATGTTTATGA  ACAAATTTTC  CCAATCCGGA  AAAGGTCTGT  CCGGTTTCTT
51  CTTCGGTTTG  ATACTGGCAA  CGGTCATTAT  TGCCGGTATT  TTGCTTTATC
101 TGAACCAGGG  CGGTCAAAAT  GCGTTCAAAA  TCCCGGCTCC  GTCGAAGCAG
151 CCTGCAGAAA  CGGAAATCCT  GAAACTGAAA  AACCAGCCTA  AGGAAGACAT
201 CCAACCTGAA  CCGGCCGATC  AAAACGCCTT  GTCCGAACCG  GATGTTGCGA
251 AAGAGGCAGA  GCAGTCGGAT  GCGGAAAAAG  CTGCCGACAA  GCAGCCCCTT
301 GCCGACAAAG  CCGACGAGGT  TGAAGAAAAG  GCGGCGGAGC  CGGAACGGGA
351 AGAGCCGGAC  GGACAGGCAG  TGCGCAAGAA  AGCACTGACT  GAAGAGCGTG
401 AACAAACCGT  CAGGGAAAAA  GCGCAGAAGA  AAGATGCCGA  AACGGTTAAA
451 AAAAAAGCGG  TAAAACCGTC  TAAAGAAACA  GAGAAAAAAG  CTTCAAAAAG
501 AGAGAAAAAG  GCGGCGAAAG  AAAAAGTTGC  ACCCAAACCG  ACCCCGGAAC
551 AAATCCTCAA  CAGCCGCAGT  ATCGAAAAAG  CGCGTAGTGC  CGCTGCCAAA
601 GAAGTGCAGA  AAATGAAAAA  CTTTGGGCAA  GGCGGAAGCC  AACGCATTAT
651 CTGCAAATGG  GCGCGTATGC  CGAACCCCGG  AGCGCGGAAG  GGCAGCGTGC
701 CAAACTGGCA  ATCTTGGGCA  TATCTTCCGA  AGTGGTCGGC  TATCAGGCGG
751 GACATAAAAC  GCTTTACCGC  GTGCAAAGCG  GCAATATGTC  CGCCGATGCG
801 GTGA

```

This corresponds to the amino acid sequence <SEQ ID 1266; ORF 306.ng>:

```

g306.pep
1   MFMNKFQSG  KGLSGFFFGL  ILATVIIAGI  LLYLNQGGQN  AFKIPAPSKQ
51  PAETELKLLK  NQPKEDIQPE  PADQNALSEP  DVAKEAEQSD  AEKAADKQPV
101 ADKADEVEEK  AGEPEREEDP  GQAVRKKALT  EEREQTVREK  AQKKDAETVK
151 KKAVKPSKET  EKKASKEEKK  AAKEKVAPKP  TPEQILNSRS  IEKARSAAAK
201 EVQKMKNFGQ  GGSQRIICKW  ARMPNPGARK  GSVPNWQSWA  YLPKWSAIRR
251 DIKRFTACKA  AICPPMR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1267>:

```

m306.seq (partial)
1   ..GGTTTGTCT  TCGGTTTGAT  ACTGGCGACG  GTCATTATTG  CCGGTATTTT
51  GTTTTATCTG  AACCAGAGCG  GTCAAAATGC  GTCAAAATC  CCGGCTTCGT
101 CGAAGCAGCC  TGCAGAAACG  GAAATCCTGA  AACCGmAawA  CCAGCyTAAG
151 GAAGACATCC  AACCTGAwCC  GGCCGATCAA  AACGCCTTGT  CCGAACCGGA
201 TGCTGCGACA  GAGGCAGAGC  AGTCGGATGC  GGAAAawGCT  GCCGACAAGC
251 AGCCCGTTGC  CGATAAAGCC  GACGAGGTTG  AAGAAAAGGC  GGGCGAGCCG
301 GAACGGGAAG  AGCCGGACGG  ACAGGCAGTG  CGTAAGAAAG  CGCTGACGGA
351 AGAGCGTGAA  CAAACCGTCA  GGGAAAAAGC  GCAGAAGAAA  GATGCCGAAA
401 CGGTTAAAw  ACAAGCGGTA  AAACCGTCTA  AAGAAACAGA  GAAAAAAGCT
451 TCAAAAGAAG  AGAAAAAGGC  GGCGAAGGAA  AAAGTTGCAC  CCAAACCAAC
501 CCCGGAACAA  ATCCTCAACA  GCGGCAGCAT  CGAAAAAGCG  CGCAGTGCCG
551 CCGCCAAAGA  AGTGCAGAAA  ATGAAAACGC  CGACAAGGCG  GAAGCAACGC

```

702

```

601   ATTATCTGCA AATGGGCGCG TATGCCGACC GTCAGAGCGC GGAAGGGCAG
651   CGTGCCAAAC TGGCAATCTT GGGCATATCT TCCAAGGTGG TCGGTTATCA
701   GGCGGGACAT AAAACGCTTT ACCGGGTGCA AAGCGGCAAT ATGTCTGCCG
751   ATGCGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1268; ORF 306>:

```

m306.pep (partial)
  1   ..GLFFGLILAT VVIAGILFYLNQSGQNAFKI PASSKQPAET EILKPXNQXK
 51   EDIQXPADQ NALSEPDAAT EAEQSDAEXA ADKQPVADKA DEVEEKAGEP
101   EREEPDGQAV RKKALTEERE QTVREKAQKK DAETVKXQAV KPSKETEKKA
151   SKEEKKAAKE KVAPKPTPEQ ILNSGSIEKA RSAAAKEVQK MKTPTRRKQR
201   IICKWARMPT VRARKGSVPN WQSWAYLPRW SVIRRDIKRF TGCKAAICLP
251   MR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 306 shows 88.9% identity over a 253 aa overlap with a predicted ORF (ORF 306.ng) from *N. gonorrhoeae*:

```

m306/g306

          10          20          30          40
m306.pep      GLFFGLILATVVIAGILFYLNQSGQNAFKI PASSKQPAETEILKPX
                |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g306           MFMNKFSQSGKLSGFFFLILATVVIAGILLYLNQGGQNAFKIPAPSKQPAETEILKLK
                10          20          30          40          50          60

          50          60          70          80          90          100
m306.pep      NQXKEDIQXPADQNALSEPDAATEAEQSDAEXAADKQPVADKADEVEEKAGEPEREEDP
                |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g306           NQPKEDIQPEPADQNALSEPDAEAEQSDAEKAADKQPVADKADEVEEKAGEPEREEDP
                70          80          90          100          110          120

          110         120         130         140         150         160
m306.pep      GQAVRKKALTEEREQTVREKAQKKDAETVKXQAVKPSKETEKKASKEEKKAAKEKVAPKP
                |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g306           GQAVRKKALTEEREQTVREKAQKKDAETVKKAVKPSKETEKKASKEEKKAAKEKVAPKP
                130         140         150         160         170         180

          170         180         190         200         210         220
m306.pep      TPEQILNSGSIEKARSAAAKEVQKMKTPTRR-KQRIICKWARMPTVRARKGSVPNWQSWA
                |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g306           TPEQILNSRSIEKARSAAAKEVQKMKNFQGGGSRQRIICKWARMPNPGARKGSVPNWQSWA
                190         200         210         220         230         240

          230         240         250
m306.pep      YLPRWSVIRRDIKRFTGCKAAICLPMRX
                |||:|||:|||:|||:|||:|||:|||
g306           YLPKWSAIRRDIKRFTACKAAICPPMRX
                250         260

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1269>:

```

a306.seq
  1   ATGTTTATGA ACAATTTTC CCAATCCGGA AAAGGTCTGT CCGGTTTTTTT
 51   CTTCGGTTTG ATACTGGCGA CGGTCATTAT TGCCGGTATT TTGTTTTATC
101   TGAACCAGAG CGGTCAAAAT GCGTTCAAAA TCCCGGTTCC GTCGAAGCAG
151   CCTGCAGAAA CGGAAATCCT GAAACCGAAA AACCAGCCTA AGGAAGACAT
201   CCAACCTGAA CCGGCCGATC AAAACGCCTT GTCCGAACCG GATGCTGCGA
251   AAGAGGCAGA GCAGTCGGAT GCGGAAAAAG CTGCCGACAA GCAGCCCGTT
301   GCCGACAAAG CCGACGAGGT TGAGGAAAAG GCGGACGAGC CGGAGCGGGA
351   AAAGTCGGAC GGACAGGCAG TGCGCAAGAA AGCACTGACG GAAGAGCGTG
401   AACAAACCGT CGGGGAAAAA GCGCAGAAGA AAGATGCCGA AACGGTTAAA
451   AAACAAGCGG TAAACCATC TAAAGAAACA GAGAAAAAAG CTTCAAAAGA
501   AGAGAAAAAG GCGGAGAAGG AAAAAGTTGC ACCCAAACCG ACCCGGAAC
551   AAATCCTCAA CAGCGGCAGC ATCGAAAAAG CGCGCAGTGC CGCTGCCAAA

```

a306.pep

1	MFMNKFSSQS	KGLSGFFFGL	ILATVIIAGI	LFYLNQSGQN	AFKIPVPSKQ
51	PAETELKPK	NQPKEDIQE	PADQNALSEP	DAAKEAEQSD	AEKAADKQPV
101	ADKADEVEEK	ADEPEREKSD	GQAVRKKALT	EEREQTVGEK	AQKKDAETVK
151	KQAVKPSKET	EKKASKEEKK	AEKEKVAPKP	TPEQILNSGS	IEKARSAAAK
201	EVQKMKTPTR	RKQRIICKWA	RMPTAGARKG	SVPNWQSWAY	LFRWSVIRRD
251	IKRFTGCKAA	ICLPMR*			

		10	20	30	40
m306.pep		GLFFGLILATVIIAGILFYLNQSGQNAFKIPASSKQPAETEILKPY			
		:			
a306		MFMNKFSGGKGLSGFFGLILATVIIAGILFYLNQSGQNAFKIPVPSKQPAETEILKPK			
	10	20	30	40	50
	60	70	80	90	100
m306.pep	NQXKEDIQXPADQNALSEPDAAEAEQSDAEAXADKQPVADKADEVEEKAGEPEREEDP				
a306	NQPKEDIQPEPADQNALSEPDAAEAEQSDAEAKADKQPVADKADEVEEKADEPEREKSD				
	70	80	90	100	110
	120				
	110	120	130	140	150
m306.pep	GQAVRKKALTEEREQTVREKAQKKDAETVKKQAVKPSKETEKKASKEEKKAAKEKVAPKP				
a306	GQAVRKKALTEEREQTVGEKAQKKDAETVKKQAVKPSKETEKKASKEEKKAEKEKVAPKP				
	130	140	150	160	170
	180				
	170	180	190	200	210
m306.pep	TPEQILNSGSIEKARSAAAKEVQMKMTPTRRKQRIICKWARMPTVRARKGSPVNQSWAY				
a306	TPEQILNSGSIEKARSAAAKEVQMKMTPTRRKQRIICKWARMPTAGARKGSPVNQSWAY				
	190	200	210	220	230
	240				
	230	240	250		
m306.pep	LPRWSVIRDDIKRFTGCKAAICLPMRX				
a306	LPRWSVIRDDIKRFTGCKAAICLPMRX				
	250	260			

```
g307.seq
1  atgaaaacct tcttcaaaac ctttcgacc gcgctactcg cgctcatcct
51  cgcagcctgc ggcggtcaaa aagacagcgc gcccgcgacc tctgcgcgcg
101 cccctttcgc cgataacggc gcggcgaaaa aagaatcgtg cttcggcacg
151 accgttggcg acttcggcga tatggtcaaa gaacaaatcc aagccgagct
201 ggagaaaaaa ggctacaccg tcaaattggg cgaatttacc gactatgtgc
251 gcccgaaatc ggcataggcg gagggcgagt tggacatcaa cgtcttccaa
301 cacaaacctt atcttgacga tttcaaaaaa gaacacaacc tggacatcac
351 cgaagccttc caagtgcgca ccgcgccttt gggactgtat ccggggcaac
401 tgaatcgtct ggaagaagtc aaagacggca gcaccgtatc cgcgccaac
451 gaccggtcca acttcgcacg cgcttgggtg atgctgaacg aactgggttg
501 gatcaaactc aaagacggca tcaatccgct gaccgcatcc aaagccgaca
551 tcgcggaaaa cctgaaaaaa atcaaaatcg tcgagcttga agccgcacaa
601 ctgcgcgcga gcgcgcgcga cgtggatttt gcgctcgcta acgggaacta
651 cqccataagc agcggcatga agctgaccga gccctgttc caaqaaccga
```

```

701 gctttgccta tgtcaactgg tctgccgtca aaaccgccga caaagacagc
751 caatggctta aagacgtaac cgaggcctat aactccgacg cgttcaaagc
801 ctacgcgcac aaacgcttcg agggctacaa ataccctgcc gcatggaatg
851 aaggcgcagc caaataa

```

g307.pcp

1	<u>MKTFFKTLST</u>	<u>ASLALILAAC</u>	<u>GGQKDSAPAA</u>	SAAAPSA	DNG	AAKKEIVFGT
51	TVGDFGDMVK	EQIQAELEKK	GYTVKLVEFT	DYVRPNLALA		EGELDINVFQ
101	HKPYLDDFKV	EHNLDTIEAF	QVPTAPLGLY	PGKLKSLEEV		KDGTSTVSAPN
151	DPSNFARALV	MLNELGWIKL	KDGINPLTAS	KADIAENLKN		IKIVELEAAQ
201	LPRSRAVDVF	AVVNGNYAIS	SGMKLTEALF	QEPSFAYVNW		SAVKTADKDS
251	QWLKDVTEAY	NSDAFKAYAH	KRFEGYKYPA	AWNEGAAK*		

m307.seq (partial)

```

1      .CAATGGCTTA AAGACGTAAC CGAGGCCTAT AACTCCGACG CGTTCAAAGC
51     CTACGCGCAC AAACGCTTCG AGGGCTACAA ATCCCTGCC GCATGGAATG
101    AAGGCGCAGC CAAATAA

```

m307.pep (partial)

1 ..QWLKDVTEAY NSDAFKAYAH KRFEGYKSPA AWNEGAAK*

Homology with a predicted ORF from *N. gonorrhoeae*

m307/g307

Position	m307.pep	g307
230	QWLKDVTEAYNSDAFKAYAHKRFEGYKSPA	SGMKLTEALFQEPSFAYVNWSAVKTADKDS
240		SGMKLTEALFQEPSFAYVNWSAVKTADKDS
250		SGMKLTEALFQEPSFAYVNWSAVKTADKDS
260		SGMKLTEALFQEPSFAYVNWSAVKTADKDS
270		SGMKLTEALFQEPSFAYVNWSAVKTADKDS
280		SGMKLTEALFQEPSFAYVNWSAVKTADKDS
39	AWNEGAAXKX	AWNEGAAXKX

a307.seq

1	ATGAAAACCT	TCTTCAAAAC	CCTTTCGCC	GCCGACTCG	CGCTCATCCT
51	CGCCGCGCTGC	GGCGGTCAAA	AAGATAGCGC	GCCCGCCGCA	TCCGCTTCTG
101	CCGCGCGCCGA	CAACGGCGCG	GCGAAAAAG	NAATCGTCTT	CGGCACGCC
151	GTCGGCGACT	TCGGCGATAT	GGTCAAAAG	CAATCCAAC	CCGAGCTGGA
201	GAAAAAAGGC	TACACCGTCA	AACTGGTCGA	GTTTACCGAC	TATGTGCGCC
251	CGAATCTGGC	ATTGGCTGAG	GGCGAGTNGG	ACATCAACGT	CTTCCAACAC
301	AAACCTTATC	TTGACGACTT	CAAAAAAGAA	CACATCTGG	ACATCACCGA
351	AGTCTTCCAA	GTGCCGACCG	CGCCTTTGG	ACTGTACCCG	GGCAAGCTGA
401	AATCGCTGGA	AGAAGTCAAA	GACGGCAGCA	CCGTATCCCG	GGCAACGAC
451	CCGTCCAAC	TCGCCCCGCT	CTTGGTGTATG	CTCGACGAAC	TGGGTTGGAT
501	CAAACTCAAA	GANGGCATCA	ATCCGCTGAC	CGCATCCAA	GCGGACATTG
551	CCGAAAACCT	GAAAAACATC	AAAATCTGCG	AGCTTGAAGC	CGCGCAACTG
601	CCGCGTAGCC	GCGCGGACGT	GGATTTTGN	GTCGTCAACG	GCAANTACGC
651	CATAAGCAGC	GGCATGAAGC	TGACCGAAGC	CCTGTTCCAA	GAACCGAGCT
701	TTGCCTATGT	CAACTGGTCT	GCCGTCAAAA	CCGCCGACAA	AGACAGCCAA
751	TGGCTTAAAG	ACGTAACCGA	GGCCTATAAC	TCCGACGCGT	TCAAAGCCTA
801	GCGGCACAAA	GCCTTCGAGG	GCTACAAATC	CCCTGCCGCA	TGGAATGAAG
851	GCGGACCCAA	ATAA			

a307.pcp

1 MKTFFKTL SA AALALILAAC GGQKDSAPAA SASAAADNGA AKKXIVFGTT

705

```

51  VGDFGDMVKE  QIQPELEKKG  YTVKLVEFTD  YVRPNLALAE  GEXDINVFQH
101 KPYLDDFKKE  HNLDITEVFQ  VPTAPLGLYP  GKLSLEEVK  DGSTVSAPND
151 PSNFARVLVM  LDELGWIKLK  XGINPLTASK  ADIAENLKN  KIVELEAAQL
201 PRSRADVDFX  VVNGXYAISS  GMKLTEALFQ  EPSFAYVNWS  AVKTADKDSQ
251 WLKDVTEAYN  SDAFKAYAHK  RFEGYKSPAA  WNEGAAK*

```

m307/a307 100.0% identity in 38 aa overlap

```

                                10      20      30
m307.pep                      QWLKDVTEAYNSDAFKAYAHKRFEGYKSPA
                                |||||
a307      SGMKLTEALFQEPSFAYVNWSAVKTADKDSQWLKDVTEAYNSDAFKAYAHKRFEGYKSPA
          220      230      240      250      260      270

                                39
m307.pep      AWNEGAAXX
              |||||
a307          AWNEGAAXX
          280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1277>:

```

g308.seq
1  ATGTTAAATC  GGGTATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGTGTTTA  TCGGATTTCT  GTTTTTTCAC  TATAATAGCC  GGTTTGCCGT
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGCG  GGGCGAGCGG  TTTCCAATAC  GCGGTGAAGG  CTTTGGAACT
201 TTTGCGCGCG  CAAGATGTCT  AAACGCACCT  TGTGGTATCG  AAAGGCGCGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGATTATA  CGAAAGACGA  AGTATATGCC
301 TTGGCTGATT  TCGTCCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CGGTACGTTT  AAAACGGACG  GGATGCTGGT  CGCACCTGT  TCGATGCCGA
401 CGCTTGCTC  TGTGCGCAC  GGCTTCGGCG  ACAACCTCTT  GACGCGTGCG
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAAGCGG  GTAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCTTG  CGATGTACCG  CAAGCCGCAG
601 ACGGCGGACG  ACATAGTGGC  GCACAGTATC  GCACACACGC  TGTGCTGTT
651 CGGAATCGAT  ACGCCGATT  TGGCGGAATG  GCAGGGAATG  GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1278; ORF 308.ng>:

```

g308.pep
1  MLNRVYRIL  GVADNLYPCL  SDFCFFTIIA  GLPLQAVLWE  RRMVRLII
51  GISGASGFQY  GVKALELLRA  QDVETHLVVS  KGAEMARASE  TDYTKDEVYA
101 LADFVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVAH  GFGDNLTRA
151 ADVVLKERRR  LVLVRETPL  NLAHLNMR  VTEMGGVVFP  PVPAMYRKPO
201 TADDIVAHSI  AHTLSLFGID  TPDLAEWQGM  AD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1279>:

```

m308.seq (partial)
1  ATGTTAAATC  GGGTATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGCGTTTA  TCGGATTTCT  GTTTTTTCAC  TATAATAGCC  GGTTTGCCGT
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGCG  GGGCGAGCGG  TTTCCAATAC  GCGGTGAAGG  CTTTGGAACT
201 TTTGCGCGCG  CAAGATGTCT  AAACGCACCT  TGTGGTATCG  AAAGGTGCGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGCTTATG  CGAGAGACGA  GGTATATGCC
301 TTGGCGGACT  TCGTGCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CGGTACGTTT  AAAACGGATG  GGATGCTGGT  CGCCCCCTGT  TCGATGCCGA
401 CGCTTGCTC  TGTGCGCAC  GGCTTCGGCG  ACAATCTGcT  GACGCGTGCG
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAAGCGG  GwAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCTTG  CGATGTACCG  CAAACCGCAG
601 ACGGCGGACG  ACATAGTGGC  GCACAGTGTT  GCACACGcT  TGTGCTGTT
651 CGGAATCGAT  ACGCCGATT  CGGCGGAATG  GCAGGGAATG  gcG...

```

This corresponds to the amino acid sequence <SEQ ID 1280; ORF 308>:

```

m308.pep (partial)

```

706

```

1  MLNRVFYRIL  GVADNLYPRL  SDFCFFTIIA  GLPLQAVLWE  RMMVRRLLII
51  GISGASGFQY  GVKALELLRA  QDVETHLVVS  KGAEMARASE  TAYARDEVYA
101 LADVFHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVAH  GFGDNLTRA
151 ADVVLKERRR  LVLVRETPL  NLAHLDNMKR  XTEMGGVVFP  PVPAMYRKPO
201 TADDIVAHSV  AHASLFGID  TPDSAEOQGM  A..

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 308 shows 96.5% identity over a 231 aa overlap with a predicted ORF (ORF 308.ng) from *N. gonorrhoeae*:

m308/g308

	10	20	30	40	50	60
m308.pep	MLNRVFYRILGVADNLYPRLSDFCFFTIIAGLPLQAVLWERRMMVRRLLIIIGISGASGFQY					
g308	MLNRVFYRILGVADNLYPCLSDFCFFFTIIAGLPLQAVLWERRMMVRRLLIIIGISGASGFQY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m308.pep	GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADVFHPIGNIGACIASGTF					
g308	GVKALELLRAQDVETHLVVSKGAEMARASETDYTKDEVYALADVFHPIGNIGACIASGTF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m308.pep	KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR					
g308	KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR					
	130	140	150	160	170	180
	190	200	210	220	230	
m308.pep	XTEMGGVVFPVPAMYRKPOQTADDIVAHSAHALSLFGIDTPDSAEOQGM					
g308	VTEMGGVVFPVPAMYRKPOQTADDIVAHSAHTLSLFGIDTPDLAEWQGMAD					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1281>:

a308.seq

```

1  ATGTTAAATC  GGATATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGTATTTA  TCGGATTTCT  GTTTTTTCAC  TATAATAGCC  GGTTTGCCGT
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGTG  GGGCGAGCGG  TTTCCAATAC  GGCCTGAAGG  CTTTGGANCT
201 TTTACGCGCG  CAAGATATCG  AAACGCACCT  TGTGGTATCG  AAAGGTGCGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGNTTATG  CGAGAGACGA  NGTATATGCC
301 TTGGCGGACT  TNGTGCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CGGTACGTTT  AAAACGGACG  GGATGCTGGT  CGCCCCCTGT  TCGATGCGGA
401 CGCTTGCCCT  GGTCGTGCAC  GGCTTCGGCG  ACAACCTCTT  GACGCGTGCG
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAANCGG  GTAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCCCT  CGATGTACCG  CAAACCGCAG
601 ACGGCGGACG  ACATAGTGGC  GCACAGTGTT  GCACACGCTT  TGTCGCTGTT
651 CGGAATCGAT  ACGCCGGATT  CGGCGGAATG  GCAGGGAATG  GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1282; ORF 308.a>:

a308.pep

```

1  MLNRIFYRIL  GVADNLYPYL  SDFCFFTIIA  GLPLQAVLWE  RMMVRRLLII
51  GISGASGFQY  GVKALXLLRA  QDIETHLVVS  KGAEMARASE  TXYARDXVYA
101 LADXVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVVH  GFGDNLTRA
151 ADVVLKERRR  LVLVRETPL  NLAHLDNMXR  VTEMGGVVFP  PVPAMYRKPO
201 TADDIVAHSV  AHASLFGID  TPDSAEOQGM  AD*

```

707

m308/a308 95.7% identity in 231 aa overlap

	10	20	30	40	50	60
m308.pep	MLNRVFYRILGVADNLYPRLSDFCFFTTIIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
	: : : : : : : : : : :					
a308	MLNRIFYRILGVADNLYPYLSDFCFFTTIIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m308.pep	GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADVFHPIGNIGACIASGTF					
	: : : : : : : : : :					
a308	GVKALXLLRAQDIETHLVVSKGAEMARASETXYARDXVYALADXVHPIGNIGACIASGTF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m308.pep	KTDGMLVAPCSMRTLASVAHGFGDNLLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR					
	: : : : : : : : : :					
a308	KTDGMLVAPCSMRTLASVVHGFGDNLLTRAADVVLKERRRLVLMVRETPLNLAHLDNMXR					
	130	140	150	160	170	180
	190	200	210	220	230	
m308.pep	XTEMGGVVFPVPAMYRKQPQTADDIVAHSAHALSLFGIDTPDSA EWQGM A					
	: : : : : : : : : :					
a308	VTEMGGVVFPVPAMYRKQPQTADDIVAHSAHALSLFGIDTPDSA EWQGM ADX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1283>:

g308-1.seq

```

1  ATGTTAAATC GGGTATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
51  TCCGTGTTTA TCGGATTTCT GTTTTTTCAC TATAATAGCC GGTTTGCCGT
101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTTCCAATAC GGCGTGAAGG CTTTGGAAC
201 TTTGCGCGCG CAAGATGTCG AAACGCACCT TGTGGTATCG AAAGGCGCGG
251 AGATGGCGCG CGCTTCGGAA ACGGATTATA CGAAAGACGA AGTATATGCC
301 TTGGCTGATT TCGTCCATCC GATCGGCAAT ATCGGGGCGT GCATTGCCAG
351 CGGTACGTTT AAAACGGACG GGATGCTGGT CGCACCTGT TCGATGCGGA
401 CGCTTGCCTC TGTCGCGCAC GGCTTCGGCG ACAACCTCTT GACGCGTGCG
451 GCGGATGTGG TTTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGCGCGA
501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
551 TGGGCGGCGT GGTGTTTCCC CCGTTCCTG CGATGTACCG CAAGCCGCG
601 ACGGCGGACG ACATAGTGGC GCACAGTATC GCACACACGC TGTCGCTGTT
651 CGGAATCGAT ACGCCGGATT TGGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1284; ORF 308-1.ng>:

g308-1.pep

```

1  MLNRVFYRIL GVADNLYPCL SDFCFFTTIIA GLPLQAVLWE RRMVRRLLI
51  GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TDYTKDEVYA
101 LADVFHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFGDNLLTRA
151 ADVVLKERRR LVLVRETPL NLAHLDNMKR VTEMGGVVFP PVPAMYRKPO
201 TADDIVAHSI AHTLSLFGID TPDLA EWQGM AD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1285>:

m308-1.seq

```

1  ATGTTAAATC GGGTATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
51  TCCGCGTTTA TCGGATTTCT GTTTTTTCAC TATAATAGCC GGTTTGCCGT
101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTTCCAATAC GGCGTGAAGG CTTTGGAAC
201 TTTGCGCGCG CAAGATGTCG AAACGCACCT TGTGGTATCG AAAGGTGCGG
251 AGATGGCGCG CGCTTCGGAA ACGGCTTATG CGAGAGACGA GGTATATGCC
301 TTGGCGGACT TCGTGATCC GATCGGCAAT ATCGGGGCGT GCATTGCCAG
351 CGGTACGTTT AAAACGGATG GGATGCTGGT CGCCCCCTGT TCGATGCGGA
401 CGCTTGCCTC TGTCGCGCAC GGCTTCGGCG ACAATCTGCT GACGCGTGCG
451 GCGGATGTGG TTTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGCGCGA
501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
551 TGGGCGGCGT GGTGTTTCCC CCGTTCCTG CGATGTACCG CAAACCGCAG
601 ACGGCGGACG ACATAGTGGC GCACAGTGTG GCACACGCTT TGTCGCTGTT
651 CGGAATCGAT ACGCCGGATT CGGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1286; ORF 308-1>:

m308-1.pep

```

1  MLNRVFYRIL GVADNLYPRL SDFCFFTTIIA GLPLQAVLWE RRMVRRLLI

```

708

```

51  GISGASGFQY  GVKALELLRA  QDVETHLVVS  KGAEMARASE  TAYARDEVYA
101 LADVFVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVAH  GFGDNLTRA
151 ADVVLKERRR  LVLMVRETPL  NLAHLDNMKR  VTEMGGVVFP  PVPAMYRKPK
201 TADDIVAHSV  AHALSFLGID  TPDSA EWQGM  AD*

```

m308-1/g308-1 97.0% identity in 232 aa overlap

```

          10      20      30      40      50      60
m308-1.pep MLNRVFYRILGVADNLYPRLSDFCFFTTIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY
          |||||
g308-1      MLNRVFYRILGVADNLYPRLSDFCFFTTIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY
          10      20      30      40      50      60

          70      80      90     100     110     120
m308-1.pep GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADVFVHPIGNIGACIASGTF
          |||||
g308-1      GVKALELLRAQDVETHLVVSKGAEMARASETDYTKDEVYALADVFVHPIGNIGACIASGTF
          70      80      90     100     110     120

          130     140     150     160     170     180
m308-1.pep KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR
          |||||
g308-1      KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR
          130     140     150     160     170     180

          190     200     210     220     230
m308-1.pep VTEMGGVVFPVPAMYRKPKQTADDIVAHSVAHALSFLGIDTPDSA EWQGMADX
          |||||
g308-1      VTEMGGVVFPVPAMYRKPKQTADDIVAHSLAHTLSLFGIDTPDLA EWQGMADX
          190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1287>:

a308-1.seq

```

1  ATGTTAAATC  GGATATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGTATTTA  TCGGATTTCT  GTTTTTTCAC  TATAATAGCC  GGTTTGCCGT
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGTG  GGGCGAGCGG  TTCCAATAC  GGCGTGAAGG  CTTGGANCT
201 TTTACGCGCG  CAAGATATCG  AAACGCACCT  TGTGGTATCG  AAAGGTGCGG
251 AGATGCGCGC  CGCTTCGGAA  ACGGNTTATG  CGAGAGACGA  NGTATATGCC
301 TTGGCGGACT  TNGTGCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CGGTACGTTT  AAAACGGACG  GGATGCTGGT  CGCCCCCTGT  TCGATGCGGA
401 CGCTTGCTC  GGTCTGTCAC  GGCTTCGGCG  ACAACCTCTT  GACGCGTGCG
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAANCGG  GTAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCTCG  CGATGTACCG  CAAACCGCAG
601 ACGGCGGACG  ACATAGTGGC  GCACAGTGTT  GCACACGCTT  TGTCGCTGTT
651 CGGAATCGAT  ACGCCGGATT  CGGCGGAATG  GCAGGGAATG  GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1288; ORF 308-1.a>:

a308-1.pep

```

1  MLNRIFYRIL  GVADNLYPYL  SDFCFFTTIA  GLPLQAVLWE  RRMVRRLLII
51  GISGASGFQY  GVKALXLLRA  QDIETHLVVS  KGAEMARASE  TXYARDXVYA
101 LADXVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVVH  GFGDNLTRA
151 ADVVLKERRR  LVLMVRETPL  NLAHLDNMXR  VTEMGGVVFP  PVPAMYRKPK
201 TADDIVAHSV  AHALSFLGID  TPDSA EWQGM  AD*

```

a308-1/m308-1 96.1% identity in 232 aa overlap

```

          10      20      30      40      50      60
a308-1      MLNRIFYRILGVADNLYPYLSDFCFFTTIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY
          |||||
m308-1      MLNRVFYRILGVADNLYPRLSDFCFFTTIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY
          10      20      30      40      50      60

          70      80      90     100     110     120
a308-1      GVKALXLLRAQDIETHLVVSKGAEMARASETXYARDXVYALADXVHPIGNIGACIASGTF
          |||||
m308-1      GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADVFVHPIGNIGACIASGTF
          70      80      90     100     110     120

          130     140     150     160     170     180
a308-1      KTDGMLVAPCSMRTLASVVHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMXR
          |||||

```

m308-1	KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLHLDNMKR
	130 140 150 160 170 180
a308-1	VTGEMGGVVFPPVPAMYRKQPQTADDIVAHSAHALSLFGIDTPDSA EWQGMADX
	190 200 210 220 230
m308-1	VTGEMGGVVFPPVPAMYRKQPQTADDIVAHSAHALSLFGIDTPDSA EWQGMADX
	190 200 210 220 230

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1289>:

g311.seq

```

1   atgttcagtt tcggctgggc gtttgaccgc ccgcagtatg agttgggttc
51  gctgtcgccct gttgcggcac ttgcgtgccg gcgcgctttg ggggtgtttg
101 gtttggaacac gcaaatcaag tggccaaacg atttggtcgt cggacgcgac
151 aaattgggctg gcattctgat tgaaacagtc agggcgggctg gtaaaacggg
201 tgccgtgggtc ggtatcggca tcaatttcgt gctgcccaag gaagtggaaa
251 acgccgcttc cgtgcagtcg ctgtttcaga cggcatcgcg gcggggcaat
301 gccgatgccg ccgtattgct ggaaacattg cttgcggaac tggcgcggt
351 gttggaacaa tatgcggaag aagggttcgc gccattttta aatgagtatg
401 aaacggccaa ccgcgaccac ggcaaggcgg tattgctgtt gcgcgacggc
451 gaaaccgtgt gcgaaggcac ggttaaaggc gtggacggac gaggcgttct
501 gcacttggaac acggcagaag gcgaacagac ggtcgtcagc ggcgaatca
551 gcctgcggcc cgacaacagg tcggtttccg tgccgaagcg gccggattcg
601 gaacgttttt tgctgttgga aggcgggaac agccggctca agtggcgctg
651 ggtggaaaac ggcacgttcg caaccgtggg cagcgcgcgc taccgcgatt
701 tgtcgccttt gggcgcgag tgggcggaag aggcggatgg aaatgtccgc
751 atcgtcggtt gcgccgtgtg cggagaatcc aaaaaggcac aagtgaagga
801 acagctcgcc cgaaaaatcg agtggctgcc gtcttcgcga caggctttgg
851 gcatacgcaa ccactaccgc caccgccgaag aacacgggtc cgaccgttgg
901 ttcaacgcct tgggcagccg ccgcttcagc cgcaacgcct gcgtcgctgt
951 cagttgcggc acggcggtaa cggttgacgc gctcaccgat gacggcatt
1001 atctcgccgg aaccatcatg cccggcttcc acctgatgaa agaatcgctc
1051 gccgtccgaa ccgccaacct caaccgcccc gccggcaaac gttacccttt
1101 cccgaccaca acgggcaacg ccgtcgcaag cggcatgatg gacgcggttt
1151 gcggctcgat aatgatgatg cacggccggt tgaaagaaaa aaacggcgcg
1201 ggcaagcctg tcgatgtcat cattaccggc ggcggcgcgg cgaaagtcgc
1251 cgaagccctg ccgcctgcat ttttggcgga aaataccgtg cgctggcg
1301 acaacctcgt catccacggg ctgctgaacc tgattgccgc cgaagcggg
1351 gaatcggaac acgcttaa

```

This corresponds to the amino acid sequence <SEQ ID 1290; ORF 311.ng>:

g311.pep

```

1   MFSFGWAFDR PQYELGSLSP VAALACRRAL GCLGLETQIK WPNDLVVGRD
51  KLGGILITV RAGGKTAVV GIGINFLPK EVENAASVQS LFQTASRRGN
101 ADAAVLLET LLAELGAVLEQ YAEFGFAPFL NEYETANRDH GKAVLLLRDG
151 ETVCEGTVKG VDGRGVLHLE TAEGEQTVVS GEISLRPDNR SVSVPKRPDS
201 ERFLLEGGN SRLKAWVEN GTFATVGSAP YRDLSPGAE WAEKADGNVR
251 IVGCAVCGES KKAQVKEQLA RKIEWLPSSA QALGIRNHYR HPPEHGS DRW
301 FNALGSR RFS RNACVVVSCG TAVTVDALTD DGHYLG GTIM PGFHLMKESL
351 AVRTANL NRP AGKRYPFPTT TGNVAVSGMM DAVCGS IMMM HGRLKEKNGA
401 GKPVDVI ITG GGAAKVAEAL PPAFLAENTV RVADNLVIHG LLNLIAAEGG
451 ESEHA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1291>:

m311.seq (partial)

```

1   ATGTTCA GTT TTGGCTGGGT GTTTGACCGG CCGCAGTATG AGTTGGGTTC
51  GCTGTG CCT GTTGCGGCAG TGGCGTGTG GCGCGCCTTG TCGCGTTTAG
101 GTTTGGATGT GCArATTAAG TGGCCCAATG ATTTGGTTGT CGGACGCGAC
151 AAATTGGGCG GCATTCTGAT TGAAACGGTC AGGACGGGCG GCAAAACGGT
201 TGCCGTGGTC GGTATCGGCA TCAATTTTGT CCTGCCCAAn GAAGTAGAAA
251 ATGCCGCTTC CGTGCAATCG CTGTTTCAGA CGGCATCGCG GCGGGGCAAT
301 GCCGATGCCG CCGTGCTGCT nnnnnnnnnn nnnnnnnnnn nnnnGGAAAT
351 CAGCCTGCGG TCCGACnACA GGCCGGTTTC CGTGnCGAAG CGGCGGATT

```

710

```

401 CGGAACGTTT TCTGCTGTTG GACGGCGGCA ACAGCCGGCT CAAGTGGgCG
451 TGGGTGGAAG ACGGCACGTT CGCAACCGTC GGTAGCGCGC CGTACCgCGA
501 TTTGTGCCTT TTGGGCGCGG AGTGGGCGGA AAAGGCGGAT GGAAATGTCC
551 GCATCGTCGG TTGCGCTGTG TCGGAGAAAT TCAAAAAGGC ACAAGTGCAG
601 GAACAGCTCG CCCGAAAAAT CGAGTGGCTG CCGTCTTCCG CACAGGCTTT
651 GTTTGGCATA CGCAACCACT ACCGCCACCC CGAAGAACAC GGTTCGGACC
701 GCTGGTTCAA CGCCTTGGGC AGCCGCCGCT TCAGCCGCAA CGCyTGCCTC
751 GTCGTCAGTT GCGGCACGGC GGTAACGGTT GACGCGCTCA CCGATGACGG
801 ACATTATCTC GGrgGAACCA TCATGCCCGG TTCCACCTG ATGAAAGAAT
851 CGCTCGCCGT CCGAACCGCC AACCTCAACC GGCACGCCGG TAAGCGTTAT
901 CCTTTCCCGA CCACAACGGG CAATGCCGTC GCCAGCGGCA TGATGGATGC
951 GGTTTGCGGC TCGGTTATGA TGATGCACGG GCGTTTGAAA GAAAAAACCG
1001 GGGCGGGCAA GCCTGTCTGAT GTCATCATT CCGGCGGGCG CGCGGCAAAA
1051 GTTGCCGAAG CCCTGCCGCC TGCATTTTGT GCGGAAAATA CCGTGCGCGT
1101 GCGGACAAC CTCGTCATTT ACGGGTTGTT GAACATGATT GCCGCCGAAG
1151 GCAGGGAATA TGAACAT...

```

This corresponds to the amino acid sequence <SEQ ID 1292; ORF 311>:

```

m311.pep (partial)
  1 MFSFGWVFDR PQYELGSLSP VAAVACRRAL SRLGLDVQIK WPNDLVVGRD
 51 KLGGILIETV RTGGKTVAVV GIGINFLVPX EVENAASVQS LFQTASRRGN
101 ADAAVLLXXX XXXXXEISLR SDXRPVSVXK RRDSEFLLL DGGNSRLKWA
151 WVNGTFATV GSAPYRDLSP LGAEWAEEKAD GNVRIVGCAG CGEFKKAQVQ
201 EQLARKIEWL PSSAQALFGI RNHYRHPEEH GSDRWFNALG SRRFSRNACV
251 VVSCGTAVTV DALTDDGHYL GGTIMPGFHL MKESLAVRTA NLNRHAGKRY
301 PFPTTGNNAV ASGMMDAVCG SVMMMHGRLL EKTGAGKPVD VIITGGGAAG
351 VAEALPPAFL AENTVRVADN LVIYGLLNMI AAEGREYEH....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 311 shows 78.5% identity over a 455 aa overlap with a predicted ORF (ORF 311.ng) from *N. gonorrhoeae*:

```

m311/g311

      10      20      30      40      50      60
m311.pep MFSFGWVFDRPQYELGSLSPVAAVACRRALSRLGLDVQIKWPNDLVVGRDKLGGILIETV
          |||||:|||||||||||||||:|||||: |||::|||||||||||||||||||
g311      MFSFGWAFDRPQYELGSLSPVAAALACRRALGCLGLETQIKWPNDLVVGRDKLGGILIETV
          10      20      30      40      50      60

      70      80      90      100     110
m311.pep RTGGKTVAVVGIGINFLVPXEVENAASVQSLFQTASRRGNADA AVLLXXX-----
          |:||||||||||||||| ||||||||||||||||||| :
g311      RAGGKTVAVVGIGINFLVPKEVENAASVQSLFQTASRRGNADA AVLLLETLAELGAVLEQ
          70      80      90      100     110     120

m311.pep -----XXXXXXXX
g311      YAEEGFAPFLNEYETANRDHGKAVLLLLRDGETVCEGTVKGV DGRGV LHLETAEGEQTVVS
          130     140     150     160     170     180

      120     130     140     150     160     170
m311.pep XEISLRSDXRPVSVXKRRDSEFLLL DGGNSRLKWA WVNGTFATVGSAPYRDLSP LGAE
          ||||| | ||| | |||||||:|||||||||||||||||
g311      GEISLRPDNRSVSVKRPDSEFLLLEGGNSRLKWA WVNGTFATVGSAPYRDLSP LGAE
          190     200     210     220     230     240

      180     190     200     210     220     230
m311.pep WAEKADGNVRIVGCAVCGEFKKAQVQEQLARKIEWLPSSAQALFGIRNHYRHPEEHGSDR
          ||||||| |||||:|||||||||||||||
g311      WAEKADGNVRIVGCAVCGESKKAQVKEQLARKIEWLPSSAQAL-GIRNHYRHPEEHGSDR
          250     260     270     280     290

```

711

	240	250	260	270	280	290
m311.pep	WFNALGSRRFSRNACVVVSCGTAVTVDALTDGHYLGGTIMPGFHLMKESLAVRTANLNR					
g311	WFNALGSRRFSRNACVVVSCGTAVTVDALTDGHYLGGTIMPGFHLMKESLAVRTANLNR					
	300	310	320	330	340	350
	300	310	320	330	340	350
m311.pep	HAGKRYFPFPTTTGNAVASGMMDAVCGSVMMHGRLEKKTGAGKPVVDVIIITGGGAAKVAEA					
g311	PAGKRYFPFPTTTGNAVASGMMDAVCGSIMMHGRLEKKNAGKPVVDVIIITGGGAAKVAEA					
	360	370	380	390	400	410
	360	370	380	390	400	410
m311.pep	LPPAFLAENTVRVADNLVIYGLLNLMIAAEGREYEH					
g311	LPPAFLAENTVRVADNLVIHGLLNLMIAAEGGESEHAX					
	420	430	440	450		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1293>:

```

a311.seq
1   ATGTTCAAGTT TTGGCTGGGT GTTTGACCGG CCGCAGTATG AGTTGGGTTC
51  GCTGTCGCCT GTTGCGGCAG TGGCGTGCCG GCGCGCCTTG TCGCGTTTGG
101 GTTTGAAAAC GCAATCAAG TGGCCAAACG ATTTGGTCGT CGGACGCGAC
151 AAATTGGGCG GCATTCTGAT TGAAACGGTC AGGACGGGCG GCAAAACGGT
201 TGCCGTGGTC GGTATCGGCA TCAATTTCGT GCTGCCAAG GAAGTGGAAA
251 ACGCCGCTTC CGTGCATCG CTGTTTCAGA CGGCATCGCG GCGGGGAAAT
301 GCCGATGCCG CCGTGTGCT GGAAACGCTG TTGGCGGAAC TTGATGCGGT
351 GTTGTTGCAA TATGCGCGGG ACGGATTTGC GCCTTTTGTG GCGGAATATC
401 AGGCTGCCAA CCGCGACCAC GGCAAGCGCG TATTGCTGTT GCGCGACGGC
451 GAAACCGTGT TCGAAGGCAC GGTAAAGGC GTGGACGGAC AAGGCGTTCT
501 GCACTTGGAA ACGGCAGAGG GCAAACAGAC GGTCTGCAGC GCGGAAATCA
551 GCCTGCGGTC CGACGACAGG CCGGTTTCG TGCCGAAGCG GCGGGATTTCG
601 GAACGTTTTT TGCTGTTGGA CGGCGGCAAC AGCCGGCTCA AGTGGGCGTG
651 GGTGGAAAAC GGCACGTTTC CAACCGTCGG TAGCGCGCCG TACCGCGATT
701 TGTCGCCTTT GGGCGCGGAG TGGGCGGAAA AGGTGGATGG AAATGTCCGC
751 ATCGTCGGTT GCGCCGTGTG CGGAGAATTC AAAAAAGCAC AAGTGCAGGA
801 ACAGCTCGCC CGAAAAATCG AGTGGCTGCC GTCTTCCGCA CAGGCTTTGG
851 GCATACGCAA CCACTACCGC CACCCGAAG AACACGGTTC CGACCGCTGG
901 TTCAACGCCT TGGGCGGCCG CCGCTTCAGC CGCAACGCCT GCGTCGTCGT
951 CAGTTGCGGC ACGGCGGTAA CGGTTGACGC GCTCACCGAT GACGGACATT
1001 ATCTCGGGG AACCATCATG CCCGTTTCC ACCTGATGAA AGAATCGCTC
1051 GCCGTCCGAA CCGCCAACCT CAACCGGCAC GCCGTAAGC GTTATCCTTT
1101 CCCGACCACA ACGGCAATG CCGTCGCCAG CGGCATGATG GATGCGGTTT
1151 GCGGCTCGGT TATGATGATG CACGGGCGTT TGAAAGAAAA AACCAGGGCG
1201 GGCAAGCCTG TCGATGTCAT CATTACCGGC GGCGGCGCGG CAAAAGTTGC
1251 CGAAGCCCTG CCGCTGCAT TTTTGGCGGA AAATACCGTG CCGTGGCGG
1301 ACAACCTCGT CATTACGGG CTGCTGAACC TGATTGCCGC CGAAGCGGG
1351 GAATCGGAAC ATACTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1294; ORF 311.a>:

```

a311.pep
1   MFSFGWVFDR PQYELGSLSP VAAVACRRAL SRLGLKTQIK WPNDLVVGRD
51  KLGGILIETV RTGGKTVAVV GIGINFVLPK EVENAASVQS LFTASRRGN
101 ADAAVLLET L LAELDAVLLQ YARDGFAPFV AEYQAANRDH GKAVLLLRDG
151 ETVFEGTVKG VDGQGVHLLE TAEGKQTVVS GEISLRSDDR PVSVPKRDS
201 ERFLLDGGN SRLKWAVVEN GTFATVGSAP YRDLSPLGAE WAEKVDGNVR
251 IVGCAVCEGF KKAQVQEQLA RKIEWLPSSA QALGIRNHYR HPEEHGSDRW
301 FNALGSRRFS RNACVVVSCG TAVTVDALTD DGHYLGGTIM PGFHLMKESL
351 AVRTANLNRH AGKRYFPFPTT TGNASGMM DAVCGSVMM HGRLEKKTGA
401 GKPVVDVIIT GGAAKVAEAL PPAFLAENTV RVADNLVIHG LLNLIAAEGG
451 ESEHT*

```

m311/a311 81.3% identity in 455 aa overlap

712

	10	20	30	40	50	60
m311.pep	MFSFGWVFD	RQYELGSL	SPVAACRR	ALSRLGLD	VQIKWPND	LVVGRDKLGGIL
a311	MFSFGWVFD	RQYELGSL	SPVAACRR	ALSRLGLK	TQIKWPND	LVVGRDKLGGIL
	10	20	30	40	50	60
	70	80	90	100	110	
m311.pep	RTGGKTVAV	VGIGINFV	LPXEVENA	ASVQSLFQ	TASRRGNAD	AAVLLXXXXXX
a311	RTGGKTVAV	VGIGINFV	LPXEVENA	ASVQSLFQ	TASRRGNAD	AAVLLTLLAELDAVLLQ
	70	80	90	100	110	120
m311.pep	-----					
a311	YARDGFAPF	VAEYQAAN	RDHGKAVL	LLLRDGET	VFEGTVKG	VDGQGV LHLETAEGKQTVVS
	130	140	150	160	170	180
	120	130	140	150	160	170
m311.pep	-EISLRSDX	RPVSVXKR	RDSERFLL	LDGGNSRL	KWAWVENG	TFATVGSAPYRDLSP
a311	GEISLRSD	RPVSVPKR	RDSERFLL	LDGGNSRL	KWAWVENG	TFATVGSAPYRDLSP
	190	200	210	220	230	240
	180	190	200	210	220	230
m311.pep	WAEKADGN	VRIVGCAV	CGEFKKAQ	VQEQ LARK	IEWLPSSA	QALFGIRNHYP
a311	WAEKVDGN	VRIVGCAV	CGEFKKAQ	VQEQ LARK	IEWLPSSA	QAL-GIRNHYP
	250	260	270	280	290	
	240	250	260	270	280	290
m311.pep	WFNALGSR	RFSRNACV	VVSCGTAV	TVTDALTD	DGHYLG	GGTIMPGFHLMKESLAVRTANLNR
a311	WFNALGSR	RFSRNACV	VVSCGTAV	TVTDALTD	DGHYLG	GGTIMPGFHLMKESLAVRTANLNR
	300	310	320	330	340	350
	300	310	320	330	340	350
m311.pep	HAGKRYPF	PPTTGN	AVASGMM	DAVCGSV	MMHGR	LKEKTGAGKPV
a311	HAGKRYPF	PPTTGN	AVASGMM	DAVCGSV	MMHGR	LKEKTGAGKPV
	360	370	380	390	400	410
	360	370	380	389		
m311.pep	LPPAFLA	ENTVRVAD	NLVIYGL	LLNMIAA	EAGREYEH	
a311	LPPAFLA	ENTVRVAD	NLVIHGL	LLNLIAA	EAGGESEHTX	
	420	430	440	450		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1295>:

g311-1.seq

```

1  ATGACGGTTT TGAAGCCTTC GCATTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTGCCG CAACACGTAT CGCAATTGGC GCGTGAGGCG GACATGAAGC
101 CGCAGCAGCT CAACGGTTT TGGCAGCAGA TGCCGGCGCA TATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CCTTGCGCGT
201 TTTCGATGCC GAAGGTTTGC GCGATCTGGG GGAAAGGTCG GGTTTTCAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GCGCACAAA ACCATATGCG TGACCCACCT
351 GCAAAGTAAG GGCAGGGGGC GGCAGGGGGC GAAAGTGGTC CACCGTTTGG
401 GCGAGTGCCT GATGTTTCA GTTCGGCTGGG CGTTTGACCG GCCGCAGTAT
451 GAGTTGGGTT CGCTGTCGCC TGTGCGGCA CTTGCGTGCC GGC GCGCTTT
501 GGGGTGTTTG GGTTTGAAA CGCAAATCAA GTGGCCAAAC GATTGGTTCG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACAGT CAGGGCGGGC
601 GGTAACACGG TTGCGGTGGT CGGTATCGGC ATCAATTTCC TGCTGCCCAA
651 GGAAAGTGAA AACGCCGCTT CCGTGCAGTC GCTGTTTCAG ACGGCATCGC
701 GGCGGGGCAA TGCCGATGCC GCCGTATTGC TGGAACATT GCTTGCGGAA
751 CTGGGCGCGG TGTGGAACA ATATGCGGAA GAAGGTTTCG CGCCATTTT

```



```

801 AAATGAGTAT GAAACGGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TCGCGACGCG CGAAACCGTG TCGGAAGGCA CGGTTAAAGG CGTGGACGGA
901 CGAGGCGGTC TGCACCTTGA AACGCGAGaa ggCGAACAGa cggctGtcag
951 cggcGaaaTC AGccTGCGGc CCGacaacag gtcggtttcc GTgccgaagc
1001 gGccggatTC GgaacgttTT tTGCTgttgg aagcggggaa cagccggctc
1051 aAGTGGgctt gGGTggAAAA Cggcacgttc gcaaccgtgg gcAGCGCgCC
1101 gtaCCGCGAT TTGTCGCCTT TGGGCGCGGA GTGGGCGGAA AAGGCGGATG
1151 GAAATGTCCG CATCGTCGGT TGCGCCGTGT GCGGAGAATC CAAAAGGCA
1201 CAAGTGAAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGTTG GTTCAACGCC TTGGGCAGCC GCCGCTTCAG CCGCAACGCC
1351 TCGCTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACCAG
1401 TGACGGACAT TATCTCGGCG GAACCATCAT GCCCGGCTTC CACCTGATGA
1451 AAGAATCGCT CGCCGTCCGA ACCGCCAACC TCAACCGCCC CGCCGGCAAA
1501 CGTTACCTTT TCCCGACCAC AACGGGCAAC GCCGTCGCAA CCGGCATGAT
1551 GGACGCGGTT TCGGCTCGA TAATGATGAT GCACGGCCGT TTGAAAGAAA
1601 AAAACGGCGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CGGCGGCGCG
1651 GCGAAAGTCG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATCCACGG GCTGCTGAAC CTGATTGCCG
1751 CCGAAGCGCG GGAATCGGAA CACGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1296; ORF 311-1.ng>:

g311-1.pep

```

1   MTVLKPSHWR VLAELADGLP QHVSQALAREA DMKPQQLNGF WQOMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRDLGERS GFQTALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECLMFS FGWAFDRPQY
151 ELGSLSPVAA LACRRALGCL GLETQIKWPN DLVVGRDKLG GILIETVRAG
201 GKTVAUVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLAE
251 LGAVLEQYAE EGFAPFLNEY ETANRDHGKA VLLLRDGETV CEGTVKGVDG
301 RGVLHLETAE GEQTVVSGEI SLRPDNRVS VPKRPDSERF LLLEGNSRL
351 KWAVVENGTG ATVGSAPYRD LSPGAEWAE KADGNVRIVG CAVCGESKKA
401 QVKEQLARKI EWLPSAQAL GIRNHRYRHE EHGS DRWFNA LGSRRFSRNA
451 CVVVSCGTAV TVDALTDG YLGGTIMPGF HLMKESLAVR TANLNRPAKG
501 RYFPPTTTGN AVASGMDAV CGSIMMHGR LKEKNAGKP VDVITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIHGLLN LIAAEGGESE HA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1297>:

m311-1.seq

```

1   ATGACGGTTT TGAAGCTTTC GCACTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CCGTTTGCCG CAACACGTCT CGCAACTGGC GCGTATGGCG GATATGAAGC
101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGGCGCA CATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CATTGGCGGT
201 TTTCGATGCC GAAGGTTTGC GCGAGCTGGG GGAAAGGTCG GGTTTTCAGA
251 CCGCATTTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GCGGCACAAA ACCATATGCG TGACCCACCT
351 GCAAAGTAAG GGCAGGGGGC GGCAGGGGCG GAAGTGGTCG CACCGTTTGG
401 GCGAGTGTCT GATGTTCACT TTTGGCTGGG TGTTTGACCG GCCGCGATAT
451 GAGTTGGGTT CGCTGTCGCC TGTTGCGGCA GTGGCGTGTC GGCGCGCCTT
501 GTCGCGTTTA GGTTTGGATG TGCAGATTAA GTGGCCCAAT GATTGTGTTG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACGGT CAGGACGGGC
601 GGCAAAACGG TTGCCGTGGT CCGTATCGGC ATCAATTTTG TCCTGCCCAA
651 GGAAGTAGAA AATGCCGCTT CCGTGCAATC GCTGTTTCAG ACGGCATCGC
701 GCGGGGGCAA TGCCGATGCC GCCGTGCTGC TGGAAACGCT GTTGGTGGAA
751 CTGGACGCGG TGTTGTTGCA ATATGCGCGG GACGGATTTC CGCCTTTTGT
801 GCGGGAATAT CAGGCTGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TGCGCGACGG CGAAACCGTG TTCGAAGGCA CGGTTAAAGG CGTGGACGGA
901 CAAGGCGTTT TGCACCTTGA AACGGCAGAG GGCAACAGAG CGGTCGTCAG
951 CCGCGAAATC AGCCTGCGGT CCGACGACAG GCCGGTTTCC GTGCCGAAGC
1001 GGCGGGATTG GGAACGTTTT CTGCTGTTGG ACGGCGGCAA CAGCCGGCTC
1051 AAGTGGGCGT GGGTGGAATA CGGCACGTTT GCAACCGTCG GTAGCGCGCC
1101 GTACCGCGAT TTGTCGCCTT TGGGCGCGGA GTGGGCGGAA AAGGCGGATG
1151 GAAATGTCCG CATCGTCGGT TCGCTGTGTG GCGGAGAATT CAAAAGGCA
1201 CAAGTGCAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGCTG GTTCAACGCC TTGGGCAGCC GCCGCTTCAG CCGCAACGCC
1351 TCGCTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACCAG
1401 TGACGGACAT TATCTCGGGG GAACCATCAT GCCCGGTTTC CACCTGATGA
1451 AAGAATCGCT CGCCGTCCGA ACCGCCAACC TCAACCGGCA CGCCGTAAG
1501 CGTTATCCTT TCCCGACCAC AACGGGCAAT GCCGTCGCAA GCGGCATGAT
1551 GGATGCGGTT TGCGGCTCGG TTATGATGAT GCACGGCGCT TTGAAAGAAA
1601 AAACCGGGGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CGGCGGCGCG
1651 GCAAAAGTTG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATTACCGG GTTGTGAAC ATGATTGCCG

```

1751 CCGAAGGCAG GGAATATGAA CATATTTAA

This corresponds to the amino acid sequence <SEQ ID 1298; ORF 311-1>:

m311-1.pep

```

1   MTVLKLSHWR VLAELADGLP QHVSQALARMA DMKPQQLNGF WQOMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRELGERS GFQTALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECLMFS FGWVFDPRQY
151 ELGSLSPVAA VACRRALSRL GLDVQIKWPN DLVVGRDKLG GILIETVRTG
201 GKTVAUVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLVE
251 LDAVLLQYAR DGFAPFVAEY QAANRDHGKA VLLLRDGETV FEGTVKGVGD
301 QGVLHLETAE GKQTVVSGEI SLRSDDRPVS VPKRRDSERF LLLDGGNSRL
351 KWAVVENGTF ATVGSAPYRD LSPLGAEWAE KADGNVRIVG CAVCGEFKKA
401 QVQEQALARKI EWLPSSAQAL GIRNHYRHPE EHGS DRWFNA LGSRRFSRNA
451 CVVVSCGTAV TVDALTDGHL YLGGTIMPGF HLMKESLAVR TANLNRHAGK
501 RYPPFTTTGN AVASGMMDAV CGSVMMHGR LKEKTGAGKP VDVITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIYGLLN MIAAEGREYE HI*

```

m311-1/g311-1 93.9% identity in 591 aa overlap

	10	20	30	40	50	60
m311-1.pep	MTVLKLSHWRVLAELADGLPQHVSQALARMADMKPQQLNGFWQOMPAHIRG	LLRQHDGYWR				
g311-1	MTVLKPSHWRVLAELADGLPQHVSQALAREADMKPQQLNGFWQOMPAHIRG	LLRQHDGYWR				
	10	20	30	40	50	60
	70	80	90	100	110	120
m311-1.pep	LVRPLAVFDAEGLRELGERSGFQTALKHECASSNDEILELARIAPDKAHKTICVTHLQSK					
g311-1	LVRPLAVFDAEGLRDLGERSGFQTALKHECASSNDEILELARIAPDKAHKTICVTHLQSK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m311-1.pep	GRGRQGRKWSHRLGECLMFSFGWVFDPRQYELGSLSPVAACRRALSRLGLDVQIKWPN					
g311-1	GRGRQGRKWSHRLGECLMFSFGWAFDRPQYELGSLSPVAALACRRALGCLGLETQIKWPN					
	130	140	150	160	170	180
	190	200	210	220	230	240
m311-1.pep	DLVVGRDKLGGGILIETVRTGGKTVAVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA					
g311-1	DLVVGRDKLGGGILIETVRAGGKTVAVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m311-1.pep	AVLLETLLVELDAVLLQYARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGVGD					
g311-1	AVLLETLLAELGAVLEQYAEEGFAPFLNEYETANRDHGKAVLLLRDGETVCEGTVKGVGD					
	250	260	270	280	290	300
	310	320	330	340	350	360
m311-1.pep	QGVLHLETAEGKQTVVSGEISLRSDDRPVSVPKRRDSERFLLLDGGNSRLKWAVVENGTF					
g311-1	RGVLHLETAEGEQTVVSGEISLRPDNRVSVPKRPDSERFLLLEGNSRLKWAVVENGTF					
	310	320	330	340	350	360
	370	380	390	400	410	420
m311-1.pep	ATVGSAPYRDLSPPLGAEWAEKADGNVRIVGCAVCGEFKKAQVQEQALARKIEWLPSSAQAL					
g311-1	ATVGSAPYRDLSPPLGAEWAEKADGNVRIVGCAVCGESKKAQVKEQLARKIEWLPSSAQAL					
	370	380	390	400	410	420
	430	440	450	460	470	480
m311-1.pep	GIRNHYRHPEEHGS DRWFNALGSRRFSRNACVVVSCGTAVTVDALTDGHYLGGTIMPGF					
g311-1	GIRNHYRHPEEHGS DRWFNALGSRRFSRNACVVVSCGTAVTVDALTDGHYLGGTIMPGF					
	430	440	450	460	470	480
	490	500	510	520	530	540
m311-1.pep	HLMKESLAVRTANLNRHAGKRYPPFTTTGNASGMMDAVCGSVMMHGRLEKKTGAGKP					
g311-1	HLMKESLAVRTANLNRHAGKRYPPFTTTGNASGMMDAVCGSIMMHGRLEKKTGAGKP					
	490	500	510	520	530	540
	550	560	570	580	590	

```

m311-1.pep  VDVIITGGGAAKVAELPPAFLAENTVRVADNLVIYGLLNLMIAAEGREYEHIX
              |||||
g311-1      VDVIITGGGAAKVAELPPAFLAENTVRVADNLVIHGLLNLMIAAEGGESEHAX
              550      560      570      580      590

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1299>:

```

a311-1.seq
1  ATGACGGTTT TGAAGCCTTC GCACTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTGCCG CAACACGTCT CGCAACTGGC GCGTATGGCG GATATGAAGC
101 CGCAGCAGCT CAACGGTTT TGGCAGCAGA TGCCGCGCCA CATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CATTGGCGGT
201 TTTCGATGCC GAAGGTTTGC GCGAGCTGGG GGAAAGGTCG GGTTTTCAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG GCCCGACAA GGCGCACAAA ACCATATGTG TGACCCACCT
351 GCAAAGTAAG GGCAGGGGGC GGCAGGGGCG GAAAGTGGTCG CACCGTTTGG
401 GCGAGTGTCT GATGTTTCACT TTTGGCTGGG TGTTTGACCG GCCGCAGTAT
451 GAGTTGGGTT CGCTGTCGCC TGTTGCGGCA GTGGCGTGCC GGCGCGCCTT
501 GTCGCGTTTG GGTGTTGAAA CGCAAATCAA GTGGCCAAAC GATTTGGTCTG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACGGT CAGGACGGGC
601 GGCAAAACGG TTGCCGTGGT CCGTATCGGC ATCAATTTCG TGCTGCCCAA
651 GGAAGTGGAA AACGCCGCTT CCGTGCAATC GCTGTTTCAG ACGGCATCGC
701 GCGGGGAAA TGCCGATGCC GCCGTGTTGC TGGAAACGCT GTTGGCGGAA
751 CTTGATGCGG TGTGTTGCA ATATGCGCGG GACGGATTG CGCCTTTTGT
801 GCGGGAATAT CAGGCTGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TCGCGACGCG CGAAACCGTG TTCGAAGGCA CGGTTAAAGG CGTGGACGGA
901 CAAGGCGTTC TGCACTTGGG AACGGCAGAG GGCAAACAGA CGGTCGTCAG
951 CGCGGAAATC AGCCTGCGGT CCGACGACAG GCCGGTTTCC GTGCCGAAGC
1001 GCGGGGATTC GGAACGTTTT CTGCTGTTGG ACGGCGGCAA CAGCCGGCTC
1051 AAGTGGGCGT GGTGGAATA CGGCACGTTT GCAACCGTCG GTAGCGCGCC
1101 GTACCGCGAT TTGTCGCCTT TGGGCGCGGA GTGGGCGGAA AAGGTGGATG
1151 GAAATGTCCG CATCGTCGGT TCGCGCGTGT GCGGAGAATT CAAAAGGCA
1201 CAAGTGCAGG AACAGCTCGC CCGAAAATC GAGTGGCTGC CGTCTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGCTG GTTCAACGCC TTGGGAGGCC GCCGCTTACG CCGCAACGCC
1351 TGCGTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTACCGA
1401 TGACGGACAT TATCTCGGGG GAACCATCAT GCCCGGTTTC CACCTGATGA
1451 AAGAATCGCT CGCGCTCGA ACCGCCAACC TCAACCGGCA CGCCGGTAAG
1501 CGTTATCCTT TCCCGACCAC AACGGGCAAT GCCGTCGCCA GCGGCATGAT
1551 GGATGCGGTT TCGGCTCGG TTATGATGAT GCACGGGCGT TTGAAAGAAA
1601 AAACCGGGGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CGGCGGCGCG
1651 GCAAAAGTTG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATTACCGG GCTGCTGAAC CTGATGCCG
1751 CCGAAGGCGG GGAATCGGAA CATACTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1300; ORF 311-1.a>:

```

a311-1.pep
1  MTVLKPSHWR VLAELADGLP QHVSQALARMA DMKPOQLNGF WQOMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRELTERS GFQALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECLMFS FGWVFD RPQY
151 ELGSLSPVAA VACRRALSRL GLKTQIKWPN DLVVGDRKLG GILIEVTRTG
201 GKTVAVVVIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLE
251 LDAVLLQYAR DGFAPFVAEY QANRDHGKA VLLLRDGETV FEGTVKGVDG
301 QGVHLHLETA GKQTVVSGEI SLRSDRPVVS VPKRRDSERF LLLDGGNSRL
351 KWAUVENGTF ATVGSAFYRD LSPLGAEWAE KVDGNVRIVG CAVCGEFKKA
401 QVQEQLARKI EWLPSAQAL GIRNHYRHPE EHGSDRWFNA LGSRRFSRNA
451 CVVVSCTAV TVDALTDGHH YLGGTIMPGF HLMKESLAVR TANLNRHAGK
501 RYFPFTTGN AVASGMMDAV CGSVMMHGR LKEKTGAGKP VDVITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIHGLLN LIAAEGGESE HT*

```

a311-1/m311-1 98.5% identity in 591 aa overlap

```

a311-1.pep      10      20      30      40      50      60
MTVLKPSHWRVLAELADGLPQHVSQALARMADMKPQQLNGFWQOMPAHIRGLLRQHDGYWR
|||||
m311-1          10      20      30      40      50      60
MTVLKLSHWRVLAELADGLPQHVSQALARMADMKPQQLNGFWQOMPAHIRGLLRQHDGYWR

a311-1.pep      70      80      90      100     110     120
LVRPLAVFDAEGLRELTERS GFQALKHECASSNDEILELARIAPDKAHKTICVTHLQSK
|||||
m311-1          70      80      90      100     110     120
LVRPLAVFDAEGLRELTERS GFQALKHECASSNDEILELARIAPDKAHKTICVTHLQSK

```

a311-1.pep	130	140	150	160	170	180
	GRGRQGRKWSHRLGECIMFSFGWVFDPRQYELGSLSPVAAVACRRALSRLGLKTQIKWPN					
m311-1	130	140	150	160	170	180
	GRGRQGRKWSHRLGECIMFSFGWVFDPRQYELGSLSPVAAVACRRALSRLGLDVQIKWPN					
a311-1.pep	190	200	210	220	230	240
	DLVVGRDKLGGILIEVTRTGGKTVAVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA					
m311-1	190	200	210	220	230	240
	DLVVGRDKLGGILIEVTRTGGKTVAVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA					
a311-1.pep	250	260	270	280	290	300
	AVLLETLLAELDAVLLQYARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGVVDG					
m311-1	250	260	270	280	290	300
	AVLLETLLVELDAVLLQYARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGVVDG					
a311-1.pep	310	320	330	340	350	360
	QGVHLHLETAEGKQTVVSGEISLRSDDRPVSVPKRRDSEFLLLDGGNSRLKWAWVENGT					
m311-1	310	320	330	340	350	360
	QGVHLHLETAEGKQTVVSGEISLRSDDRPVSVPKRRDSEFLLLDGGNSRLKWAWVENGT					
a311-1.pep	370	380	390	400	410	420
	ATVGSAPYRDLSPGAEWAEEKVDGNVRIVGCAVCGEFKKAQVQEQQLARKIEWLPSSAQAL					
m311-1	370	380	390	400	410	420
	ATVGSAPYRDLSPGAEWAEEKADGNVRIVGCAVCGEFKKAQVQEQQLARKIEWLPSSAQAL					
a311-1.pep	430	440	450	460	470	480
	GIRNHYRHPPEHSGDRWFNALGSRFRSRNACVVVSCGTAVTVDALTDGHHYLGGTIMPGF					
m311-1	430	440	450	460	470	480
	GIRNHYRHPPEHSGDRWFNALGSRFRSRNACVVVSCGTAVTVDALTDGHHYLGGTIMPGF					
a311-1.pep	490	500	510	520	530	540
	HLMKESLAVRTANLNRHAGKRYPFPTTTGNAVASGMMDAVCGSVMMHGRLEKKTGAGKP					
m311-1	490	500	510	520	530	540
	HLMKESLAVRTANLNRHAGKRYPFPTTTGNAVASGMMDAVCGSVMMHGRLEKKTGAGKP					
a311-1.pep	550	560	570	580	590	
	VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIHGLLNLI AEGGESEHTX					
m311-1	550	560	570	580	590	
	VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIYGLNMI AEGGREYEHIX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1301>:

g312.seq

```

1  atgaGtatCc aatCcGgcga AATTTtagaa accgtCAAAA TGGTTGCCGA
51  ccggaATttt gAtgtccgCA CCATTAccat cggcaTTgaT ttgcacgact
101 gcatcagcac cgacatcgac gtgttaAACC AAAACATtta caaCAaaaTc
151 accacggtcg gcaaagactT GGTGGCAacg Gcgaaacacc tTTccgcCAA
201 ATACGGCGTG CCGATTGTGA ATCAGCGCAT TTCCGTTACG CCGAttgccc
251 AaatcGCGGC GGcgaccaAa gccgaCAGTT AtgtcAGCgt ggcgcAGact
301 tTGGACAAGG CAGCCAAAGC CATCGGCGTG TCCTTTATCG GcggCTTTTC
351 CGCGCTGGTG CAAAAAGGTA TGTCGCCTTC GGATGAGGTG TTGATCCGTT
401 CCGTTCCCGA AGCGATGAAA ACTACCGATA TCGTGTGCAG CTCCATCAAT
451 ATCGGCAGCA CGCGTGCCGG TATCAATATG GATGCGGTCA AGCTGGCAGG
501 CGAAACCATC AAACGCACGG CTGAAATCAC ACCCGAAGGT TTCGCTGCG
551 CCAAAATCGT CGTGTTCTGC AACCGGTGG AAGACAAATCC GTTTATGGCG
601 GGTGCGTTCT ACGGCTCGGG CGAAGCGGAT GCTGTGATTA ATGTCGGCGT
651 ATCCGGTCCA GGCGTGGTCA AAGCCGCGCT GGAAAAATTCG GACGCGGTCA
701 GCCTGACCGA GGTGCGCGAA GTCGTGAAGA AAACCGCTTT CAAAAATCACC
751 CGCGTGGGCG AACTCATCGG TCGCGAAGCC TCAAAAATGC TGAATATCCC
801 GTTCGGCATT CTCGATTGTG CGCTGGCACC GACCCCGGCC GTCGGCGACT
851 CCGTGGCGCG CATTCTTGAA GAAATGGGCT TGAGCGTCTG CCGTACGCAC

```

717

```

901 GGCACAACAG CAGCTTTGGC ATTGCTGAAC GATGCCGTGA AAAAGGGCGG
951 CATGATGGCT TCCAGCGCGG TCGGCGGTTT GAGCGGCGCG TTTATCCCCG
1001 TTTCCGAAGA CGAAGGTATG ATTGCCGCCG CCGAGGCAGG CGTGTTGACG
1051 CTGGACAAAC TCGAAGCCAT GACCGCCGTC TGCTCCGTTG GTTTGGACAT
1101 GATTGCCGTT CCCGGCGACA CGCCCGCGCA CACCATTTCG GGCATCATCG
1151 CCGACGAAGC CGCCATCGGC ATGATCAACA GCAAAACCAC CGCCGTGCGC
1201 ATTATTCGGG TAACGGGCAA AACCGTCGGC GACAGCGTCG AGTTCGGCGG
1251 TCTGTTGGGC TACGCGCCTG TAATGCCGGC AAAAGAAGGT TCGTGCGAAG
1301 TGTTCTGCAA CCGGGGCGGC AGGATTCCTG CACCGGTTCA ATCGATGAAA
1351 AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1302; ORF 312.ng>:

g312.pep

```

1 MSIQSGEILE TVKMVADRNF DVRTITIGID LHDCISTDID VLNQNIYNKI
51 TTVGKDLVAT AKHLSAKYGV PIVNQRISVT PIAQIAAATK ADSYVSVAQ
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSVPEAMK TTDIVCSSIN
151 IGSTRAGINM DAVKLAGETI KRTAEITPEG FGC AKIVVFC NAVEDNPFMA
201 GAFHGSGEAD AVINVGVSGP GVVKAALENS DAVSLTEVAE VVKKTAFKIT
251 RVGELIGREA SKMLNIPFGI LDLSLAPTPA VGDSVARILE EMGLSVCGTH
301 GTTAALALLN DAVKKGGMMA SSAVGGLSGA FIPVSEDEGM IAAAEAGVLT
351 LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR
401 IIPVTGKTVG DSVEFGGLLG YAPVMPAKEG SCEVFNRRGG RIPAPVQSMK
451 N*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1303>:

m312.seq

```

1 ATGAGTATCC AATCCGGCGA AATTTTAGAA ACCGTCAAAA TGTTGCCGGA
51 CCAGAATTTT GATGTCCGCA CCATTACCAT CGGCATTGAT TTGCACGACT
101 GCATCAGCAG CGATATCAAT GTGTTGAACC AAAATATTTA CAATAAAATT
151 ACCACAGTCG GCAAAGACTT GGTCACACG GCAAATATC TGTCTGCCAA
201 ATACGGCGTA CCGATTGTGA ATCAGCGCAT TTCCGTTACG CCGATTGCCC
251 AAATCGCGGC GGCCACCCAT GCTGATTCTT ACGTCAGCGT GGCGCAAAC
301 TTGGATAAAG CTGCCAAAGC CATCGGTGTG TCTTTTATCG GCGGTTTTTC
351 CGCGTTGGTG CAAAAGGGA TGTGCGCTTC GGATGAGGTG TTAATCCGCT
401 CCATTCCCGA AGCGATGAAG ACTACCGATA TTGTGTGCwG CTCCATCAAT
451 ATCGGCAGTA CGCGTGCCGG TATCAATATG GATGCGGTCA AGCTGGCGGG
501 CGAAACCGTc AAACGCACGG CGGAAATCAC GCCCGAAGGT TTCGGTGCGG
551 CTAAAATTGT CGTGTCTGCG AACGCGGTGG AAGACAACCC GTTTWTGCGG
601 GGCGCGTTTC ATGGTTCGGG CGATGCCGTT ATCAATGTCT GCGTATCCGG
651 CCCAGGTGTC GTAAAAGCCG CGTTGGAAAA TTCAGATGCA ACGACATTGA
701 CCGAAGTTGC GGAAGTAGTG AAGAAAAC TGCTTCAAAT TACCCGCGTG
751 GGCGAACTCA TCGGCCGCGA AGCCTCAAAA ATGCTGAATA TCCCGTTTGG
801 TATTCTCGAC TTGTCGCCGA CCCCGCCGT CGGCGACTCA GTGCGACGCA
851 TTCTTGAAGA AATGGGCTTG AGCGTCTGCG GTACGCACGG CACAACGCA
901 GCTTTGGCAT TGCTGAACGA TGCCGTGAAA AAAGGCGGCA TGATGGCTTC
951 CAGCGCGGTC GGGGTTTGA GTGGCGCGTT TATCCCGGTT TCCGAAGACG
1001 AAGGTATGAT yGmCgCcGCC GAAGCAGGCG TGCTGACGCT GGACAAACTC
1051 GAAGCCATGA CCGCCGTTTG TTCGGTCGGC TTGGATATGA TTGCCGTTCC
1101 CGGCGACACG CCCGCGCACA CCATTTCGG CATCATTGCC GACGAAGCCG
1151 CCATCGGCAt GATCAACAGC AAAACCACTG CCGTGCGCAT TATTCCGGTA
1201 ACCGGTAAAA CCGTCGGCGA CACGGTCGAG TTCGGCGGCT TGTTGGGCTA
1251 CGCGCTGTG ATGCCGGTCA AAGAAGGTTT GTGCGAAGTA TTCGTCAACC
1301 GAGGCGGCAG AATTCGGGCT CCGGTTCAAT CGATGAAAAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1304; ORF 312>:

m312.pep

```

1 MSIQSGEILE TVKMVADQNF DVRTITIGID LHDCISSDIN VLNQNIYNKI
51 TTVGKDLVTT AKYLSAKYGV PIVNQRISVT PIAQIAAATH ADSYVSVAQ
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSIPEAMK TTDIVCX SIN
151 IGSTRAGINM DAVKLAGETV KRTAEITPEG FGC AKIVVFC NAVEDNPFXA
201 GAFHGSGLAV INVGVSGPGV VKAALENS DA TTLTEVAE VV KKTAFKITRV
251 GELIGREASK MLNIPFGILD LSPTPPVGD S VARILEEMGL SVCGTHGTTA
301 ALALLNDAVK KGGMMASAV GGLSGAFIPV SEDEGMIXAA EAGVLTLDKL
351 AMTAVCSVG LDMIAVPGDT PAHTISGIIA DEAAIGMINS KTTAVRIIPV
401 TGKTVGDTVE FGGLLGYPV MPVKEGSCEV FVNRGGRI PA PVQSMKN*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 312 shows 95.6% identity over a 451 aa overlap with a predicted ORF (ORF 312.ng) from *N. gonorrhoeae*:

m312/g312

m312.pep	10	20	30	40	50	60
	MSIQSGEILETVKMVADQNFVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT					
g312	10	20	30	40	50	60
	MSIQSGEILETVKMVADRNFVRTITIGIDLHDCISTDIDVLNQNIYNKITTVGKDLVAT					
m312.pep	70	80	90	100	110	120
	AKYLSAKYGVPIVNQRISVTPIAQIAAATHADSYVSVSAQTLDKAAKAIGVSFIGGFSALV					
g312	70	80	90	100	110	120
	AKHLSAKYGVPIVNQRISVTPIAQIAAATKADSYVSVSAQTLDKAAKAIGVSFIGGFSALV					
m312.pep	130	140	150	160	170	180
	QKGMSPSDEVLIRSIPEAMKTTDIVCXSNIGSTRAGINMDAVKLAGETVKRTAEITPEG					
g312	130	140	150	160	170	180
	QKGMSPSDEVLIRSVPEAMKTTDIVCSSINIGSTRAGINMDAVKLAGETIKRTAEITPEG					
m312.pep	190	200	210	220	230	
	FGCAKIVVFCNAVEDNPFXAGAFHGSG--DAVINVGVS GPGVVKAALENS DATTLTEVAE					
g312	190	200	210	220	230	
	FGCAKIVVFCNAVEDNPFMAGAFHGSGEADAVINVGVS GPGVVKAALENS DAVSLTEVAE					
m312.pep	240	250	260	270	280	290
	VVKKTAFKITRVGELIGREASKMLNIPFGILDLS--PTPPVGDSVARILEEMGLSVCGTH					
g312	240	250	260	270	280	290
	VVKKTAFKITRVGELIGREASKMLNIPFGILDLSLAPTAVGDSVARILEEMGLSVCGTH					
m312.pep	300	310	320	330	340	350
	GTTAALALLNDAVKKGGMMASSAVGGLSGAFIPVSEDEGMIXAAEAGVLTLDKLEAMTAV					
g312	300	310	320	330	340	350
	GTTAALALLNDAVKKGGMMASSAVGGLSGAFIPVSEDEGMIAAAEAGVLTLDKLEAMTAV					
m312.pep	360	370	380	390	400	410
	CSVGLDMIAPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDSVEFGGLLG					
g312	360	370	380	390	400	410
	CSVGLDMIAPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDSVEFGGLLG					
m312.pep	420	430	440			
	YAPVMPVKEGSCEVFVNRGGRI PAPVQSMKNX					
g312	420	430	440			
	YAPVMPAKEGSCEVFVNRGGRI PAPVQSMKNX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1305>:

a312.seq

1	ATGAGTATCC	AATCCGGCGA	AATTTTAGAA	ACCGTCAAAA	TGGTTGCCGA
51	CCAGAATTTC	GATGTCCGCA	CCATTACCAT	CGGCATTGAT	TTGCACGACT
101	GCATCAGCAC	CGACATCGAC	GTGTGAACC	AAAATATTTA	CAACAAAATT
151	ACCACGGTCG	GCAAAGACTT	GGTGGCGACA	GCAAATATC	TGCTGCCAA
201	ATACGGCGTG	CCGATTGTGA	ATCAGCGCAT	TTCTGTCACG	CCGATTGCCC
251	AAATCGCGGC	GGCCACCCAT	GCTGATTCTT	ACGTCAGCGT	GGCGCAAAT

```
a312.pep
1  MSIQSGEILE TVKMVADQNF DVRTITIGID LHDCISTDID VLNQNIYNKI
51  TTVGKDLVAT AKYLSAKYGV PIVNQIRISVT PIAQIAAATH ADSYVSVAQT
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSIPEAMK TTDIVCSSIN
151 IGSTRAGINM DAVRLAGETI KRTAEITLEG FGCAKIVVFC NAVEDNPFMA
201 GAFHGSGEAD AVINVGVS GP VGVKAALENS DATTITTEVAE VVKKTAFKIT
251 RVGELIGREA SKMLNIPFGI LDLSLAPTPA VGDSVARILE EMGLSVCGTH
301 GTTAALALLN DAVKKGGGMA SSAVGGLSGA FIPVSEDEGM IAAEAGVLT
351 LDKLEAMTAV CSVGLDMIIV PGDTPAHTIS GIIADEAAIG MINSKTTAVR
401 IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK
451 N*
```

	10	20	30	40	50	60
m312.pep	MSIQSGEILETVKMQVADQNF	DVRTITIGIDLHDCISSDINVL	NQNIYNKITT	VGKDLVTT		
a312	MSIQSGEILETVKMQVADQNF	DVRTITIGIDLHDCISTDIDVL	NQNIYNKITT	VGKDLVAT		
	10	20	30	40	50	60
m312.pep	70	80	90	100	110	120
a312	AKYLSAKYGVPIVNQRISVTPIAQIAAATHADSYV	SVAQTLDKA	AKAIGVSFIGGFSALV			
	70	80	90	100	110	120
m312.pep	130	140	150	160	170	180
a312	QKGMSPSDEVLIRSIPEAMKTTDIVCX	SINIGSTRAGINMDAVKLAGETVKRTAEITPEG				
	130	140	150	160	170	180
m312.pep	190	200	210	220	230	
a312	FGCAKIVVFCNAVEDNPFEXAGAFHGS	G--DAVINVGVS	SGPGVVKAAL	ENS	DATTLTEVAE	
	190	200	210	220	230	240
m312.pep	240	250	260	270	280	290
a312	VVKKTAFKITRVGELIGREASKMLNIPFGILD	LS--PTPPVGDS	VARILEEMGLS	VCGTH		
	240	250	260	270	280	290
m312.pep	300	310	320	330	340	350
a312	QKGMSPSDEVLIRSIPEAMKTTDIVCS	SINIGSTRAGINMDAVRLAGETIKRTAEITLEG				

720

	250	260	270	280	290	300
	300	310	320	330	340	350
m312.pep	GTTAALALLNDAVKKGGMMASSAVGGLSGAFIPVSEDEGMIXAAEAGVLTLDKLEAMTAV					
a312	GTTAALALLNDAVKKGGMMASSAVGGLSGAFIPVSEDEGMIAAAEAGVLTLDKLEAMTAV					
	310	320	330	340	350	360
	360	370	380	390	400	410
m312.pep	CSVGLDMIAPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDTVEFGGLLG					
a312	CSVGLDMIAPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDSVEFGGLLG					
	370	380	390	400	410	420
	420	430	440			
m312.pep	YAPVMPVKEGSCEVFVNRGGRIAPVQSMKNX					
a312	YAPVMPVKEGSCEVFVNRGGRIAPVQSMKNX					
	430	440	450			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1307>:

```

g313.seq
1  atggacgacc cgcgcaccta cggatcgggc aatcccgggc cgaccaatgt
51  tttagcgagc ggcaaaaaaa aggcggccgc gctgacgctc ttgggcgatg
101 ccgccaaagg tttggttgcc gttttgcttg cacgcgtgct tcaagaaccg
151 ctcggtttat ccgacagcgc aatcgccgcc gtcgcactcg ccgcgctggt
201 cgggcatatg tggccggtgt ttttcggatt taaggcgggc aaaggcgtgg
251 caacggcatt gggcgtgctt ctggcactct ctctgcaac tgccttggtc
301 tgcgcgttga tttggttgt gatggcattc ggcttcaaag tatcctccct
351 tgccgcgctg gtcgccacaa ccgccgcccc ccttgccgca ctgtttttta
401 tgccgcatac ttcttggtt ttcgcaaccc tcgcaatcgc catattgggtg
451 ttgctccgcc ataagagcaa catcctcaac ctgattaaag gcaaagaaag
501 caaaatcggc gaaaaacgct ga

```

This corresponds to the amino acid sequence <SEQ ID 1308; ORF 313.ng>:

```

g313.pep
1  MDDPRTYGSG NPGATNVLRS GKKKAAALTL LGDAAKGLVA VLLARVLQEP
51  LGLSDSAIAA VALAALVGHM WPVFFGFKGG KGVATALGLV LALSPATALV
101 CALIWLVMFA GFKVSSLAAL VATTAAPLAA LFFMPHTSWI FATLAIAILV
151 LLRHKSNIILN LIKGESKIG EKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1309>:

```

m313.seq
1  ATGGACGACC CGCGCACCTA CGGATCGGGC AATCCGGGGG CAACCAATGT
51  TTTACGCAGC GGCAAAAAAA AGGCGGCCGC GCTGACGCTC TTGGGCGATG
101 CCGCCAAAGG TTTAGTTGCC GTTTTGCTTG CACGCGTGCT TCAAGAACCG
151 CTCGTTTAT CCGACAGCGC AATCGCGGCC GTCGCACTCG CCGCGCTGGT
201 CGGGCATATG TGGCCGGTGT TTTTCGGATT TAAAGGCGGC AAAGGCGTGG
251 CAACGGCATT GGGCGTGCTT CTGGCACTCT CTCCCACAAC TGCCTTGCTC
301 TGCGCGTTGA TTTGGCTTGT TATGGCATTG GGCTTCAAGG TGTCTCCCT
351 TGCCGCATTA ACCGCCACAA TCGCCGCACC GGTGCGCGCA TCCTTCTTAA
401 TGCCGCACGT CTCGTGGGTT TGGGCGACCG TCGCCATTGC TTTGCTGGTG
451 TTGTTCCGCC ACAAAGTAA TATCGTCAAG CTGCTCGAAG GCAGAGAAAG
501 CAAAATCGGC GGCAGCCGCT GA

```

This corresponds to the amino acid sequence <SEQ ID 1310; ORF 313>:

```

m313.pep
1  MDDPRTYGSG NPGATNVLRS GKKKAAALTL LGDAAKGLVA VLLARVLQEP
51  LGLSDSAIAA VALAALVGHM WPVFFGFKGG KGVATALGLV LALSPATALV
101 CALIWLVMFA GFKVSSLAAL TATIAAPVAA SFFMPHVSWS WATVAIALLV
151 LFRHKSNIIVK LLEGRESKIG GSR*

```

Computer analysis of this amino acid sequence gave the following results:

721

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 313 shows 90.2% identity over a 173 aa overlap with a predicted ORF (ORF 313.ng) from *N. gonorrhoeae*:

m313/g313

	10	20	30	40	50	60
m313.pep	MDDPRTYGSNPGATNVLRSGKKKAAALTLGDAAKGLVAVLLARVLQEPGLGLSDSAIAA					
g313	MDDPRTYGSNPGATNVLRSGKKKAAALTLGDAAKGLVAVLLARVLQEPGLGLSDSAIAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m313.pep	VALAALVGHMWPVFFGFKGGKVATALGVLLALSPATALVCALIWLVMFAGFKVSSLAAL					
g313	VALAALVGHMWPVFFGFKGGKVATALGVLLALSPATALVCALIWLVMFAGFKVSSLAAL					
	70	80	90	100	110	120
	130	140	150	160	170	
m313.pep	TATIAAPVAASFFMPHVSWWATVAIALLVLRHKSNIIVKLLLEGRESKIGGSRX					
g313	VATTAAPLAALFFMPHTSWIFATLAIAILVLLRHKSNIILNLIKGESKIGEKRX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1311>:

a313.seq

```

1  ATGGACGACC CGCGCACCTA CGGATCGGGC AATCCGGGGG CAACCAATGT
51  TTTACGCAGC GGCAAAAAAA AGGCGGCCGC GCTGACGCTC TTGGGCGATG
101 CCGCCAAAGG TTTGGTTGCC GTTTTGCTTG CACGCGTGCT TCAAGAACCG
151 CTCGGTTTAT CCGACAGCGC AATCGCGGCC GTCGCACTCG CCGCGCTGGT
201 CGGGCATATG TGGCCGGTGT TTTTCGGATT TAAAGGCGGC AAAGGCGTGG
251 CAACGGCATT GGGCGTGCTT CTGGCACTCT CTCCCACAAC TGCCTTGCTC
301 TCGCGTTTGA TTTGGCTTGT GATGGCATTC GGCTTCAAGG TGTCTCCCT
351 TGCCGCATTA ACCGCCACAA TCGCCGCCCC CCTTGCCGCA CTGTTTTTTA
401 TGCCGCATAC TTCTTGGATT TTCGCAACCC TCGCAATCGC CATATTGGTG
451 TTGCTCCGCC ATAAGAGCAA CATCCTCAAC CTGATTAAAG GCAAAGAAAG
501 CAAAATCGGC GAAAAACGCT GA

```

This corresponds to the amino acid sequence <SEQ ID 1312; ORF 313.a>:

a313.pep

```

1  MDDPRTYGS NPGATNVLR S GKKKAAALTL LGDAAKGLVA VLLARVLQEP
51  LGLSDSAIAA VALAALVGHM WPVFFGFKGG KGVATALGV LALSPTTALV
101 CALIWLVMF GFKVSSLAAL TATIAAPLAA LFFMPHTSWI FATLAIAILV
151 LLRHKSNIIL LIKGESKIG EKR*

```

m313/a313 90.8% identity in 173 aa overlap

	10	20	30	40	50	60
m313.pep	MDDPRTYGSNPGATNVLRSGKKKAAALTLGDAAKGLVAVLLARVLQEPGLGLSDSAIAA					
a313	MDDPRTYGSNPGATNVLRSGKKKAAALTLGDAAKGLVAVLLARVLQEPGLGLSDSAIAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m313.pep	VALAALVGHMWPVFFGFKGGKVATALGVLLALSPATALVCALIWLVMFAGFKVSSLAAL					
a313	VALAALVGHMWPVFFGFKGGKVATALGVLLALSPPTALVCALIWLVMFAGFKVSSLAAL					
	70	80	90	100	110	120
	130	140	150	160	170	
m313.pep	TATIAAPVAASFFMPHVSWWATVAIALLVLRHKSNIIVKLLLEGRESKIGGSRX					
a313	TATIAAPLAALFFMPHTSWIFATLAIAILVLLRHKSNIILNLIKGESKIGEKRX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1313>:

```
g401.seq
1   atgaaattac aacaattggc tgaagaaaaa atcggcggttc tgatttgtgtt
51  cacgctgctt gtagtcagtg tcggtctgtt gattgaagtt gtgcccttgg
101 cctttaccaa ggcggaaca cagccggcgc cggcggtgaa gccttacaat
151 gccctgcagg ttgccggacg cgatatttac atccgtgagg gctgttacaa
201 ctgccactct caaatgattc gtccgttccg tgcggaaacc gagcggtacg
251 gtcattactc tgttgccgga gagtcggttt acgaccatcc gttccaatgg
301 ggttccaaac gtaccggtcc tgatttggca cgtgtgggag gccgctattc
351 cgacgaatgg caccgcatcc acctgctgaa tccccgtgat gtcgtgcctg
401 agtccaatat gccggcattc ccgtggcttg cacgcaataa agtcgatgtc
451 gatgcaaccg ttgccaacat gaaggctttg cgtaaagtag gtactcctta
501 cagtgatgag gaaattgcca aagcgcttga ggctttggca aacaaatccg
551 agctggatgc ttagtcgcc tatctgcaag gattgggtct ggctttgaaa
601 aacgtaaggc aa
```

This corresponds to the amino acid sequence <SEQ ID 1314; ORF 401.ng>:

```
g401.pep
1   MKLQQLAEEK IGV LIVFTLL VSVGLLIEV VPLAFTKAAT QPAPGVKPYN
51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVDHDPFQW
101 GSKRTGPDLA RVGGRYSEW HRIHLLNPRD VVPESNMPAF PWLARNKVDV
151 DATVANMKAL RKVGTPYSDE EIAKAPEALA NKSELDVVA YLQGLGLALK
201 NVR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1315>:

```
m401.seq
1   ATGAAATTAC AaCAATTGGC TGAAGAAAAA ATCGGCGTTC TGATTGTGTT
51  CACGCTGCTT GTAGTCAGTG TCGGTCTGTT GATTGAAGTT GTGCCCTTGG
101 CCTTTACCAA GGCGGCAACA CAGCCGGCGC CGGGCGTGAA GCCTTACAAT
151 GCCCTGCAGG TTGCCGGACG CGATATTTAC ATCCGTGAGG GCTGTACAA
201 CTGCCACTCG CAAATGATTG GTCCGTTCCG TGCggAAACC GAGCGTTACG
251 GTCATTACTC TGTGCGGGA GAGTCGGTTT ACGACCATCC GTTCCAATGG
301 GGTTCCAAAC GTACCGGTCC TGATTGGCA CGTGTGGGCG GTCGCTATTC
351 CGACGAATGG CACCGTATCC ACCTGCTGAA TCCCCGTGAT GTCGTGCCTG
401 AGTCCAATAT GCCGGCATTG CCGTGGCTTG CACGCAATAA AGTCGATGTC
451 GATGCAACCG TTGCCAACAT GAAGGCTTTG CGTAAAGTAG GTACTCCTTA
501 CAGTGATGAG GAAATTGCGA AAGCACCTGA GGCTTTGGCA AACAAATCCG
551 AGCTGGATGC TGTAGTCGCC TATCTGCAAG GATTGGGTCT GGCTTTGAAA
601 AACGTAAGGT AA
```

This corresponds to the amino acid sequence <SEQ ID 1316; ORF 401>:

```
m401.pep
1   MKLQQLAEEK IGV LIVFTLL VSVGLLIEV VPLAFTKAAT QPAPGVKPYN
51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVDHDPFQW
101 GSKRTGPDLA RVGGRYSEW HRIHLLNPRD VVPESNMPAF PWLARNKVDV
151 DATVANMKAL RKVGTPYSDE EIAKAPEALA NKSELDVVA YLQGLGLALK
201 NVR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 401 shows 100.0% identity over a 203 aa overlap with a predicted ORF (ORF 401.ng) from *N. gonorrhoeae*:

```
m401/g401
10      20      30      40      50      60
m401.pep  MKLQQLAEEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
          |||
g401      MKLQQLAEEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
          |||
10      20      30      40      50      60
m401.pep  IREGCYNCHSQMIRPFRAETERYGHYSVAGESVVDHDPFQW GSKRTGPDLARVGGRYSEW
```

723

```

      |||
g401  IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGGRYSDEW
      70      80      90      100     110     120

      130     140     150     160     170     180
m401.ppep HRIHLLNPRDVPESNMPAFPLARNKVDVDATVANMKALRKVGTPYSDEEIIAKAPEALA
      |||
g401  HRIHLLNPRDVPESNMPAFPLARNKVDVDATVANMKALRKVGTPYSDEEIIAKAPEALA
      130     140     150     160     170     180

      190     200
m401.ppep NKSELDAVVAYLQGLGLALKNVRX
      |||
g401  NKSELDAVVAYLQGLGLALKNVRX
      190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1317>:

```

a401.seq
1   ATGAAATTAC AACAATTGGC TGAAGAAAAA ATCGGCGTTC TGATTGTGTT
51  CACGCTGCTT GTAGTCAGTG TCGGTCTGTT GATTGAAGTT GTGCCCTTGG
101 CCTTTACCAA GCGCGCAACA CAGCCGGCGT CGGGCGTGAA GCCTTACAAT
151 GCCCTGCAGG TTGCCGGACG CGATATTAC ATCCGTGAGG GCTGTTACAA
201 CTGCCACTCG CAAATGATTC GTCCGTTCCG TCGGGAACC GAGCGTTACG
251 GTCATTACTC TGTGCGCGGA GAGTCGGTTT ACGACCATCC GTTCCAATGG
301 GGTTCCAAAC GTACCGGTCC TGATTGGGCA CGTGTGGGCG GTCGCTATTC
351 CGACGAATGG CACCGTATCC ACCTGCTGAA TCCCGTGAT GTCGTGCTG
401 AGTCCAATAT GCCGGCATT CCGTGGCTTG CACGCAATAA AGTCGATGTC
451 GATGCAACCG TTGCAACAT GAAGGCTTTG CGTAAAGTAG GTACTCCTTA
501 CAGTGATGAG GAAATTGCGA AAGCGCCTGA GGCTTTGGCA AACAAATCCG
551 AGCTGGATGC TGTAGTCGCC TATCTGCAAG GATTGGGTCT GGCTTTGAAA
601 AACGTAAGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1318; ORF 401.a>:

```

a401.ppep
1   MKLQQLAEEK IGV LIVFTLL VVSVGLLIEV VPLAFTKAAT QPASGVKPYN
51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVYDHPFQW
101 GSKRTGPDLA RVGGGRYSDEW HRIHLLNPRD VVPESNMPAF PLARNKVDV
151 DATVANMKAL RKVGTPYSDE EIAKAPEALA NKSELDAVVA YLQGLGLALK
201 NVR*

```

m401/a401 99.5% identity in 203 aa overlap

```

      10      20      30      40      50      60
m401.ppep MKLQQLAEEKIGVLIVFTLLVVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
      |||
a401  MKLQQLAEEKIGVLIVFTLLVVSVGLLIEVVPLAFTKAATQPASGVKPYNALQVAGRDIY
      10      20      30      40      50      60

      70      80      90      100     110     120
m401.ppep IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGGRYSDEW
      |||
a401  IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGGRYSDEW
      70      80      90      100     110     120

      130     140     150     160     170     180
m401.ppep HRIHLLNPRDVPESNMPAFPLARNKVDVDATVANMKALRKVGTPYSDEEIIAKAPEALA
      |||
a401  HRIHLLNPRDVPESNMPAFPLARNKVDVDATVANMKALRKVGTPYSDEEIIAKAPEALA
      130     140     150     160     170     180

      190     200
m401.ppep NKSELDAVVAYLQGLGLALKNVRX
      |||
a401  NKSELDAVVAYLQGLGLALKNVRX
      190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1319>:

g402.seq

```

1  ATGGATATGG TGAACACTAA Accgaatact agtgtgatta atatgctttc
51  tttccttacc ggatTATTGA GCTTGGGTat agaagtCtTg tGGGTAAGGA
101 TGttttcgtT CGCagcAcag tccgtgcctc aggCATTtTC atttattcct
151 gcctGttttc tgACCGtat cgccgtcggc gCgTATTtTG GCAAACGGAT
201 TTGCCGCAGC CGCTTTGTG ATATTCCctT TATCGGGCAG TgcttcttgT
251 GGGCGGGTAT TgccgaTttt ttgatTTGG GTGCTGCGTG GTTGTGACG
301 GGTtTTTccg gtttcGTCCA CCACGCCGGT AtttTCATTA CCCTgtctgc
351 CGtcGTCAGG GGGTTGATT TCCCACTGT ACACCATgtg GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTTCcAATG TTTATTTCGC CAACGTTGCC
451 GGCAGTGCAT TGGGTCCGGT CCTTATCGGC TTTGTGATAC TTGATtTgtt
501 gTCCACCCAA CAGATTtacc tgctcatCTG TTTGATTtCT GCTGctgtcc
551 cTTTGTtTg tacaCTGtTC CAAAAAGTC TCCGACTGAA TGCAGTGTCG
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTcCTAC TGCCGGATTc
651 TGTCTTTCAA AATATTGCTG GCCGTCCGGA TAGGTGATT GAAAAAAAC
701 ACGGCATTGT TGCGGTTTAC CATAGAGATG GTGATAAGGT TGTtTATGGG
751 GCGAATGTAT ACGACGGCGC ATACAATACC GATATATTCA ATAGTGTCAA
801 CGGCATCGAA CGTGCCTATC TGCTACCCTC CCTGAAGTCC GGCATACGCC
851 GCATTTTCGT CGTTGGATTG AGTACAGGTT CGTGGGCGCG CGTCTGTCT
901 GCCATTCCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
951 CCGTAGCCTT ATCGCGGAcg agccgcAAAT CGCACCGCTT TTGCAGGACA
1001 AACGTGTGA AATTGTATTG GATGACGGTA GGAAATGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTCGACCT GATTTTGATG AATTCGACTT GGTACTGGCG
1101 TGCCTATTCC ACTAACCTGT TGAGTGCGGA ATTTTAAAA CAGGTGCAAA
1151 GCCACCTTAC CCCGGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCG
1201 CATgctTTG CTACCGCCGT ACACAGTATT CCCTATGCAT ACCGCTACGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTTCcct AATAAAGAAC
1301 TGCTCaagca aCGCCTTtcc cgGTTGATTT GGCCGAAAG CGGCAGgcac
1351 gtATTtGACA GCAGCACCGT GGATGTGCA GCACAAAAGG TTGctctcCG
1401 TATGCTGATT CGGATGACGG AAcctTCGGC TGGGGCGGAA GTCATTACTG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1320; ORF 402.ng>:

g402.pep

```

1  MDMVNTKPNT SVINMLSFLT GLLSLGIEVL WVRMFSFAAQ SVPQAFSFLI
51  ACFLTGIavg AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAawLLT
101 GFSGFVHHAG IFITLSAVVR GLIFPLVHHV GTDGNKSGRQ VSNVYFANVA
151 GSALGPVLIG FVILDLLSTQ QIYLLICLIS AAVPLFCTLF QKSLRLNAVS
201 VAVSLMFGIL MFLLPDSVFQ NIAGRPDRLI ENKHGIVAVY HRDGDKVYVY
251 ANVYDGAYNT DIFNSVNGIE RAYLLPSLKS GIRRIFFVGL STGSwARVLS
301 AIPEMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRRH
351 PDEKFDLILM NSTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP
401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLKQRLS RLIWPESGRH
451 VFDSSTVDAA AQKVVSRLI RMTEPSAGAE VITDDNMIVE YKYGRGI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1321>:

m402.seq

```

1  ATGGATATAG TGAACACTAA ACCGAATACT AGTTTGATT ATATGChTTC
51  TTTCTTAGC GGCTTATTGA GCTTGGGTAT AGAAGTCTTG TGGGTGAGGA
101 TGTTTTCGTT CGCAGCACAG TCCGTGCCTC AGGCATTtTC ATTTACCCTT
151 GCCTGTTTTc TGACCGGTAT CGCCGTCGGC GCGTATTtTG GCAAACGGAT
201 TTGCCGCAGC CGCTTTGTG ATATTCCCTT TATCGGGCAG TGCTCTTGT
251 GGGCGGGTAT TGCCGACTTT TTGATTtTG GTGCTGCGTG GTTGTGACG
301 GGTtTTTCCG GCTTCGTCCA CCACGCCGGT ATCTTCATTA CCCTGTCTGC
351 CGTCTTCAsA sGGTTGATT TCCCGCTCGT ACACCATGTG GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTTCcAATG TTTATTTCGC CAmCGTTGCC
451 GGCAGTGCAT TGGGTCCGGT CCTTATCGGC TTTGTGATAC TTGATTtCTT
501 GTCCACCCAA CAGATTtACC TGCTCATCTG TwTGATTtCT GCTGCTGTCC
551 CTTTGTtTTG TACACTGTTC CAAAAAGTC TCCGACTGAA TGCAGTGTCG
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTcyTAC TGCCGGATTc

```

725

```

651 TGTCTTTCAA AATATTGCTG ACCGTCCGGA TAGGCTGATT GAAAACAAAC
701 ACGGCATTGT TCGGTTTTAC CATAGAGATG GTGATAAGGT TGTTTTATGGG
751 GCGAATGTAT ACGACGGCGC ATACAATACC GATGTATTCA ATAGTGTCAA
801 CGGCATCGAA CGTGCCTATC TGCTACCCTC CCTGAAGTCT GGCATACGCC
851 GCATTTTCGT CGTTGGACTG AGTACAGGT CGTGGGCGCG CGTCTTGCTCT
901 GCCATTCCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
951 CCGTAGCCTT ATCGCGGACG AGCCGCAAAT CGCCCCGCTT TTGCAGGACA
1001 AACGTGTTGA AATTGTATTG GATGACGGTA GGAATAGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTCGACCT GATTTTGATG AATACGACTT GGTACTGGCG
1101 TGCCTATTCC ACCAACCTGT TGAGTGC GGA ATTTTAAAA CAGGTGCAAA
1151 GCCACCTTAC CCCGGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCG
1201 CATGCTTTTG CTACCGCCGT ACACAGTATT CCCTATGCAT ACCGCTATGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTTCCTT AATAAGAAG
1301 TGCTCAAGCA ACGTCTCTCC CGGTTGATT GGCCGGAAG CGGCAGGCAC
1351 GTATTTGACA GCAGACCGT GGATGCTGCA GCACAAAAG TTGTCTCTCG
1401 TATGCTGATT CAGATGACGG aAcCTTCGGC TGGGGCGGAA GTTATTACCG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1322; ORF 402>:

m402.pep

```

1 MDIVNTKPNT SLIYMXSFLS GLLSLGIEVL WVRMFSFAAQ SVPQAFSFTL
51 ACFLTGI AVG AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAWLLT
101 GFSGFVHHAG IFITLSAVVX XLIFPLVHHV GTDGNKSGRQ VSNVYFAXVA
151 GSALGPVLIG FVILDFLSTQ QIYLLICXIS AAVPLFCTLF QKSLRLNAVS
201 VAVSLMFGIL MFLLPDSVFQ NIADRPDRLI ENKHGIVAVY HRDGDKV VYG
251 ANVYDGAYNT DVFNSVNGIE RAYLLPSLKS GIRRI FV VGL STGSWARVLS
301 AIPEMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRRH
351 PDEKFDLILM NTTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP
401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLKQRLS RLIWPESGRH
451 VFDSSTVDAA AQKVSRMLI QMTEPSAGAE VITDDNMIVE YKYGRGI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 402 shows 97.0% identity over a 497 aa overlap with a predicted ORF (ORF 402.ng) from *N. gonorrhoeae*:

m402/g402

	10	20	30	40	50	60
m402.pep	MDIVNTKPNTSLIYMXSFLSGLLSLGIEVLWVRMFSFAAQSVPAFSTLACFLTGI AVG					
	: : :					
g402	MDMVNTKPNTSVINMLSFLTGLLSLGIEVLWVRMFSFAAQSVPAFSTFILACFLTGI AVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m402.pep	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAWLLTGFSGFVHHAGIFITLSAVVX					
g402	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAWLLTGFSGFVHHAGIFITLSAVVR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m402.pep	XLIFPLVHHVGTGDNKSGRQVSNVYFAXVAGSALGPVLIGFVILDFLSTQQIYLLICXIS					
g402	GLIFPLVHHVGTGDNKSGRQVSNVYFANVAGSALGPVLIGFVILDLLSTQQIYLLICLIS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m402.pep	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY					
g402	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIAGRDRPDRLIENKHGIVAVY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m402.pep	HRDGDKV VYGANVYDGAYNTDVFNSVNGIERAYLLPSLKS GIRRI FV VGLSTGSWARVLS					

726

```

g402      |||||:|||||
          250   260   270   280   290   300
          310   320   330   340   350   360
m402.pep  AIPQMISMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRRHPDEKFDLILM
          |||||:|||||
g402      AIPQMISMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRRHPDEKFDLILM
          310   320   330   340   350   360

          370   380   390   400   410   420
m402.pep  NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV
          |||||:|||||
g402      NSTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV
          370   380   390   400   410   420

          430   440   450   460   470   480
m402.pep  VGSATPVVFPNKELLKQRLSRLIWPESGRHVFDSSSTDAAAQKVVSRLIQMTEPSAGAE
          |||||:|||||
g402      VGSATPVVFPNKELLKQRLSRLIWPESGRHVFDSSSTDAAAQKVVSRLIRMTEPSAGAE
          430   440   450   460   470   480

          490
m402.pep  VITDDNMIVEYKYGRGIX
          |||||
g402      VITDDNMIVEYKYGRGI
          490

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1323>:

```

a402.seq
1  ATGGATATAG TGAACACTAA ACCGAATACT AGTTTGATTT ATATGCTTTC
51  TTTCCTTAGC GGCTTATTGA GCTTGGGTAT AGAAGTCTTG TGGGTAAGGA
101 TGTTTTCGTT CGCAGCACAG TCCGTGCCTC AGGCATTTTC ATTTACTCTT
151 GCCTGTTTTT TGACCGGTAT CGCCGTCGGC GCGTATTTTG GCAAACGGAT
201 TTGCCGCAGC CGCTTTGTTG ATATTCCCTT TATCGGGCAG TGCTTCTTGT
251 GGGCGGGTAT TGCCGACTTT TTGATTTTGG GTGCTGCGTG GTTGTGACG
301 GGTTTTTCG GCTTCGTCCA CCACGCCGGT ATCTTCATTA CCCTGTCTGC
351 CGTCGTCAGA GGGTTGATTT TCCCGCTCGT ACACCATGTG GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTTCCAATG TTTATTTTCG CAACGTTGCC
451 GGCAGTGCAT TGGGTCCGGT CCTTATCGGC TTTGTGATAC TTGATTTCTT
501 GTCCACCCAA CAGATTTACC TGCTCATCTG TTTGATTCTT GCTGCTGTCC
551 CTTTGTTTTG TACACTGTTT CAAAAAAGTC TCCGACTGAA TGCAGTGTCTG
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTCTCTAC TGCCGGATTTC
651 TGTCTTTCAA AATATTGCTG ACCGTCCGGA TAGGCTGATT GAAAAACAAC
701 ACGGCATTGT TCGGTTTAC CATAGAGATG GTGATAAGGT TGTATTATGGG
751 GCGAATGTAT ACGACGGCGC ATACAATACC GATGTATTCA ATAGTGTCAA
801 CGGCATCGAA CGTGCCTATC TGCTACCCTC CCTGAAGTCT GGCATACGCC
851 GCATTTTCGT CGTTGGATTG AGTACAGGTT CGTGGGCGCG CGTCTTGTCT
901 GCCATTCCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
951 CCGTAGCCTT ATCGCGGACG AGCCGCAAAT CGCCCCGCTT TTGCAGGACA
1001 AACGTGTTGA AATTGTATTG GATGACGGTA GGAAATGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTCGACCT GATTTTGATG AATACGACTT GGTACTGGCG
1101 TGCCTATTCC ACCAACCTGT TGAGTGCAGG ATTTTAAAAA CAGGTGCAAA
1151 GCCACCTTAC CCCGGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCG
1201 CATGCTTTTG CTACCGCCGT ACACAGTATT CCCTATGCAT ACCGCTATGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTTCCTT AATAAAGAAC
1301 TGCTCAAGCA ACGTCTCTCC CGGTTGATTT GGCCGGAAG CCGCAGGCAC
1351 GTATTTGACA GCAGCACCGT GGATGCTGCA GCACAAAAGG TTGTCTCTCG
1401 TATGCTGATT CAGATGACGG AACCTTCGGC TGGTGCGGAA GTCATTACCG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1324; ORF 402.a>:

```

a402.pep
1  MDIVNTKPNT SLIYMLSFLS GLLSLGIEVL WVRMFSAAG SVPOAFSFTL

```

```

51 ACFLTGI AVG AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAAWLLT
101 GFSGFVHHAG IFITLSAVVR GLIFPLVHHV GTDGNKSGRQ VSNVYFANVA
151 GSALGPVLIG FVILDFLSTQ QIYLLICLIS AAVPLFCTLF QKSLRLNAVS
201 VAVSLMFGIL MFLLPDSVFQ NIADRPDRLI ENKHGIVAVY HRDGDKVYVG
251 ANVYDGAYNT DVFNSVNGIE RAYLLPSLKS GIRRIFFVGL STGSWARVLS
301 AIPMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRRH
351 PDEKFDLILM NTTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP
401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLQRLS RLIWPESGRH
451 VFDSSTVDAA AQKVSRMLI QMTEPSAGAE VITDDNMIVE YKYGRGI*

```

m402/a402 99.0% identity in 497 aa overlap

	10	20	30	40	50	60
m402.pep	MDIVNTKPNTSLIYMXSFLSGLLSLGLIEVLWVRMFSFAAQSVPAFSTLACFLTGI AVG					
a402	MDIVNTKPNTSLIYMLSFLSGLLSLGLIEVLWVRMFSFAAQSVPAFSTLACFLTGI AVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m402.pep	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVX					
a402	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m402.pep	XLIFPLVHHVGTGDNKSGRQVSNVYFAXVAGSALGPVLIGFVILDFLSTQQIYLLICXIS					
a402	GLIFPLVHHVGTGDNKSGRQVSNVYFANVAGSALGPVLIGFVILDFLSTQQIYLLICLIS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m402.pep	AAVPLFCTLFQKSLRLNAVS VAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY					
a402	AAVPLFCTLFQKSLRLNAVS VAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m402.pep	HRDGDKVYVGANVYDGAYNTDVFNSVNGIERAYLLPSLKS GIRRIFFVGLSTGSWARVLS					
a402	HRDGDKVYVGANVYDGAYNTDVFNSVNGIERAYLLPSLKS GIRRIFFVGLSTGSWARVLS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m402.pep	AIPMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRRHPDEKFDLILM					
a402	AIPMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRRHPDEKFDLILM					
	310	320	330	340	350	360
	370	380	390	400	410	420
m402.pep	NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV					
a402	NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV					
	370	380	390	400	410	420
	430	440	450	460	470	480
m402.pep	VGSATPVVFPNKELLQRLSRLIWPESGRHVFDSSTVDAAAQKVSRMLIQMTEPSAGAE					
a402	VGSATPVVFPNKELLQRLSRLIWPESGRHVFDSSTVDAAAQKVSRMLIQMTEPSAGAE					
	430	440	450	460	470	480
	490					
m402.pep	VITDDNMIVEYKYGRGIX					
a402	VITDDNMIVEYKYGRGIX					
	490					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1325>:

```

g406.seq
  1  ATGCGGGCAC  GGCTGCTGAT  ACCTATTCTT  TTTTCAGTTT  TTATTTTATC
 51  CGCCTGCGGG  AACTGACAG  GTATTCCATC  GCATGGCGGA  GGCAAACGCT
101  TCGCGGTCGA  ACAAGAACTT  GTGGCCGCTT  CTGCCAGAGC  TGCCGTTAAA
151  GACATGGATT  TACAGGCATT  ACACGGACGA  AAAGTTGCAT  TGTACATTGC
201  AACTATGGGC  GACCAAGGTT  CAGGCAGTTT  GACAGGGGGT  CGCTACTCCA
251  TTGATGCACT  GATTGCGGCG  GAATACATAA  ACAGCCCTGC  CGTCCGCACC
301  GATTACACCT  ATCCGCGTTA  CGAAACCACC  GCTGAAACAA  CATCAGGCGG
351  TTTGACGGGT  TTAACCACTT  CTTTATCTAC  ACTTAATGCC  CCTGCACTCT
401  CGCGCACCCA  ATCAGACGGT  AGCGGAAGTA  GGAGCAGTCT  GGGCTTAAAT
451  ATTGGCGGGA  TGGGGGATTA  TCGAAATGAA  ACCTTGACGA  CCAACCCGCG
501  CGACACTGCC  TTTCTTTCCC  ACTTGGTGCA  GACCGTATTT  TTCCTGCGCG
551  GCATAGACGT  TGTTTCTCCT  GCCAATGCCG  ATACAGATGT  GTTTATTAAC
601  ATCGACGTAT  TCGGAACGAT  ACGCAACAGA  ACCGAAATGC  ACCTATACAA
651  TGCCGAAACA  CTGAAAGCCC  AAACAAACT  GGAATATTTT  GCAGTAGACA
701  GAACCAATAA  AAAATTGCTC  ATCAAACCCA  AAACCAATGC  GTTTGAAGCT
751  GCCTATAAAG  AAAATTACGC  ATTGTGGATG  GGGCCGTATA  AAGTAAGCAA
801  AGGAATCAAA  CCGACGGAAG  GATTGATGGT  CGATTTCTCC  GATATCCAAC
851  CATACGGCAA  TCATACGGGT  AACTCCGCCC  CATCCGTAGA  GGCTGATAAC
901  AGTCATGAGG  GGTATGGATA  CAGCGATGAA  GCAGTGCGAC  AACATAGACA
951  AGGGCAACCT  TGA

```

This corresponds to the amino acid sequence <SEQ ID 1326; ORF 406>:

```

g406.pep
  1  MRARLLIPIL  FSVFILSACG  TLTGIPSHGG  GKRFAVEQEL  VAASARAAVK
 51  DMDLQALHGR  KVALYIATMG  DQSGSLTGG  RYSIDALIRG  EYINSPAVRT
101  DYTYPRIYET  AETTSGLTGT  LTSLSTLNA  PALSRTQSDG  SGSRSSLGLN
151  IGGMGDYRNE  TLTTNPRDTA  FLSHLVQTVF  FLRGIDVVSP  ANADTDVFIN
201  IDVFGTIRNR  TEMHLYNAET  LKAQTKLEYF  AVDRTNKKLL  IKPKTNAFEA
251  AYKENYALWM  GPYKVSIGIK  PTEGLMVDPS  DIQPYGNHTG  NSAPSVEADN
301  SHEGYGYSDE  AVRQHRQGP  *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1327>:

```

m406.seq
  1  ATGCAAGCAC  GGCTGCTGAT  ACCTATTCTT  TTTTCAGTTT  TTATTTTATC
 51  CGCCTGCGGG  AACTGACAG  GTATTCCATC  GCATGGCGGA  GGTAAACGCT
101  TTGCGGTCGA  ACAAGAACTT  GTGGCCGCTT  CTGCCAGAGC  TGCCGTTAAA
151  GACATGGATT  TACAGGCATT  ACACGGACGA  AAAGTTGCAT  TGTACATTGC
201  CACTATGGGC  GACCAAGGTT  CAGGCAGTTT  GACAGGGGGT  CGCTACTCCA
251  TTGATGCACT  GATTGCGGCG  GAATACATAA  ACAGCCCTGC  CGTCCGTACC
301  GATTACACCT  ATCCACGTTA  CGAAACCACC  GCTGAAACAA  CATCAGGCGG
351  TTTGACAGGT  TTAACCACTT  CTTTATCTAC  ACTTAATGCC  CCTGCACTCT
401  CTCGCACCCA  ATCAGACGGT  AGCGGAAGTA  AAAGCAGTCT  GGGCTTAAAT
451  ATTGGCGGGA  TGGGGGATTA  TCGAAATGAA  ACCTTGACGA  CTAACCCGCG
501  CGACACTGCC  TTTCTTTCCC  ACTTGGTACA  GACCGTATTT  TTCCTGCGCG
551  GCATAGACGT  TGTTTCTCCT  GCCAATGCCG  ATACAGATGT  GTTTATTAAC
601  ATCGACGTAT  TCGGAACGAT  ACGCAACAGA  ACCGAAATGC  ACCTATACAA
651  TGCCGAAACA  CTGAAAGCCC  AAACAAACT  GGAATATTTT  GCAGTAGACA
701  GAACCAATAA  AAAATTGCTC  ATCAAACCAA  AAACCAATGC  GTTTGAAGCT
751  GCCTATAAAG  AAAATTACGC  ATTGTGGATG  GGGCCGTATA  AAGTAAGCAA
801  AGGAATTAAG  CCGACGGAAG  GATTAATGGT  CGATTTCTCC  GATATCCGAC
851  CATACGGCAA  TCATACGGGT  AACTCCGCCC  CATCCGTAGA  GGCTGATAAC
901  AGTCATGAGG  GGTATGGATA  CAGCGATGAA  GTAGTGCGAC  AACATAGACA
951  AGGACAACCT  TGA

```

This corresponds to the amino acid sequence <SEQ ID 1328; ORF 406>:

```

m406.pep
  1  MQARLLIPIL  FSVFILSACG  TLTGIPSHGG  GKRFAVEQEL  VAASARAAVK

```



```

51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPRYETT AETTSGGLTG LTTSLSTLNA PALSRTQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVS KGIK PTEGLMVDFS DIRPYGNHTG NSAPSVEADN
301 SHEGYGYSDE VVRQHRQGPX *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 406 shows 98.8% identity over a 320 aa overlap with a predicted ORF (ORF406.a) from *N. gonorrhoeae*:

g406/m406

	10	20	30	40	50	60
g406 . pep	MRARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARA AVKDMDLQALHGR					
	:					
m406	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARA AVKDMDLQALHGR					
	10	20	30	40	50	60
	70	80	90	100	110	120
g406 . pep	KVALYIATMGDQSGSLTGG RYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGGLTG					
m406	KVALYIATMGDQSGSLTGG RYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGGLTG					
	70	80	90	100	110	120
	130	140	150	160	170	180
g406 . pep	LTTSLSTLNAPALSRTQSDGSGSRSSLGLNIGGMGDYRNETLTNPRDTAFLSHLVQTVF					
m406	LTTSLSTLNAPALSRTQSDGSGSKSSLGLNIGGMGDYRNETLTNPRDTAFLSHLVQTVF					
	130	140	150	160	170	180
	190	200	210	220	230	240
g406 . pep	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
m406	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	190	200	210	220	230	240
	250	260	270	280	290	300
g406 . pep	IKPKTNAFEAAAYKENYALWMGPYKVS KGIK PTEGLMVDFS DIQPYGNHTGNSAPSVEADN					
m406	IKPKTNAFEAAAYKENYALWMGPYKVS KGIK PTEGLMVDFS DIRPYGNHTGNSAPSVEADN					
	250	260	270	280	290	300
	310	320				
g406 . pep	SHEGYGYSDEAVRQHRQGPX					
m406	SHEGYGYSDEVVRQHRQGPX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1329>:

a406 . seq

```

1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGTAAACGCT
101 TCGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTCGTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTGACAGGT TTAACCACTT CTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG

```

730

```

501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTCCTCCT GCCAATGCCG ATACGGATGT GTTTATTAAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAACT GGAATATTTC GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGACCGTATA AAGTAAGCAA
801 AGGAATTAAA CCGACAGAAG GATTAATGGT CGATTCTCC GATATCCAAC
851 CATACGGCAA TCATATGGGT AACTCTGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCAC GACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1330; ORF 406.a>:

```

a406.pep
1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFQVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPRYETT AETTSAGGLTG LTSSLSTLNA PALSRTQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSIGIK PTEGLMVDFFS DIQPYGNHMG NSAPSVEADN
301 SHEGYGYSDE AVRRHRQGP *

m406/a406 98.8% identity in 320 aa overlap

              10      20      30      40      50      60
m406.pep      MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFQVEQELVAASARAAVKDMDLQALHGR
              |||
a406           MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFQVEQELVAASARAAVKDMDLQALHGR
              10      20      30      40      50      60

              70      80      90      100     110     120
m406.pep      KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSAGGLTG
              |||
a406           KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSAGGLTG
              70      80      90      100     110     120

              130     140     150     160     170     180
m406.pep      LTSSLSTLNAPALSRTQSDGSGSKSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF
              |||
a406           LTSSLSTLNAPALSRTQSDGSGSKSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF
              130     140     150     160     170     180

              190     200     210     220     230     240
m406.pep      FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL
              |||
a406           FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL
              190     200     210     220     230     240

              250     260     270     280     290     300
m406.pep      IKPKTNAFEAAAYKENYALWMGPYKVSIGIKPTEGLMVDFFS DIRPYGNHTGNSAPSVEADN
              |||
a406           IKPKTNAFEAAAYKENYALWMGPYKVSIGIKPTEGLMVDFFS DIQPYGNHMGNSAPSVEADN
              250     260     270     280     290     300

              310     320
m406.pep      SHEGYGYSDEVVRQHRQGPX
              |||
a406           SHEGYGYSDEAVRRHRQGPX
              310     320

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1331>:

```

g501.seq
1  atggctcggac ggaccttgac cgcagatacc gacatatttg ttctgcttgc,
51  ggcaggcgga gatggcaaga tgcagcatca ctttgacggc aggggttgct

```

```

101  tcgtcaaacg attcggacac caagccgctg tctcggtcga ggccgaggggt
151  cagctgggtc atgtcgttcg agccgatgga gaagccgtcg aagtattgca
201  ggaattgttc cgccaatacc gcgttgctcg gcagctcgca catcataatc
251  aggcgcaggc cgtttttgcc gcgttccaag ccgttttctt tcaatgcctt
301  aaccactgct tcggcttcgc ccaaagtgcg gacgaacgga atcatgattt
351  cgacgttggt cagaccattt tcgtcacgaa cgcgtttcaa ggctttgcat
401  tccaaggcga aacagtcttt gaagctctcg gcaacataac gcgccgcacc
451  acggaagccc aacatcgggt tttcttcatt cggttcgtat acgtgccgc
501  cgaccagggt ggcgatttcg ttggatttga agtcggacat acggacgatg
551  gttttacgcg gataaaccga tgcggcaagc gttgccacgc cttcggcgat
601  tttatcgacg tagaagtcga caggggatgc gtaaccggcg atgcggcgga
651  taatttccgc tttcagttcg tcgtcttggt tgtcaaattc caacaaggct
701  ttcgggtgga tgccgatttg gcggttgatg ataaattcca tacgcgccaa
751  gccgatgcct tcgctgggca gattggcgaa gctgaatgcg agttcgggat
801  tgccgacggt catcatgact ttgacgggtg cttttggcat attgtccaag
851  gcgacatcgg taatttgtac gtccagcagg ccggcataga taaagccgggt
901  atcgcccttc gcacaggata cggtaacttc ctgaccgttt tccaagagtt
951  cggtcgcatt gccgcagccg acgacggcag gaatacccag ttcgcgcgcg
1001 atgatggcgg cgtggcagggt gcgtccgccg cggttggtca cgatggcgga
1051 agcacgtttc atcacgggtt cccaatccgg atcggtcatt tcggtaacca
1101 gtacgtcgcc ggcttcgacg gaatccatct cggaagcatt ttaatacagg
1151 cgcaccttgc cctgaccgac tttttgaccg atggcacgac cttcgacaaa
1201 gacggttttt tcgccgttga tggcgtagcg gcgcagggtg cggctgcctt
1251 cttcttgga tttgacggtt tcggggcggg cttgcaggat gtagagtttg
1301 ccgtccaggc cgtcgcgtcc ccattcgata tccatcgggc ggccgtagtg
1351 tttttcgatg gtcagcgctg agtgtgcaa ctcggtgatt tcttcgtcgg
1401 taatggagaa gcggttgccg tcttcttcgg ggacttcgac gttggttacc
1451 gatttgccgg cttcggcttt gtcggtgaaa atcattttga tgtgtttcga
1501 acccatggtc ttgcgcagga tggcggttt gcctgctttg agcgtgggtt
1551 tgaacacata aaattcgtcc gggttgaccg cgccttgtag gacgttttcg
1601 cccagaccgt aagaggaggt aacaaagacg acttggttgt agccggattc
1651 ggtgtcgagg gtgaacatca cacctga

```

This corresponds to the amino acid sequence <SEQ ID 1332; ORF 501.ng>:

```

g501.pep
1  MVGRTLTA DT DIFVLLAAGG DGKMQHHFDG RFAFVKRFGH QAAVSVEAEG
51  QLGHVVRA DG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQCL
101 NHCFGFAQ SA DERNHDFDVG QTHFVTNAFQ GFAFQGETVF EALGNITRRT
151 TEAQHRVFF M RFVYAAADQV GVFGFVGVGH TDDGFTRINR CGKRCHAFGD
201 FIDVEVDRC G VTGDAADNFR FQFVVLVFKF QQGFRVDADL AVDDKFHTRQ
251 ADAFAGQIG E AECEFGIADV HHDFDGCFWH IVQGDIGNLY VQQAGIDKAG
301 IAFGTGYGN F LTVFQEFGR I AAADDGRNTQ FARDDGGVAG ASAAVGHDDG
351 STFHHGFPI R IGHVGNQYVA GFDGIHLGSI FNQAHLALTD FLTDGTTFAQ
401 DGFFAVDGA A AQVAAFFLG FDGFGAGLQD VEFVQAVAS PFDIHRAAVV
451 FFDGQRVVC Q LGDFFVGNGE AVAVFFGDFD VGYRFAGFGF VGENHFDVFR
501 THGLAQDGG F ACFERGF EHI KFVRVDRALY DVFAQTVRGG NKDDL VVAGF
551 GVEGEHHT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1333>:

```

m501.seq
1  atggtcggac sggccttgac cgcagatgcc gacatatttg ttctgcttgc
51  ggaggcgga gatggcaagg tgcagcatca ctttgacggc agggttgcgt
101 tcgtcaaacg attcggatac caagccgctg tcgcggtcga gaccgaggggt
151 cagttgggtc atgtcgttcg agccgatgga gaagccgtcg aagtattgca
201 ggaattgttc cgccaatacc gcgttgctcg gcagctcgca catcataatc
251 aggcgcaggc cgtttttgcc gcgttccaag ccgttttctt tcagggtctt
301 gacaacggmt tcggcttcgc ccaaagtgcg gacgaacgga atcatgattt
351 caacgttggy caacccattt tcatcgcgga cgcgtttcaa ggctttgcat
401 tccaaggcga aacagtcttt gaagttgtcg gcgacataac gcgccgcacc
451 acggaagccc aacatcgggt tttcttcatt cggttcgtat acgttgccgc
501 cgaccagggt ggcgatttcg ttggatttga agtcggacat acggacgatg
551 gttttacgcg gataaaccga tgcggccaat gtcgccacgc cttcggcgat
601 tttatcgacg tagaagtcga caggggacgc gtaaccggcg atacggcggg
651 taatttccgc ttttaattcg tcgtcttggt tgtcaaattc caacaargct

```

732

```

701 ttggggtgga taccgatttg gcggttgatg ataaattcca tacgcgccaa
751 gccgatgcct tcgctgggca ggttggcgaa gctgaatgcg agttcgggat
801 tgccgacggt catcatgact ttacaggtg ctttaggcac attgtctaag
851 gcgacatcgg taatctgtac gtccaacaga ccggcataga taaagccggt
901 atcgcccttc gcacaggata cggttaactt ttgaccgttt ttcagcaatt
951 cgggtgcatt gccgcagccg acaacggcag gaatgcccaa ttcacgcgcg
1001 atgatggcgg cgtggcaggt acggccgccg cggttggtaa cgatggcaga
1051 agcacgtttc atcacgggtt cccaatccgg atcggtcatg tcggtaacga
1101 gtacgtcgcc ggcttcgacg gaatccatct cggaagcatc tttaatcagg
1151 cgcaccttgc cctgaccgac tttctgaccg atggcgcggc cttcgcataa
1201 tacggttttg tcgccgttga tggcgaagcg gcgcagggtg cggttgccct
1251 cttcttgagg ttttacggtt tcgggacggg cttgcaggat gtagagtttg
1301 ccgtccaagc cgtcgcgctc ccattcgata tccatcgggc ggccgtagtg
1351 tttttcgatg gtcagtgcgt aatgcgccaa cttagtaatt tcttcgtcgg
1401 taatggagaa gcggttgccg tcttcctcgg ggacatcgac gttggttacg
1451 gatttaccgg cttctgcttt gtcggtaaaa atcattttga tgtgtttga
1501 acccatggtt ttacgcagga tggcgggctt gcccgtyttg agcgtgggtt
1551 tgaacacatr aaattcgctc gggttgaccg caccttgtag gacgttttcg
1601 cccagaccgt aagaggaggt acaaaagacg acytgatcgt akccggattc
1651 ggtgtcgagg gtgaacatca cacctga

```

This corresponds to the amino acid sequence <SEQ ID 1334; ORF 501>:

```

m501.pep
1  MVGXALTADA DIFVLLAAGG DGKVQHFDG RFAFVKRFGY QAAVAVETEG
51  QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQGF
101 DNGFGFAQSA DERNHDFNVG QPHFIADAFQ GFAFQGETVF EVVGDITRRT
151 TEAQHRVFFM RFVYVAADQV GVFVGFEVGH TDDGFTRINR CGQCRHAFGD
201 FIDVEVDRGR VTGDTAGNFR FXFVVLVVKF QXFGVDTDL AVDDKFHTRO
251 ADAFAGQVGE AECEFGIADV HHDFYRCFRH IVXGDIGNLY VQQTGIDKAG
301 IAFGTGYGNF LTVFQQFGCI AAADNGRNAQ FTRDDGGVAG TAAAVGNDRG
351 STFHHGFPIR IGHVNEYVA GFDGIHLGSI FNQAHALTD FLTDGAFAFX
401 YGFVAVDGEA AQVAVALFLG FYGFGTGLQD VEFVQAVAS PFDIHRAAVV
451 FFDGQCVMRQ LSNFFVNGE AVAVFLGDI VGYGFTGFCF VGKNHFDVFX
501 THGFTQDGLL ARFERGFEXH KFRVVDRTLY DVFAQTVRGG NKDDLIVXGF
551 GVEGEHHT*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 501 shows 86.2% identity over a 558 aa overlap with a predicted ORF (ORF 501.ng) from *N. gonorrhoeae*:

m501/g501

```

              10      20      30      40      50      60
m501.pep      MVGXALTADADIFVLLAAGGDGKVQHFDGRFAFVKRFGYQAAVAVETEGQLGHVVRADG
              ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g501           MVGRTLTAADTDIFVLLAAGGDGKMQHFDGRFAFVKRFGHQAASVEAEGQLGHVVRADG
              10      20      30      40      50      60

              70      80      90      100     110     120
m501.pep      EAVEVLQELFRQYRVARQLAHHNQAQAVFAAFQAVFFQGFQDNGFGFAQSADERNHDFNVG
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g501           EAVEVLQELFRQYRVARQLAHHNQAQAVFAAFQAVFFQCLNHCFGFAQSADERNHDFDVG
              70      80      90      100     110     120

              130     140     150     160     170     180
m501.pep      QPHFIADAFQGFQAFQGETVFEVVDITRRTTEAQHRVFFMRVYVAADQVGVFVGFEVGH
              | ||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||
g501           QTHFVTNAFQGFQAFQGETVFEALGNITRRTTEAQHRVFFMRVYVAADQVGVFVGFEVGH
              130     140     150     160     170     180

              190     200     210     220     230     240
m501.pep      TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVVKFQXFGVDTDL
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

733

g501	TDDGFTRINRCGKRCHAFGDFIDVEVDRGCVTGDAADNFRFQFVVLFVKFQQGFRVDADL
	190 200 210 220 230 240
m501.pep	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFYRCFRHIVXGDIIGNLYVQQTGIDKAG
	250 260 270 280 290 300
g501	AVDDKFHTRQADAFAGQIGAECEFGIADVHHDFDGCFWHIVQGDIGNLYVQQAGIDKAG
	250 260 270 280 290 300
m501.pep	IAFGTGYGNFLTTFVQQFGCIAAADNGRNAQFTRDDGGVAGTAAVGNDRSTFHHGFPPIR
	310 320 330 340 350 360
g501	IAFGTGYGNFLTTFVQEFGRIAAADNGRNTQFARDDGGVAGASAAVGHGDSSTFHHGFPPIR
	310 320 330 340 350 360
m501.pep	IGHVGNQYVAGFDGIHLGSI FNQAHALALTDFLTDGAFAFYGFVAVDGEAAQVAVALFLG
	370 380 390 400 410 420
g501	IGHVGNQYVAGFDGIHLGSI FNQAHALALTDFLTDGTTFAQDGFFAVDGVAAQVAALFLG
	370 380 390 400 410 420
m501.pep	FYGFGLQDVEFAVQAVASPFDIHRAAVVFFDQCVMRQLSNFFVNGEAVAVFLGDID
	430 440 450 460 470 480
g501	FDGFGAGLQDVEFAVQAVASPFDIHRAAVVFFDQQRVVCQLGDDFFVNGEAVAVFFGDFD
	430 440 450 460 470 480
m501.pep	VGYGFTGFVGVGNHFDVFXTHGFTQDGLARFERGFEXHKKFVRVDRTLVDVFAQTVRGG
	490 500 510 520 530 540
g501	VGYRFAGFGFVGENHFDVFRTHGLAQDGGFACFERGFEXHKKFVRVDRALYDVFAQTVRGG
	490 500 510 520 530 540
m501.pep	NKDDLIVXGFGVEGEHHT
	550
g501	NKDDLIVVAGFGVEGEHHT
	550

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1335>:

a501.seq	(partial)
1	ATGGTCGGAC GGGCCTTGAC CGCAGATGCC GACATATTTG TTCTGCTTGC
51	GGCAGGCGGA GATGGCAAGG TGCAGCATCA CTTTGACGGC AGGGTTGCGT
101	TCGTCAAACG ATTCGGATAC CAAGCCGCTG TCGCGGTCGA GACCGAGGGT
151	CAGTTGGGTC ATGTCGTTTC AGCCGATGGA GAAGCCGTCG AAGTATTGCA
201	GGAATTGTTC CGCCAATACC GCGTTGCTCG GCAGCTCGCA CATCATAAATC
251	AGGCGCAGGC CGTTTTTGCC GCGTTCCAAG CCGTTTTCTT TCAGGGCTTT
301	GACAACGGCT TCGGCTTCGC CCAAAGTGCG GACGAACGGA ATCATGATTT
351	CAACGTTGGT CAACCCCATC TCATCGCGGA CGCGTTTCAA GGCTTTGCAT
401	TCCAAGGCGA AACAGTCTTT GAAGTTGTCG GCGACATAAC GCGCCGACCC
451	ACGGAAGCCC AACATCGGGT TTTCTTCATG CCGTTTCGTAT ACGTTGCCGC
501	CGACCAGGTT GCGGTATTCG TTGGATTTGA AGTCGGACAT ACGGACGATG
551	GTTTTACGCG GATAAACCAG TGCGGCCAAT GTCGCCACGC CTTCGGCGAT
601	TTTATCGACG TAGAAGTCGA CAGGGGACGC GTAACCGGCG ATACGGCGGG
651	TAATTTCCGC TTTTAATTTC TCGCTTGTTT TGTCAAATTC CAACAAGGCT
701	TTGGGGTGGT TACCGATTTG GCGGTTGATG ATAAATTCCA TACGCGCCAA
751	GCCGATGCCT TCGCTGGGCA GGTGCGGAA GCTGAATGCG AGTTCGGGAT
801	TGCCGACGTT CATCATGACT TTTACAGGTG CTTTAGGCAT GTTGTCCTAA
851	GCAACATCGG TAATTTGTAC GTCCAGCAGG CCGGAGTAGA TGAAGCCGGT
901	ATCGCCTTCG GCACAGGATA CGGTAACCTC TTGACCGTTT TTCAGCAATT
951	CGGTTGCATT GCCGACGCCG ACAACGGCAG GAATACCCAG TTCGCGCGCG

```

1001 ATGATGGCGG CGTGGCAGGT ACGTCCGCCC CTGTTGGTCA CGATGGCGGA
1051 AGCGCGTTTC ATCACCAGGT CCCAATCTGG GTCGGTCATG TCGGTAACCA
1101 GTACGTCGCC GGCTTCGACG GAATCCATCT CGGAAGCATC TTTAATCAGG
1151 CGTACCTTGC CCTGACCGAC TTTCTGACCG ATGGCGCGGC CTTTCGCACAA
1201 GACGGTTTTT TCGCCGTTGA TAGAAAAGCG GCGCAGGTTG CGGCTGCCTT
1251 CTTCTGCGGA TTTGACGGTT TCGGGACGGG CTTGCAGGAT GTAGAGTTTG
1301 CCGTCCAAGC CGTCGCGTCC CCATTTCGATG TCCATCGGGC GGCCGTAGTG
1351 TTTTTCGATG GTCAGTTCGT AATGCGCCAA CTCGGTGATT TCTTCGTCGG
1401 TAATGGAGAA GCGGTTGCGG TCTTCTTCGG GGACATCGAC GTTGGTTACC
1451 GATTTGCCGG CTTCTGCTTT GTCGGTAAAA ATCATTTTGA TGTGTTTTGA
1501 GCCCATGGTT TTGCGCAGGA TGGCAGGTTT GCCTGCTTTC AGCGTGGGTT
1551 TGAACACATA GAATTCGTCG GGATTGACTG CGCCTTGAC GACGTTTTCG
1601 CCCAGACCGT AGGATGAAGT GACAAAGACG ACTTGTCGT AACCGGATTC
1651 GGTATCGAGG GTGAACATCA C

```

This corresponds to the amino acid sequence <SEQ ID 1336; ORF 501.a>:

a501.pep

```

1 MVGRALTADA DIFVLLAAGG DGKVQHFDG RFAFVKRFGY QAAVAVETEG
51 QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQGF
101 DNGFGFAQSA DERNHDFNVG QPHFIADAFQ GFAFQGETVF EVVGDITRRT
151 TEAQHRVFFM RFVYVAADQV GVFGFVEVGH TDDGFTRINR CGQCRHAFGD
201 FIDVEVDRGR VTGDTAGNFR F*FVVLVVKF QQGFVVDL AVDDKFHTRQ
251 ADAFAGQVGE AECEFGIADV HHDFFRCFRH VVQSNIGNLY VQAGVDEAG
301 IAFGTGYGNF LTVFQQFGCI AAADNGRNTQ FARDDGGVAG TSAPVGHG
351 SAFHHRFPIW VGHVGNQYVA GFDGIHLGSI FNQAYLALTD FLTDGAAFAQ
401 DGFFAVDRKA AQVAAFFLG FDGFGTGLQD VEFVAVAVAS PFDVHRAAVV
451 FFDGQCVMRQ LGDFFVGNGE AVAVFFGDID VGYRFAGFCF VGKNHFDVF*
501 AHGFAQDGRF ACFQRGFEHI EFVGIDCALY DVFAQTVG*S DKDDLVTGTF
551 GIEGEHH

```

m501/a501 90.3% identity in 557 aa overlap

	10	20	30	40	50	60
m501.pep	MVGXALTADADIFVLLAAGGDGKVQHFDGRVAFVKRFGYQAAVAVETEGQLGHVVRADG					
a501	MVGRALTADADIFVLLAAGGDGKVQHFDGRVAFVKRFGYQAAVAVETEGQLGHVVRADG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m501.pep	EAVEVLQELFRQYRVARQLAHNQAQAVFAAFQAVFFQGFQDNGFGFAQSADERNHDFNVG					
a501	EAVEVLQELFRQYRVARQLAHNQAQAVFAAFQAVFFQGFQDNGFGFAQSADERNHDFNVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m501.pep	QPHFIADAFQGFQGETVFEVVDITRRTTEAQHRVFFMRVYVAADQVGVFGFVEVGH					
a501	QPHFIADAFQGFQGETVFEVVDITRRTTEAQHRVFFMRVYVAADQVGVFGFVEVGH					
	130	140	150	160	170	180
	190	200	210	220	230	240
m501.pep	TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVVKFQQXFGVDTDL					
a501	TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVVKFQQGFGVDTDL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m501.pep	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFYRCFRHVVQSNIGNLYVQQTGIDKAG					
a501	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFYRCFRHVVQSNIGNLYVQAGVDEAG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m501.pep	IAFGTGYGNFLTTFVQQFGCIAAADNGRNTQFARDDGGVAGTAAAVGNDGRSTFHGGFPIR					
a501	IAFGTGYGNFLTTFVQQFGCIAAADNGRNTQFARDDGGVAGTSAPVGHGGSFAFHHRFPIW					
	310	320	330	340	350	360

735

	370	380	390	400	410	420
m501.pep	IGHVGN EYVAGFDGIHLGSI FNQAH LALTDFLTDGA AFAXYGFVA VDGEAAQVAV ALFLG					
a501	VGHVGNQYVAGFDGIHLGSI FNQAYLALTDFLTDGA AFADGFFAVDRKAAQVAAFFLG					
	370	380	390	400	410	420
m501.pep	FYGFGTGLQDVEFAVQAVASPFDIHRAAVVFFDGCVMRQLSNFFVGNGEAVAVFLGDID					
a501	FDGFGTGLQDVEFAVQAVASPFDVHRAAVVFFDGCVMRQLGDFVGNGEAVAVFFGDID					
	430	440	450	460	470	480
m501.pep	VGYGFTGFCFVGK NHFVFXTHGFTQDGLARFERGF EHXKFVRVDR TLYDVFAQTVRGG					
a501	VGYRFAGFCFVGK NHFVFXAHGFAQDGRFACFQRGF EHFVGI DCALYDVFAQTVGXS					
	490	500	510	520	530	540
m501.pep	NKDDLIVXGFGVGEHHTX					
a501	DKDDLVTGFGIEGEHH					
	550	559				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1337>:

```

g502.seq
1  atgatgaaac cgcacaacct gttccaattc ctgcccgttt gtcacctgac
51  cgtcgccgtc gttccgcac aggcgggcgc ggtggacgcg ctcaagcaat
101 tcaacaacga tgccgacggt atcagcgcca gcttcaccca aaccgtccaa
151 agcaaaaaga aaaccctaac cgcgcacggc acgttcaaaa tcttgcgccc
201 gggcctcttc aaatgggaat acactttgcc ctacagacag actattgtcg
251 gcgacggtca aaccgtttgg ctctacgatg ttgatttggc acaagtgacc
301 aagtcgtccc aagaccaggc catcgcgggc agccccgcgc ccatcctgtc
351 gaacaaaacc gccctcgaaa gcagttacac gctgaaagag gacggttcgt
401 ccaacggcat cgattatgtg cggggcgaac ccaaacgca acaacgcgcg
451 ctaccaatac atccgcacgc gttcctaaag cggcaacctc gccgccatgc
501 agcttaa

```

This corresponds to the amino acid sequence <SEQ ID 1338; ORF 502.ng>:

```

g502.pep
1  MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQTQVQ
51  SKKKTQTAHG TFKILRPGLF KWEYTLPLYRQ TIVGDGQTVW LYDVDLAQVT
101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV RGNAQTQRRR
151 LPIHPHRLQR RQPRRHAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1339>:

```

m502.seq
1  atgatgaaac cgcacaacct gttccaattc ctgcccgttt gtcacctgac
51  cgtcgccgtc gttccgcac aggcgggcgc ggtagacgcg cttaagcaat
101 tcaacaacga tgccgacggt atcagcgcca gcttcaccca amccgtccaa
151 wgcaaaaaga aaaccctaac cgcgcacggc acgttcaaaa tcttgcgacc
201 gggccttttc aaatgggaat acacaaact t.acaggcaa accatcgctc
251 gcgacggtca aacygtttgg ctmtacgatg tygatctggc acaagtgacc
301 aagtcgtccc aagaccaggc cataggcgsc agccccgcgc ccatcctgtc
351 gaacaaarcc gccctcgaaa gcagctacac gctgaaagag gacggttcgt
401 ccaacggcat cgattatgtg ggcaacgccc aaacgcaaca acgccggcta
451 ccaatacatc cgcacggtc tcaaaggcgc caacctcgcc gccatgcagc
501 tyaa

```

This corresponds to the amino acid sequence <SEQ ID 1340; ORF 502.ng>:

```

m502.pep
1  MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQXVQ
51  XKKKTQTAHG TFKILRPGLF KWEYTKLYRQ TIVGDGQTVW LYDVDLAQVT
101 KSSQDQAIGX SPAAILSNKX ALESSYTLKE DGSSNGIDYV GNAQTQRRR
151 PIHPHRLQRR QPRRHAA

```

736

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 502 shows 95.8% identity over a 168 aa overlap with a predicted ORF (ORF 502.ng) from *N. gonorrhoeae*:

m502/g502

	10	20	30	40	50	60
m502.pep	MMKPHNLFQFLAVCSLT	TVAVASQAQAGAVDALKQFNNDADG	ISGSFTQXVQXKKKTQTAHG			
g502	MMKPHNLFQFLAVCSLT	TVAVASQAQAGAVDALKQFNNDADG	ISGSFTQTVQSKKKTQTAHG			
	10	20	30	40	50	60
	70	80	90	100	110	120
m502.pep	TFKILRPGLFKWEYTKLYRQTIVGDGQTVWLYD	VDLAQVTKSSQDQAIGXSPAAILSNKX				
g502	TFKILRPGLFKWEYTL	PYRQTIVGDGQTVWLYD	VDLAQVTKSSQDQAIGGSPAAILSNKT			
	70	80	90	100	110	120
	130	140	150	160		
m502.pep	ALESSYTLKEDGSSNGIDYV-GNAQTQQRRLPIHPHRLQRRQPRRHAA					
g502	ALESSYTLKEDGSSNGIDYVRGNAQTQQRRLPIHPHRLQRRQPRRHAA					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1341>:

a502.seq

1	ATGATGAAAC	CGCACAACT	GTTCCAATTC	CTCGCCGTTT	GCTCCCTGAC
51	CGTCTCCGTC	GCTTCCGCAC	AGGCGGGCGC	GGTGGACGCG	CTCAAGCAAT
101	TCAACAACGA	TGCCGACGGT	ATCAGCGGCA	GCTTCACCCA	AACCGTCCAA
151	AGCAAAAAGA	AAACCCAAAC	CGCGCACGGC	ACGTTCAAAA	TCCTGCGCCC
201	GGGCCTCTTT	AAATGGGAAT	ACACTTCGCC	TTACAAACAG	ACTATTGTGC
251	GCGACGGTCA	AACCGTTTGG	CTCTACGATG	TCGATTGGC	ACAAAGTGACC
301	AAGTCGTCCC	AAGACCAGGC	CATAGGCGGC	AGCCCCGCCG	CCATCCTGTC
351	GAACAAAACC	GCCCTCGAAA	GCAGCTACAC	GCTGAAAGAG	GACGGTTCGT
401	CCAACGGCAT	CGATTATGTG	GGCAACGCCC	AAACGCAACA	ACGCCGGCTA
451	CCAATACATC	CGCATCGGCT	TCAAAGGCGG	CAACCTCGCC	GCCATGCAGC
501	TTAA				

This corresponds to the amino acid sequence <SEQ ID 1342; 502 217.a>:

a502.pep

1	MMKPHNLFQF	LAVCSLTVSV	ASAQAGAVDA	LKQFNNDADG	ISGSFTQTVQ
51	SKKKTQTAHG	TFKILRPGLF	KWEYTSFYKQ	TIVGDGQTVW	LYDVLDAQVT
101	KSSQDQAIGG	SPAAILSNKT	ALESSYTLKE	DGSSNGIDYV	GNAQTQQRRL
151	PIHPHRLQRR	QPRRHAA*			

m502/a502 95.2% identity in 167 aa overlap

	10	20	30	40	50	60
m502.pep	MMKPHNLFQFLAVCSLT	TVAVASQAQAGAVDALKQFNNDADG	ISGSFTQXVQXKKKTQTAHG			
a502	MMKPHNLFQFLAVCSLT	TVSVASQAQAGAVDALKQFNNDADG	ISGSFTQTVQSKKKTQTAHG			
	10	20	30	40	50	60
	70	80	90	100	110	120
m502.pep	TFKILRPGLFKWEYTKLYRQTIVGDGQTVWLYD	VDLAQVTKSSQDQAIGXSPAAILSNKX				
a502	TFKILRPGLFKWEYTSFYKQTIVGDGQTVWLYD	VDLAQVTKSSQDQAIGGSPAAILSNKT				
	70	80	90	100	110	120
	130	140	150	160		
m502.pep	ALESSYTLKEDGSSNGIDYVGNAQTQQRRLPIHPHRLQRRQPRRHAA					
a502	ALESSYTLKEDGSSNGIDYVGNAQTQQRRLPIHPHRLQRRQPRRHAA					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1343>:

g502-1.seq

```

1  ATGATGAAAc  cgcaCaacct  gttccaaTtc  CTCGCCGTTT  GCTCCCTGAC
51  CGTCGCCGTC  GCTTCCGCAC  AGGCGGGCGC  GGTGGACGCG  CTCAGCAAT
101 TCAACAACGA  TGCCGACGGT  ATCAGCGGCA  GCTTCACCCA  AACCGTCCAA
151 AGCAAAAAGA  AAACCCAAAC  CGCGCACGGC  ACGTTCAAAA  TCCTGCGCCC
201 GGGCCTCTTC  AAATGGGAAT  ACACTTTGCC  CTACAGACAG  ACTATTGTCG
251 GCGACGGTCA  AACCGTTTGG  CTCTACGATG  TTGATTGGC  ACAAGTGACC
301 AAGTCGTCCC  AAGACCAGGC  CATCGGCGGC  AGCCCCGCCG  CCATCCTGTC
351 GAACAAAACC  GCCCTCGAAA  GCAGTTACAC  GCTGAAAGAG  GACGGTTCGT
401 CCAACGGCAT  CGATTATGTG  CGGGCAACGC  CCAAACGCAA  CAACGCCGGC
451 TACCAATACA  TCCGCATCGG  CTCAAAGGC  GGCAACCTCG  CCGCCATGCA
501 GCTTAAAGAC  AGCTTCGGCA  ACCAAACCTC  CATCAGTTTC  GCGGTTTGA
551 ATACCAATCC  CCAACTCTCG  CGCGGCGCGT  TCAAGTTTAC  CCCGCCCAAA
601 GCGTGGACG  TGTGAGCAA  CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1344; ORF 502-1.ng>:

g502-1.pep

```

1  MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQTVQ
51  SKKKQTQAHG TFKILRPGLF KWEYTLPLYRQ TIVGDGQTVW LYDVLDAQVT
101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV RATPKRNNAG
151 YQYIRIGFKG GNLAAMQLKD SFGNQTSSISF GGLTNPQLS  RGAFKFTPPK
201 GVDVLSN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1345>:

m502-1.seq

```

1  ATGATGAAAC  CGCACAACT  GTTCCAATTC  CTCGCCGTTT  GCTCCCTGAC
51  CGTCGCCGTC  GCTTCCGCAC  AGGCGGGCGC  GGTAGACGCG  CTTAAGCAAT
101 TCAACAACGA  TGCCGACGGT  ATCAGCGGCA  GCTTCACCCA  AACCGTCCAA
151 AGCAAAAAGA  AAACCCAAAC  CGCGCACGGC  ACGTTCAAAA  TCCTGCGACC
201 GGGCCTTTTC  AAATGGGAAT  ACACCAAACC  TTACAGGCAA  ACCATCGTCG
251 GCGACGGTCA  AACCGTTTGG  CTCTACGATG  TTGATCTGGC  ACAAGTGACC
301 AAGTCGTCCC  AAGACCAGGC  CATAGGCGGC  AGCCCCGCCG  CCATCCTGTC
351 GAACAAAACC  GCCCTCGAAA  GCAGCTACAC  GCTGAAAGAG  GACGGTTCGT
401 CCAACGGCAT  CGATTATGTG  CTGGCAACGC  CCAAACGCAA  CAACGCCGGC
451 TACCAATACA  TCCGCATCGG  CTCAAAGGC  GGCAACCTCG  CCGCCATGCA
501 GCTTAAAGAC  AGCTTCGGCA  ACCAAACCTC  CATCAGTTTC  GCGGTTTGA
551 ATACCAATCC  CCAACTCTCG  CGCGGCGCGT  TCAAGTTTAC  CCCGCCCAAA
601 GCGTGGACG  TGTGAGCAA  CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1346; ORF 502-1>:

m502-1.pep

```

1  MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQTVQ
51  SKKKQTQAHG TFKILRPGLF KWEYTKPYRQ TIVGDGQTVW LYDVLDAQVT
101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV LATPKRNNAG
151 YQYIRIGFKG GNLAAMQLKD SFGNQTSSISF GGLTNPQLS  RGAFKFTPPK
201 GVDVLSN*

```

m502-1/g502-1 99.0% identity in 207 aa overlap

	10	20	30	40	50	60
m502-1.pep	MMKPHNLFQFLAVCSLTVAVASAQAGAVDAL	LKQFNNDADGISGSFTQTVQSKKKQTQAHG				
g502-1	MMKPHNLFQFLAVCSLTVAVASAQAGAVDAL	LKQFNNDADGISGSFTQTVQSKKKQTQAHG				
	10	20	30	40	50	60
m502-1.pep	TFKILRPGLFKWEYTKPYRQTIVGDGQTVW	LYDVLDAQVTKSSQDQAIGGSPAAILSNKT				
g502-1	TFKILRPGLFKWEYTLPLYRQTIVGDGQTVW	LYDVLDAQVTKSSQDQAIGGSPAAILSNKT				
	70	80	90	100	110	120
m502-1.pep	TFKILRPGLFKWEYTKPYRQTIVGDGQTVW	LYDVLDAQVTKSSQDQAIGGSPAAILSNKT				
g502-1	TFKILRPGLFKWEYTLPLYRQTIVGDGQTVW	LYDVLDAQVTKSSQDQAIGGSPAAILSNKT				
	70	80	90	100	110	120
m502-1.pep	ALESSYTLKEDGSSNGIDYVLATPKRNNAG	YQYIRIGFKGGNLAAMQLKDSFGNQTSSISF				
g502-1	ALESSYTLKEDGSSNGIDYVRATPKRNNAG	YQYIRIGFKGGNLAAMQLKDSFGNQTSSISF				
	130	140	150	160	170	180

```

                190      200
m502-1.pep    GGLNTNPQLSRGAFKFTPPKGVVDVLSNX
                |||||
g502-1        GGLNTNPQLSRGAFKFTPPKGVVDVLSNX
                190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1347>:

a502-1.seq

```

1  ATGATGAAAC CGCACAAACCT GTTCCAATTC CTCGCCGTTT GCTCCCTGAC
51 CGTCTCCGTC GCTTCCGCAC AGGCGGGCGC GGTGGACGCG CTCAGCAAT
101 TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCCAA
151 AGCAAAAAGA AAACCCAAAC CGCGCACGGC ACGTTCAAAA TCCTGCGCCC
201 GGGCCTCTTT AAATGGGAAT ACACTTCGCC TTACAAACAG ACTATTGTCG
251 GCGACGGTCA AACCGTTTGG CTCTACGATG TCGATTGGC ACAAGTGACC
301 AAGTCGTCCC AAGACCAGGC CATAGCGGCG AGCCCCGCG CCATCCTGTC
351 GAACAAAACC GCCCTCGAAA GCAGCTACAC GCTGAAAGAG GACGGTTCGT
401 CCAACGGCAT CGATTATGTG CTGGCAACGC CCAAACGCAA CAACGCCGGC
451 TACCAATACA TCCGCATCGG CTTCAAAGGC GGCAACCTCG CCGCCATGCA
501 GCTTAAAGAC AGCTTCGGCA ATCAAACCTC CATCAGTTTC GCGGGTTGA
551 ATACCAATCC CCAACTCTCG CGCGGCGCGT TCAAGTTTAC CCCGCCCAAA
601 GCGGTGGACG TGTGAGCAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1348; ORF 502-1.a>:

a502-1.pep

```

1  MMKPHNLFQF LAVCSLTVSV ASAQAGAVDA LKQFNNDADG ISGSFTQTQVQ
51 SKKKTQTAHG TFKILRPGLF KWEYTSFYKQ TIVGDGQTVW LYDVDLAQVT
101 KSSQDQATGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV LATPKRNNAG
151 YQYIRIGFKG GNLAAMQLKD SFGNQTSISF GGLNTNPQLS RGAFKFTPPK
201 GVDVLSN*

```

a502-1/m502-1 98.6% identity in 207 aa overlap

```

                10      20      30      40      50      60
a502-1.pep    MMKPHNLFQFLAVCSLTVSVASAQAGAVDALKQFNNDADGISGSFTQTQVQSKKKTQTAHG
                |||||
m502-1        MMKPHNLFQFLAVCSLTVASAQAGAVDALKQFNNDADGISGSFTQTQVQSKKKTQTAHG
                10      20      30      40      50      60

                70      80      90      100     110     120
a502-1.pep    TFKILRPGLFKWEYTSFYKQTIVGDGQTVWLYDVDLAQVTKSSQDQAIIGGSPAAILSNKT
                |||||
m502-1        TFKILRPGLFKWEYTKPYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIIGGSPAAILSNKT
                70      80      90      100     110     120

                130     140     150     160     170     180
a502-1.pep    ALESSYTLKEDGSSNGIDYVLATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTSISF
                |||||
m502-1        ALESSYTLKEDGSSNGIDYVLATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTSISF
                130     140     150     160     170     180

                190     200
a502-1.pep    GGLNTNPQLSRGAFKFTPPKGVVDVLSNX
                |||||
m502-1        GGLNTNPQLSRGAFKFTPPKGVVDVLSNX
                190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1349>:

g503.seq

```

1  atgtccgcgc cgtcggcacg ggtaatcatt ttgttccatg ccgcttcgat
51 ttcggcatcg agctgttcgg ggaaggcggt gtccaaaatc cattggcgga
101 tttctttgcc gacgcgtgcc agttcggaaa cgtcttcgac atccaatttt
151 gccagagcgg cggaaatgcg ttcgttcaga ccgttggtg cgagaaatgc
201 gcggttag

```

This corresponds to the amino acid sequence <SEQ ID 1350; ORF 503.ng>:

g503.pep

```

1  MSAPSASVII LFHAASISAS SCSGKGVSKI HWRISLPTRA SSETSSSTSNF
51 ARAAEMRSFR PLCARNAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1351>:

739

```

m503.seq
  1  atgtccgcac cgccggcatc ggcaaccatt ttgttccatg ccgcttcgat
 51  ttcggcatcg agctgttcgg ggaaaggcgt atccaaaatc cattggcgga
101  tttctttgcc gacgcgtgcc agttcggcaa cgtcttcgac atccaatttt
151  gccagtgcgg cggaaatgcg ttcgctcaga ccgttggtgt cgaggaatgc
201  gcggtag

```

This corresponds to the amino acid sequence <SEQ ID 1352; ORF 503>:

```

m503.pep
  1  MSAPPASATI LFHAASISAS SCSGKGVSKI HWRISLPTRA SSATSSTSNF
 51  ASAAEMRSLR PLCARNAR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 503 shows 91.2% identity over a 68 aa overlap with a predicted ORF (ORF 503.ng) from *N. gonorrhoeae*:

```

m503/g503
      10      20      30      40      50      60
m503.pep  MSAPPASATILFHAASISASSCSGKGVSKIHWRI SLPTRASSATSSTSNFASAAEMRSLR
          |||||::|
g503      MSAPSASVILFHAASISASSCSGKGVSKIHWRI SLPTRASSETSTSNFARAAEMRSFR
          10      20      30      40      50      60

      69
m503.pep  PLCARNAR
          |||||
g503      PLCARNAR

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1353>:

```

a503.seq
  1  ATGTCCGCGC CGCCGGCATC GGCAACCATT TTGTTCATG CCGCTTCGAT
 51  TTCGGCATCG AGCTGTTCGG GGAAGGGCGT GTCCAAAATC CATTGGCGGA
101  TTTCTTTGCC GACGCGTGCC AGTTCGGCAA CGTCTTCGAC ATCTAATTTT
151  GCCAGTGCGG CGGAAATGCG TTCGCTCAGA CCCTTGTGTG CGAGGAATGC
201  GCGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1354; ORF 503.a>:

```

a503.pep
  1  MSAPPASATI LFHAASISAS SCSGKGVSKI HWRISLPTRA SSATSSTSNF
 51  ASAAEMRSLR PLCARNAR*

```

m503/a503 100.0% identity in 68 aa overlap

```

      10      20      30      40      50      60
m503.pep  MSAPPASATILFHAASISASSCSGKGVSKIHWRI SLPTRASSATSSTSNFASAAEMRSLR
          |||||
a503      MSAPPASATILFHAASISASSCSGKGVSKIHWRI SLPTRASSATSSTSNFASAAEMRSLR
          10      20      30      40      50      60

      69
m503.pep  PLCARNARX
          |||||
a503      PLCARNARX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1355>:

```

g503-1.seq
  1  ATGGCGCGGT CGTGTACAG GGAGGCGAAA ACGTGGCGCA TCGCTTTTTT
 51  AACGTTATCC AAGCCATTGA TATTCAGGAA GGTTTCCTGT TGGCCGGCAA
101  ATGATGCGTC GGGCAGGTCT TCGGCGGTTG CGGAAGAGCG TACGGCAACG
151  GAAATGTCCG CGCCGTCGGC ATCGGTAATC ATTTTGTTCC ATGCCGCTTC
201  GATTTTCGCA TCGAGCTGTT CGGGGAAGGG CGTGTCCAAA ATCCATTGGC
251  GGATTTCTTT GCCAGCGCGT GCCAGTTCGG AAACGTCTTC GACATCCAAT
301  TTTGCCAGAG CGGCGGAAAT GCGTTCGTTT AGACCGTTGT GTGCGAGAAA
351  TGC GCGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1356; ORF 214.ng>:

g503-1.pep

```

1  MARSLYREAK TWRI AFLTSL KPLIFRKVSC WPANDASGRS SAVAEERTAT
51 EMSAPSASVI ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSATSSTSN
101 FARAAEMRSF RPLCARNAR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1357>:

m503-1.seq

```

1  ATGGCACGGT CGTTATACAG GGAAGCGAAT ACATGGTGCA TCGCTTCTTT
51 AACGTTATCC AAGCCGTTGA TGTCAAGAA GGTTTCCTGT TGTCCAGCGA
101 ATGATGCGTC CGGCAGGTCT TCGGCAGTTG CGGAAGAACG TACGGCAACG
151 GAAATGTCCG CACCGCCGGC ATCGGCAACC ATTTTGTTC ATGCCGCTTC
201 GATTTCGGCA TCGAGCTGTT CGGGGAAAGG CGTATCCAAA ATCCATTGGC
251 GGATTCTTTT GCCGACGCGT GCCAGTTCGG CAACGTCTTC GACATCCAAT
301 TTTGCCAGTG CGGCGGAAAT GCGTTCGCTC AGACCGTTGT GTGCGAGGAA
351 TGC GCGGTAG
```

This corresponds to the amino acid sequence <SEQ ID 1358; ORF 503-1>:

m503-1.pep

```

1  MARSLYREAN TWCIA SLTSL KPLMFKKVSC CPANDASGRS SAVAEERTAT
51 EMSAPPASAT ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSATSSTSN
101 FASAAEMRSL RPLCARNAR*
```

g503-1 / m503-1 89.9% identity in 119 aa overlap

	10	20	30	40	50	60
g503-1.pep	MARSLYREAKTWRI	AFLTSLKPLIFR	KVSCWPANDASGR	SSSAVAEERTAT	EMSAPSASVI	
		:			:	
m503-1	MARSLYREANTWCI	ASLTSLKPLMFKK	VSCCPANDASGR	SSSAVAEERTAT	EMSAPPASAT	
		:			:	
	10	20	30	40	50	60
	70	80	90	100	110	120
g503-1.pep	ILFHAASISASSC	SGKGVSKIHWRIS	LPTRASSETSTSN	FARAAEMRSFR	RPLCARNARX	
		:			:	
m503-1	ILFHAASISASSC	SGKGVSKIHWRIS	LPTRASSETSTSN	FASAAEMRSLR	RPLCARNARX	
		:			:	
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1359>:

a503-1.seq

```

1  ATGGCGCGGT CGTTGTACAG GGAGGCGAAT ACATGGCGCA TCGCTTCTTT
51 AACGTTTTCC AAGCCGTTGA TATTCAGGAA GGTTTCCTGT TGGCCGGCAA
101 ATGATGCGTC GGGCAGGTCT TCGGCGGTTG CGGAAGAGCG TACGGCAACG
151 GAAATGTCCG CGCGCCGGC ATCGGCAACC ATTTTGTTC ATGCCGCTTC
201 GATTTCGGCA TCGAGCTGTT CGGGGAAAGG CGTGTCCAAA ATCCATTGGC
251 GGATTCTTTT GCCGACGCGT GCCAGTTCGG CAACGTCTTC GACATCTAAT
301 TTTGCCAGTG CGGCGGAAAT GCGTTCGCTC AGACCGTTGT GTGCGAGGAA
351 TGC GCGGTAG
```

This corresponds to the amino acid sequence <SEQ ID 1360; ORF 503-1.a>:

a503-1.pep

```

1  MARSLYREAN TWRIASLTFS KPLIFRKVSC WPANDASGRS SAVAEERTAT
51 EMSAPPASAT ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSATSSTSN
101 FASAAEMRSL RPLCARNAR*
```

a503-1 / m503-1 95.8% identity in 119 aa overlap

	10	20	30	40	50	60
a503-1.pep	MARSLYREANTWRI	ASLTFSKPLIFR	KVSCWPANDASGR	SSSAVAEERTAT	EMSAPPASAT	
		:			:	
m503-1	MARSLYREANTWCI	ASLTSLKPLMFKK	VSCCPANDASGR	SSSAVAEERTAT	EMSAPPASAT	
		:			:	
	10	20	30	40	50	60
	70	80	90	100	110	120
a503-1.pep	ILFHAASISASSC	SGKGVSKIHWRIS	LPTRASSETSTSN	FASAAEMRSLR	RPLCARNARX	
		:			:	
m503-1	ILFHAASISASSC	SGKGVSKIHWRIS	LPTRASSETSTSN	FASAAEMRSLR	RPLCARNARX	
		:			:	
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1361>:

```
g504.seq
1  atgttggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
51  cgattttttac aatacgggta tgccgcgcga ttttgccagc gatattgaag
101 taacggacaa ggcaaccggg gagaaactcg agcgaccat ccgcgtgaac
151 catcctttga ccttgacagg catcacgatt tatcaggcga gttttgccga
201 cggcggttcg gatttgacat tcaaggcgtg gaatttgagg gatgcttcgc
251 gcgaacctgt cgtgttgaag gcaacctcca tacaccagtt tccgttgga
301 atcggcaaac acaaatatcg tcttgagttc gatcagttca cttctatgaa
351 tgtggaggac atgagcgagg gtgcggaacg ggaaaaaagc ctgaaatcca
401 ctctgaacga tgtccgcgcc gttactcagg aaggtaaaaa atacaccaat
451 atcggccctt ccacgtgta ccgcacccgt gatgcggcag ggcaggcggg
501 cgaatataaa aactatatgc tgccgatttt gcaggacaaa gattattttt
551 ggctgaccgg cacgcgcagc ggcttgagc agcaataaccg ctggctgcgt
601 atcccccttg acaagcagtt gaaagcggac acctttatgg cattgcgtga
651 gtttttgaaa gatggggaag ggcgcaaacg tctggttgcc gacgcaacca
701 aagacgcacc tgccgaaatc cgcgaacaat tcatgctggc tgcggaaaaa
751 acgctgaata tctttgcgca aaaaggctat ttgggattgg acgaatttat
801 tacgtccaat atcccgaaag ggcagcagga taagatgcag ggctatttct
851 acgaaatgct ttacggcgtg atgaacgctg ctttgatga aaccatacgc
901 cggtagcggt tgcccgaatg gcagcaggat gaagcgcgga accgtttcct
951 gctgcacagt atggatgctt atacggggct gacggaatat cccgcgccta
1001 tctgtctcca gcttgacggg ttttccgagg tgcgttcctc aggtttgcag
1051 atgaccggtt cgcggggtgc gcttttggtc tatctcggct cggattgtt
1101 ggttttggtt acagtattta tgttttatgt gcccaaaaaa cgggcgtggg
1151 tattgttttc aaacdgcata atccggtttg ctatgtcttc ggcccgagc
1201 gaacgggatt tgcagaagga atttccaaaa cacgtcgaga gcctgcaacg
1251 gctcggcaag gacttgaatc atgactga
```

This corresponds to the amino acid sequence <SEQ ID 1362; ORF 504.ng>:

```
g504.pep
1  MLVQDLPEFV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
51  HPLTLHGITI YQASFADGGS DLTFAWNLR DASREPVVLK ATSIHQFPLE
101 IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLNDVRA VTQEGKKYTN
151 IGPSIVYRIR DAAGQAVEYK NYMLPILQDK DYFWLTGTRS GLQQQYRWLR
201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKDAPAEI REQFMLAAEN
251 TLNIFAQKGY LGLDEFITSN IPKGQDDKMQ GYFYEMLYGV MNAALDETIR
301 RYGLPEWQOD EARNRFLHS MDAYTGLTEY PAPMLLQLDG FSEVRSSGLQ
351 MTRSPGALLV YLGSVLLVLG TVFMFYVPPK RAWVLFNKKI RFAMSSARSE
401 RDLQKEFPKH VESLQRLGKD LNHD*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1363>:

```
m504.seq..
1  atatttggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
51  cgattttttac aatacgggta tgccgcgcga tttcgccagc gatattgaag
101 tgacggacaa ggcaaccggg gagaaactcg agcgaccat ccgcgtgaac
151 catcctttga ccttgacagg catcacgatt tatcaggcga gttttgccga
201 cggcggttcg gatttgacat tcaaggcgtg gaatttgagg gatgcttcgc
251 gcgagcctgt cgtgttgaag gcaacatcca tacaccagtt tccgttgga
301 attggcaaac acaaatatcg tcttgagttc gatcagttca cttctatgaa
351 tgtggaggac atgagcgagg gcgcggaacg ggaaaaaagc ctgaaatcca
401 cgctgmmcga tgtccgcgcc gttactcagg aaggtaaaaa atacaccaat
451 atcggccctt ccattgttta ccgtatccgt gatgcggcag ggcaggcggg
501 cgaatataaa aactatatgc tgccgggttt gcaggaaacag gattattttt
551 ggattaccgg cacgcgcagc ggcttgagc agcaataaccg ctggctgcgt
601 atcccccttg acaagcagtt gaaagcggac acctttatgg cattgcgtga
651 gtttttgaaa gatggggaag ggcgcaaacg tctggttgcc gacgcaacca
701 aaggcgcacc tgccgaaatc cgcgaacaat tcatgctggc tgcggaaaaa
751 acgctgaaca tctttgcaca aaaaggctat ttgggattgg acgaatttat
801 tacgtccaat atcccgaaag agcagcagga taagatgcag ggctatttct
851 acgaaatgct ttacggcgtg atgaacgctg ctttgatga aaccatacgc
901 cggtagcggt tgcccgaatg gcagcaggat gaagcgcgga atcgtttctt
951 gctgcacagt atggatgcgt acacgggttt gaccgaatat cccgcgccta
1001 tgctgctgca acttgatggg ttttccgagg tgcgttcgctc gggtttgagc
```

742

```

1051 atgacccgtt ccccggtgct gcttttggtc tatctcggct cgggtgctgtt
1101 ggtattgggt acggtattga tgttttatgt gcgcgaaaaa cgggcgtggg
1151 tattgttttc agacggcaaa atccgttttg ccatgtcttc ggcccgcagc
1201 gaacgggatt tgcagaagga atttccaaaa cacgtcgaga gtctgcaacg
1251 gctcggcaag gacttgaatc atga

```

This corresponds to the amino acid sequence <SEQ ID 1364; ORF 504>:

m504.pep.

```

1 ILVQDLPPFEV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
51 HPLTLHGITI YQASFADGGS DLTFKAWNLG DASREPVVLK ATSIHQFPLE
101 IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLXDVRA VTQEGKKYTN
151 IGPSIVYRIR DAAGQAVEYK NYMLPVLQEQ DYFWITGTRS GLQQYRWLR
201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKGAPAEI REQFMLAAEN
251 TLNIFAQKGY LGLDEFITSN IPKEQDKMQ GYFYEMLYGV MNAALDETIR
301 RYGLPEWQQD EARNRFLHLS MDAYTGLTEY PAPMLQLDGF SEVRSSGLQ
351 MTRSPGALLV YLGSVLLVLG TVLMFYVREK RAWVLFSDGK IRFAMSSARS
401 ERDLQKEFPK HVESLQRLGK DLNHD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 504 shows 96.7% identity over a 425 aa overlap with a predicted ORF (ORF 504.ng) from *N. gonorrhoeae*:

m504/g504

m504.pep	10	20	30	40	50	60
	ILVQDLPPFEVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLERTIRVNHPLTLHGITI					
g504	MLVQDLPPFEVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLERTIRVNHPLTLHGITI					
	10	20	30	40	50	60
m504.pep	70	80	90	100	110	120
	YQASFADGGSDLTFKAWNLDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED					
g504	YQASFADGGSDLTFKAWNLRDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED					
	70	80	90	100	110	120
m504.pep	130	140	150	160	170	180
	MSEGAREKSLKSTLXDVRVAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPVLQEQ					
g504	MSEGAREKSLKSTLNDVRVAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPILQDK					
	130	140	150	160	170	180
m504.pep	190	200	210	220	230	240
	DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI					
g504	DYFWLTGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKDAPAEI					
	190	200	210	220	230	240
m504.pep	250	260	270	280	290	300
	REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQDKMQGYFYEMLYGMNAALDETIR					
g504	REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKGQDKMQGYFYEMLYGMNAALDETIR					
	250	260	270	280	290	300
m504.pep	310	320	330	340	350	360
	RYGLPEWQQDEARNRFLHLSMDAYTGLTEYPAPMLQLDGFSEVRSSGLQMTSPGALLV					
g504	RYGLPEWQQDEARNRFLHLSMDAYTGLTEYPAPMLQLDGFSEVRSSGLQMTSPGALLV					
	310	320	330	340	350	360
m504.pep	370	380	390	400	410	420
	YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSDRLQKEFPKHVESLQRLGK					
	: : : : :					

743

g504 YLGSVLLVLGTVMFYVPKKRAWVLFNS-KIRFAMSSARSERDLQKEFPKHVESLQRLGK
 370 380 390 400 410

m504.pep DLNHD
 |||||
 g504 DLNHD
 420

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1365>:

a504.seq
 1 ATATTGGTTC AGGACTTGCC TTTTGAAGTC AAACGTAAAA AATTCCATAT
 51 CGATTTTAC AATACGGGTA TGCCGCGCGA TTTTGCCAGT GATATTGAAG
 101 TAACGGATAA GGCAACCGGT GAGAACTCG AGCGCACCAT CCGCGTGAAC
 151 CATCCTTTGA CCTTGACAGG CATCACGATT TATCAGGCGA GTTTTGCCGA
 201 CGGCGGTTTC GATTTGACAT TCAAGGCGTG GAATTTGGGT GATGCTTCGC
 251 GCGAGCCTGT CGTGTGAAG GCAACATCCA TACACCAGTT TCCGTTGGAA
 301 ATGGCAAAC ACAATATCG TCTTGAGTTC GATCAGTTTA CTCTATGAA
 351 TGTGGAGGAC ATGAGCGAGG GCGCGGAACG GGAAAAAGC CTGAAATCCA
 401 CGCTGAACGA TGTCGCGGCC GTTACTCAGG AAGGTAAAAA ATACACCAAT
 451 ATCGGCCCTT CCATTGTTTA CCGTATCCGT GATGCGGCAG GGCAGGCGGT
 501 CGAATATAAA AACTATATGC TGCCGGTTTT GCAGGAACAG GATTATTTTT
 551 GGATTACCGG CACGCGCAGC GGCTTGACAG AGCAATACCG CTGGCTGCGT
 601 ATCCCTTGG ACAAGCAGTT GAAAGCGGAC ACCTTTATGG CATTGCGTGA
 651 GTTTTGAAG GATGGGAAG GCGCGAAACG TCTGGTTGCC GACGCAACCA
 701 AAGGCGCACC TGCCGAAATC CGCGAACAAT TCATGCTGGC TGCGGAAAAC
 751 ACGCTGAACA TCTTGCACA AAAAGGCTAT TTGGGATTGG ACGAATTTAT
 801 TAGCTCCAAT ATCCCGAAAG AGCAGCAGGA TAAGATGCAG GGCTATTTCT
 851 ACGAAATGCT TTACGGCGTG ATGAACGCTG CTTTGGATGA AACCATACGC
 901 CGGTACGGCT TGCCCGAATG GCAGCAGGAT GAAGCGCGGA ATCGTTTCCT
 951 GCTGCACAGT ATGGATGCGT ACACGGGTTT GACCGAATAT CCCGCGCCTA
 1001 TGCTGCTGCA ACTTGATGGG TTTTCCGAGG TGCGTTCGTC GGGTTTGCAG
 1051 ATGACCCGTT CCCCAGGTC GCTTTTGGTC TATCTCGGCT CGGTGCTGTT
 1101 GGTATTGGGT ACGGTATTGA TGTTTATGT GCGCGAAAAA CGGGCGTGGG
 1151 TATGTTTTC AGACGGCAA ATCCGTTTTC CCATGTCTTC GGCCCGCAGC
 1201 GAACGGGATT TGCAGAAGGA ATTTCCAAAA CACGTCGAGA GTCTGCAACG
 1251 GCTCGCAAG GACTTGAATC ATGACTGA

This corresponds to the amino acid sequence <SEQ ID 1366; ORF 504.a>:

a504.pep
 1 ILVQDLPEFV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
 51 HPLTLHGITI YQASFADGGS DLTFKAWNLG DASREPVVLK ATSIHQFPLE
 101 IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLNDVRA VTQEGKKYTN
 151 IGPSIVYRIR DAAGQAVEYK NYMLPVLQEQ DYFWITGTRS GLQQQYRWLR
 201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKGAPAEI REQFMLAAEN
 251 TLNIFAQGY LGLDEFITSN IPKEQDDKMQ GYFYEMLYGV MNAALDETIR
 301 RYGLPEWQDD EARNRFLLS MDAYTGLTEY PAPMLLQLDG FSEVRSSGLQ
 351 MTRSPGALLV YLGSVLLVLG TVLMFYVREK RAWVLFSDGK IRFAMSSARS
 401 ERDLQKEFPK HVESLQRLGK DLNHD*

m504/a504 99.8% identity in 425 aa overlap

	10	20	30	40	50	60
m504.pep	ILVQDLPEFVKLKKFHIDFYNTGM	PRDFASDIEVTDKATGEKLERTIRV	NHPLTLHGITI			
a504	ILVQDLPEFVKLKKFHIDFYNTGM	PRDFASDIEVTDKATGEKLERTIRV	NHPLTLHGITI			
	10	20	30	40	50	60
m504.pep	YQASFADGGSDLTFKAWNLDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED					
a504	YQASFADGGSDLTFKAWNLDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED					
	70	80	90	100	110	120
m504.pep	MSEGAREKSLKSTLXDVRVAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPVLQEQ					
a504	MSEGAREKSLKSTLXDVRVAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPVLQEQ					
	130	140	150	160	170	180
m504.pep						

744

```

|||||
a504      MSEGAREKSLKSTLNDVRAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKKNYMLPVLQEQ
          130      140      150      160      170      180

          190      200      210      220      230      240
m504.pep  DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI
          |||||
a504      DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI
          190      200      210      220      230      240

          250      260      270      280      290      300
m504.pep  REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQQDKMQGYFYEMLYGVMNAALDETIR
          |||||
a504      REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQQDKMQGYFYEMLYGVMNAALDETIR
          250      260      270      280      290      300

          310      320      330      340      350      360
m504.pep  RYGLPEWQQDEARNRFLHSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTSPGALLV
          |||||
a504      RYGLPEWQQDEARNRFLHSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTSPGALLV
          310      320      330      340      350      360

          370      380      390      400      410      420
m504.pep  YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSDRLQKEFPKHVESLQRLGK
          |||||
a504      YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSDRLQKEFPKHVESLQRLGK
          370      380      390      400      410      420

m504.pep  DLNHDX
          |||||
a504      DLNHDX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1367>:

```

g505.seq
1   atgtttcggt tacaattcag gctgtttccc cctttgcgaa cgcacatgca
51  catcctgttg accgccctgc tcaaatgcct ctccctgctg tcgctttcct
101 gtctgcacac gctgggaaac cggctcggac atctggcggt ttacctttta
151 aaggaagacc gcgcgcgcat cgtcgccaat atgcggcagg cgggtttgaa
201 ccccgacacg cagacggtca aagccgtttt tgcggaaacg gcaaaatgcg
251 gtttgaact  tgccccgcg tttttcaaaa aaccggaaga catcgaaaca
301 atgttcaaag cggtagacgg ctgggaacac gtgcagcagg ctttggacaa
351 gggcgaaggg ctgctgttca tcacgccgca catcggcagc tacgatttgg
401 gcggacgcta catcagccag cagcttccgt tccacctgac cgccatgtac
451 aagccgccga aaatcaaagc gatagacaaa atcatgcagg cgggcagggt
501 gcgcggcaaa ggcaaaaccg cgcccaccgg catacaaggg gtcaaacaaa
551 tcatcaaggc cctgcgcgcg ggcgaggcaa ccatcatcct gcccgaccac
601 gtcccttctc cgcaggaagg cggcggcggt tgggcggatt ttttcggcaa
651 acctgcatac accatgacac tggcggcaaa attggcacac gtcaaaggcg
701 tgaaaaccct gttttcttgc tgcgaacgcc tgcccgcagg acaaggcttc
751 gtgttgacac tccgccccgt ccaaggggaa ttgaacggca acaaaagcca
801 cgatgccgcc gtgttcaacc gcaataccga atattggata cgccgttttc
851 cgacgcagta tctgtttatg tacaaccgct ataaaacgcc gtaa

```

This corresponds to the amino acid sequence <SEQ ID 1368; ORF 505.ng>:

```

g505.pep
1   MFRLQFRLFP PLRTAMHILL TALLKCLSL LL SL SCLHTLGN RLGH LAFYLL
51  KEDRARIVAN MRQAGLNPD T QTVKAVFAET AKCGLELAPA FFKKPEDIET
101 MFKAVHGW EH VQALDKGEG LLFITPHIGS YDLGGYISQ QLPFHLTAMY
151 KPPKIKAI DK IMQAGRVRGK GKTAPTGIQ G VKQIIKALRA GEATIILPDH
201 VPSPQEGGGV WADFFGKPAY TMTLAAKLAH VKGVKTLFFC CERLPDGQGF
251 VLHIRPVQGE LNGNKAHDAA VFNRNTEYWI RRFPTQYL FM YNRYKTP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1369>:

745

```

m505.seq (partial)
  1  GGCATGTTTC GTTACAATT CAGGCTGTTT CCCCTTTGTC GAACCGCCAT
  51  GCACATCCTG TTGACCGCCC TGCTCAAATG CCTCTCCCTG CTGCCGCTTT
 101  CCTGTCTGCA CACGCTGGGA AACCGGCTCG GACATCTGGC GTTTTACCTT
 151  TTAAAGGAAG ACCGCGCGCG CATCGTCGCC AATATGCGGC AGGCGGGTTT
 201  GAACCCCGAC CCCAAAACGG TCAAAGCCGT TTTGCGGAA ACGGCAAAAG
 251  GCGGTTTGGA ACTTGCCCCC GCGTTTTTCA GAAAACCGGA AGACATAGAA
 301  ACAATGTTCA AAGCGGTACA CGGCTGGGAA CATGTGCAGC AGGCTTTGGA
 351  CAAACACGAA GGGCTGCTAT TCATCACGCC GCACATCGGC AGCTACGATT
 401  TGGGCGGACG CTACATCAGC CAGCAGCTTC CGTTCCCGCT GACCGCCATG
 451  TACAAACCGC CGAAAATCAA AGCGATAGAC AAAATCATGC AGGCGGGCAG
 501  GGTTTCGCGC AAAGGAAAAA CCGCGCCTAC CAGCATACAA GGGGTCAAAC
 551  AAATCATCAA AGCCTGCGT TCGGGCGAGC AACCATCGTC CTGCCCGACC
 601  ACGTCCCTC CCCTCAAGAA GGCGGGGAAG GCGTATGGGT GGATTTCTTC
 651  GGCAAACCTG CCTATACCAT GACGCTGGCG GCAArATTGG CACACGTCAA
 701  AGGCGTGAAA ACCCTGTTTT TCTGCTGCGA ACGCCTGCCT GGCGGACAAAG
 751  GTTTCGATTT GCACATCCGC CCCGTCCAAG GGAATTGAA CGGCGACAAA
 801  GCCCATGATG CCGCGTGTT CAACCGCAAT GCCGAATATT GGATACGCCG
 851  TTTTCCGACG CATATC....

```

This corresponds to the amino acid sequence <SEQ ID 1370; ORF 505>:

```

m505.pep (partial)
  1  MFRLQFRLFP PLRTAMHILL TALLKCLSLL PLSCSLHTLGN RLGHILAFYLL
  51  KEDRARIVAN MRQAGLNPD P KTVKAVFAET AKGGLELAPA FFRKPEDIET
 101  MFKAVHGW EHVQQALDKHEG LLFITPHIGS YDLGGYISQ QLPPPLTAMY
 151  KPPKIKAI D KIMQAGRVRGK GKTAPTSIQG VKQIIKALRS GEATIVLPDH
 201  VPSPQEGG EG VVWVDFGKPA YTM TLAAXLA HVKGVKTLFF CCERLPGGQG
 251  FDLHIRPVQ G ELNGDKAHDA AVFNRNAEYW IRRFPTHI...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 505 shows 93.7% identity over a 287 aa overlap with a predicted ORF (ORF 505.ng) from *N. gonorrhoeae*:

m505/g505

	10	20	30	40	50	60
m505.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLLPLSCSLHTLGNRLGHILAFYLLKEDRARIVAN					
g505	MFRLQFRLFPPLRTAMHILLTALLKCLSLLPLSCSLHTLGNRLGHILAFYLLKEDRARIVAN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m505.pep	MRQAGLNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIETMFKAVHGW EHVQQALDKHEG					
g505	MRQAGLNPDQTVKAVFAETAKCGLELAPAFFRKPEDIETMFKAVHGW EHVQQALDKGEG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m505.pep	LLFITPHIGSYDLGGYISQQLPPPLTAMYPKPPKIKAIKIMQAGRVRGKGTAPTSIQG					
g505	LLFITPHIGSYDLGGYISQQLPFHLTAMYPKPPKIKAIKIMQAGRVRGKGTAPTGIQG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m505.pep	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVVWVDFGKPAYTMTLAAXLAHVKGVKTLFF					
g505	VKQIIKALRAGEATIILPDHVPSPQEGG-GVWADFFGKPAYTMTLAAXLAHVKGVKTLFF					
	190	200	210	220	230	
	250	260	270	280	289	
m505.pep	CCERLPGGQGFDLHIRPVQGEELNGDKAHDAVFNRNAEYWIIRFPTHI					
g505	CCERLPDGGQGFVLRPVQGEELNGNKAHDAVFNNTYWIIRFPTQYLFMYNRYKTP					
	240	250	260	270	280	290

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1371>:

a505.seq

```

1  ATGTTTCGTT TACAATTCAG GCTGTTTCCC CCTTTGCGAA CCGCCATGCA
51  CATCCTGTTG ACCGCCCTGC TCAAATGCCT CTCCCTGCTG CCGCTTTCCT
101 GTCTGCACAC GCTGGGAAAC CGGCTCGGAC ATCTGGCGTT TTACCTTTTA
151 AAGGAAGACC GCGCGCGCAT CGTCGCCAAT ATGCGTCAGG CAGGCATGAA
201 TCCCGACCCC AAAACGGTCA AAGCCGTTTT TGCGGAAACG GCAAAAGGCG
251 GTTTGGAACT TGCCCCCGCG TTTTTCAGAA AACCGBAAGA CATAGAAACA
301 ATGTTCAAAG CGGTACACGG CTGGGAACAT GTGCAGCAGG CTTTGACAAA
351 ACACGAAGGG CTGCTATTCA TCACGCCGCA CATCGGCAGC TACGATTTGG
401 GCGGACGCTA CATCAGCCAG CAGCTTCCGT TCCCCTGAC CGCCATGTAC
451 AAACCGCCGA AAATCAAAGC GATAGACAAA ATCATGCAGG CGGGCAGGGT
501 TCGCGGCAAA GGAAAAACCG CGCCTACCAG CATACAAGGG GTCAAACAAA
551 TCATCAAAGC CCTGCGTTTC GGCGAAGCAA CCATCGTCCT GCCCGACCAC
601 GTCCCCCTCC CTCAAGAAGG CGGGGAAGGC GTATGGGTGG ATTTCTTCGG
651 CAAACCTGCC TATACCATGA CGCTGGCGGC AAAATTGGCA CACGTCAAAG
701 GCGTGAAAC CCTGTTTTTC TGCTGCGAAC GCCTGCCTGG CGGACAAGGT
751 TTCGATTTGC ACATCCGCCC CGTCCAAGGG GAATTGAACG GCGACAAAGC
801 CCATGATGCC GCCGTGTTCA ACCGCAATGC CGAATATTGG ATACGCCGTT
851 TTCCGACGCA GTATCTGTTT ATGTACAACC GCTACAAAAT GCCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1372; ORF 505.a>:

a505.pep

```

1  MFRLQFRLFP PLRTAMHILL TALLKCLSL LPLSCLHTLGN RLGLHAFYLL
51  KEDRARIVAN MRQAGMNPDP KTVKAVFAET AKGGLLELAPA FFRKPEDIET
101 MFKAVHGWEH VQQALDKHEG LLFITPHIGS YDLGGYISQ QLPFPLTAMY
151 KPPKIKAIK IMQAGRVRGK GKTAPTSIQG VKQIIKALRS GEATIVLPDH
201 VPSPQEGGEG VWVDFFGKPA YTMTLAAKLA HVKGVKTLFF CCERLPGGQG
251 FDLHIRPVQG ELNGDKAHDA AVFNRNAEYW IRRFPTQYLF MYNRYKMP*

```

m505/a505 99.0% identity in 287 aa overlap

m505.pep	10	20	30	40	50	60
	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGLHAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGLHAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505.pep	70	80	90	100	110	120
	MRQAGLNPDPKTVKAVFAETAKGGLLELAPAFFRKPEDIETMFKAVHGWEHVQQALDKHEG					
a505	MRQAGMNPDPKTVKAVFAETAKGGLLELAPAFFRKPEDIETMFKAVHGWEHVQQALDKHEG					
	70	80	90	100	110	120
m505.pep	130	140	150	160	170	180
	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTSIQG					
a505	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTSIQG					
	130	140	150	160	170	180
m505.pep	190	200	210	220	230	240
	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFFGKPAYTMTLAAXLAHVKGVTLLFF					
a505	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFFGKPAYTMTLAAXLAHVKGVTLLFF					
	190	200	210	220	230	240
m505.pep	250	260	270	280		
	CCERLPGGQGFDLHIRPVQEGELNGDKAHDAVFNRNAEYWIRRFPTHI					
a505	CCERLPGGQGFDLHIRPVQEGELNGDKAHDAVFNRNAEYWIRRFPTQYLFMYNRYKMPX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1373>:

m505-1.seq

```

1  ATGTTTCGTT TACAATTCAG GCTGTTTCCC CCTTTGCGAA CCGCCATGCA
51  CATCCTGTTG ACCGCCCTGC TCAAATGCCT CTCCCTGCTG CCGCTTTCCT
101 GTCTGCACAC GCTGGGAAAC CGGCTCGGAC ATCTGGCGTT TTACCTTTTA
151 AAGGAAGACC GCGCGCGCAT CGTCGCCAAT ATGCGGCAGG CGGGTTTGAA
201 CCCCACCCCC AAAACGGTCA AAGCCGTTT TCGGAAACG GCAAAAGGCG
251 GTTTGGAAC TCCCCCGCG TTTTTCAGAA AACCGAAGA CATAGAAACA
301 ATGTTCAAAG CGGTACACGG CTGGGAACAT GTGCAGCAGG CTTTGGACAA
351 ACACGAAGGG CTGCTATTCA TCACGCCGCA CATCGGCAGC TACGATTGCG
401 GCGGACGCTA CATCAGCCAG CAGCTTCCGT TCCCGCTGAC CGCCATGTAC
451 AAACCGCCGA AAATCAAAGC GATAGACAAA ATCATGCAGG CGGGCAGGGT
501 TCGCGGCAAA GGAAAAACCG CGCTACCAG CATACAAGGG GTCAAACAAA
551 TCATCAAAGC CCTGCGTTCG GGCGAAGCAA CCATCGTCTT GCCCGACCAC
601 CCGCCCTCCC CTCAAGAAGG CGGGGAAGGC GTATGGGTGG ATTTCTTCGG
651 CAAACCTGCC TATACCATGA CGCTGGCGGC AAAATTGGCA CACGTCAAAG
701 GCGTGAAAAC CCTGTTTTTC TGCTGCGAAC GCCTGCCTGG CGGACAAGGT
751 TTCGATTGTC ACATCCGCCC CGTCCAAGGG GAATTGAACG GCGACAAAGC
801 CCATGATGCC GCGGTGTTCA ACCGCAATGC CGAATATTGG ATACGCCGTT
851 TTCCGACGCA GTATCTGTTT ATGTACAACC GCTACAAAAT GCCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1374; ORF 505-1>:

m505-1.pep

```

1  MFRLQFRLFP PLRTAMHILL TALLKCLSL LPLSCLHTLGN RLGLHAFYLL
51  KEDRARIVAN MRQAGLNPD P KTVKAVFAET AKGGLLELAPA FFRKPEDIET
101 MFKAVHGW EHVQQALDKHEG LLFITPHIGS YDLGGYISQ QLPFPLTAMY
151 KPPKIKAI DKIMQAGRVRGK GKTAPTISIQ VKQIIKALRS GEATIVLPDH
201 VSPQEGGEG VWVDFFGKPA YMTLAAKLA HVKGVKTLFF CCERLPGGQG
251 FDLHIRPVQ G ELNGDKAHDA AVFNRAEYW IRRFPTQYLF MYNRYKMP*

```

m505-1/g505 94.3% identity in 298 aa overlap

	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSL LPLSCLHTLGNRLGLHAFYLLKEDRARIVAN					
g505	MFRLQFRLFPPLRTAMHILLTALLKCLSL LSLSCLHTLGNRLGLHAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MRQAGLNPD PKTVKAVFAETAKGGLLELAPAFFRKPEDIETMFKAVHGW EHVQQALDKHEG					
g505	MRQAGLNPD TQTVKAVFAETAKCGLELAPAFFKKPEDIETMFKAVHGW EHVQQALDKGEG					
	70	80	90	100	110	120
m505-1.pep	LLFITPHIGSYDLGGYISQQLPFPLTAM YKPPKIKAI DKIMQAGRVRGKGKTAPTISIQ					
g505	LLFITPHIGSYDLGGYISQQLPFPLTAM YKPPKIKAI DKIMQAGRVRGKGKTAPTGIQ					
	130	140	150	160	170	180
m505-1.pep	VKQIIKALRSGEATIVLPDHVSPQEGGEGVWVDFFGKPAYTMTLAAKLAHVKG V KTLFF					
g505	VKQIIKALRAGEATII LPDHVSPQEGG-GVWADFFGKPAYTMTLAAKLAHVKG V KTLFF					
	190	200	210	220	230	240
m505-1.pep	CCERLPGGQGF DLHIRPVQ GELNGDKAHDA AVFNRAEYW IRRFPTQYLFMYNRYKMPX					
g505	CCERLPDGGQGFV LHIRPVQ GELNGKHA DA AVFNRT EY W IRRFPTQYLFMYNRYKTPX					
	240	250	260	270	280	290

m505-1/a505 99.7% identity in 298 aa overlap

	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSL LPLSCLHTLGNRLGLHAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSL LPLSCLHTLGNRLGLHAFYLLKEDRARIVAN					
	10	20	30	40	50	60
	70	80	90	100	110	120

748

m505-1.pep	MRQAGLNPDPKTVKAVFAETAKGGLELAPAFFRKPEDMETMFKAVHGWEHVQQALDKHEG
a505	MRQAGMNPDPKTVKAVFAETAKGGLELAPAFFRKPEDMETMFKAVHGWEHVQQALDKHEG
	70 80 90 100 110 120
m505-1.pep	LLFITPHIGSYDLGGYISQQLPFPPLTAMYKPPKIKAIKIMQAGRVRGKGTAPTSIQG
a505	LLFITPHIGSYDLGGYISQQLPFPPLTAMYKPPKIKAIKIMQAGRVRGKGTAPTSIQG
	130 140 150 160 170 180
m505-1.pep	VKQIIKALRSGEATIVLPDHVPSPOEGGEGVWVDFFGKPAYTMTLAAKLAHVKGVKTLFF
a505	VKQIIKALRSGEATIVLPDHVPSPOEGGEGVWVDFFGKPAYTMTLAAKLAHVKGVKTLFF
	190 200 210 220 230 240
m505-1.pep	CCERLPGGQGFDLHIRPVQGELNGDKAHDAAVFNRNAEYWIRRFPTQYLFMYNRYKMPX
a505	CCERLPGGQGFDLHIRPVQGELNGDKAHDAAVFNRNAEYWIRRFPTQYLFMYNRYKMPX
	250 260 270 280 290 299

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1375>:

g506.seq

```

1  ATGGCGGTAT  TTGATGAAGT  CGGGCGCATC  GCCCATGGCT  GCGGCGGTGT
51  TGTCAAACAA  AGCCTGTTTC  TCGCGTCGT  TCATCAGGTT  GAACAAGGCG
101 CGCGGTGGC  TGAAGTAGTC  GTCATCGTCT  TGGCGGTAGT  CCCAGTGTGC
151 CGCGTCGCCG  TTGATTTTCA  AAGGCGGTT  GCGGAAGTCG  GGTGTGTGCT
201 GCCATTGGCC  GAAGCTGTTG  GGTTCGTAGT  GCGGCAGGCT  GCCGTAGTTG
251 CCGTCGGCGC  GGCCTTGTC  GTCGCGCTG  TTGCTGTGAA  CAGGGCAACG
301 CGGACGATTG  ACGGGGATTT  GCGGGAAGTT  CACACCCAAG  CGGTAACGTT
351 GCGCGTCGGC  GTAATTGAAC  AAACGGGCTT  GCAACATTTT  ATCCGGGCTC
401 GCGCCGATAC  CGGGAACGAG  GTTGCTCGGT  GCGAAGGCGG  ATTGTTCAC
451 ATCGCGAAG  AAGTTTTCGG  GATTGCGGTT  CAACTCGAAT  TCGCCCACTT
501 CAATCAGCGG  ATAGTCTTTT  TTCGGCCAAA  CTTTGGTCAA  GTCAAACGGA
551 TGATAAGGCA  CTTTTTCGGC  ATCGGCTTCA  GGCATGACTT  GGATGTACAT
601 CGTCCATTTT  GGGAACTCGC  CGCGCTCGAT  GGCTTCGTAC  AGGTGCGGCT
651 GATGGCTTTC  GCGGTCGTCG  GCGATGATTT  TTGCAGCTTC  TTCGTTGGTC
701 AGGTTTTTAA  TCCCTTGCTG  GCTGCGGAAA  TGGAATTTCA  CCCAAAACG
751 TTCGCCCGCT  TCGTTCCAGA  AGCTGTAGGT  ATGCGAACCG  AAGCCGTGCA
801 TATGGCGGTA  GCTGGCGGGA  ATACCGCGGT  CGTCTATCAC  GATGGTAACT
851 TGGTGCAGGG  CTTGCGGCAG  CAGCGTCCAG  AAGTCCAGT  TGTGTGTGGC
901 GGAACGCATA  TTGGTGC GCG  GATCGCGTTT  GACGGCTTTG  TTCAGGTCCG
951 GGAATTTGCG  CGGGTCGCGC  AGGAAGAACA  CGGGCGTGTT  GTTGCCGACC
1001 ACATCCAGT  TGCCTTCTTC  GGTATAGAAT  TTCAACGCAA  AACC GCGGAT
1051 GTCGCGTTCC  GCATCGGCTG  CGCCGCGCTC  GCCTGCCACG  GTGGTGAAAC
1101 GGGCGAACAT  CTCGGTTTTT  TTGCCGACTT  CGCTGAAAA  TTTGGCGCGG
1151 GTGTATTTGG  TGATGTCGTG  TGTACGGTA  AACGTACCGA  ACGCGCCCGA
1201 ACCTTTGGCG  TGCATACGGC  GTTCGGGGAT  GACTTCGCGC  ACGAAGTCGG
1251 CGAGTTTTTC  ATTCAGCCAC  AAATCTTGCG  TCAGCAGGGG  GCCGCGCGGG
1301 CCGGCGGTCA  GGCTGTTTTG  ATTGTCGGCA  ACGGCGCGC  CGTTGTTTCA
1351 GGTCAGATGG  GTTACGGGGC  ATTTGGAGGT  AGTCATCGCT  CTTGTTCCCT
1401 TTCTCAGGTT  GGTCAAATGG  GGGGCAAACG  GCTTACAGTA  CGATTGGCG
1451 GAAAGCGTAT  TCGTAACCGG  TTTCTTGATT  GTAATAAATT  TCTGAATCG
1501 ACATTTTATT  TTCTTTTGC  AAAAATATG  GATGCGATTA  TACGCCAAGA
1551 TTTTCGTTAT  TAA

```

This corresponds to the amino acid sequence <SEQ ID 1376; ORF 506.ng>:

g506.pep

```

1  MAVFDEVGRI  AHGCGGVVKQ  SLFLRVVHQQ  EQGARLAEVV  VIVLAVVPVC
51  RVAVDQRRF  GEVGLLLPLA  EAVGFVVRQA  AVVAVGAALS  VALVAVNRAT
101  RTIDGDLAEV  HTQAVTLRVG  VIEQTGLQHF  IRARADTGNE  VARCEGGLFH
151  IGEEVFGIAV  QLEFAHFNQR  IVFFRPNFGQ  VKRMIRHFFG  IGRHDLDDVH

```

749

```

201  RPFRELAALD GFVQVALMAF AVVGDDFCFS FVGQVFNPLL AAEMEFHPKT
251  FARFVPEAVG MRTEAVHMAV AGGNTAVAHH DGNLVQGFQ QRPEVPVVC
301  GTHIGARIAF DGFVQVGEFA RVAQEEHGRV VADHIPVAFF GIEFQRKTAD
351  VAFRIGCAAL ACHGGETGEH LGFFADFAEN FGAGVFGDVV CYGKRTERAR
401  TFGVHTAFGD DFAHEVGEFF IQPQILRQQG AARAGGQAVL IVGNRAVVH
451  GQMGYGAFFG SHRSCSFSQV GQMGGKRLTV RFGGKRIRNR FLDCNKFLES
501  TFYFPFAKTM DAIIRQDFRY *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1377>:

m506.seq

```

1  ATGGCGGTAT TTGATGAAGT CGGGCGCGTC GCCCATTGCG GCGGCGGTGT
51  TGCCGAACAA TGCCGTGTTT TGCGCGTCGT TCATCAGGTT GAACAGGGCG
101 CGCGGTGGC TGAAATAGTC GTCATCGTCT TGGCGGTAGT CCCAGTGTGC
151 CGCGTCGCCG TTGATTTTCA AAGGCGGTTC GGCGAATCG GGTGTGTGCT
201 GCCATTGGCC GAAGCTGTyG GGTTCGTAGT GCGGCAGGCT GCCGyAGTTG
251 CCGTCGCGCG GGCCTTGCCC GTyGCGsTgr TTgCTGTgAA CAsGGCAACG
301 CGGACGATTG ACGGAATTT GCGGAAGTT TACGCCAAA CGGTAGCGTT
351 GTGCGTCGGC GTAATTGAAC AAACGCGCTT GCAGCATTTT ATCTsGGCTG
401 GCGCCGACAC CGGGAACGAG GTTGCTCGGT CGGAAGGCGG ATTGTTCCAC
451 ATCGGCGAAG AAGTTTTCGG GATTGCGGTT CTCAAACGGA TGATAAGGTA
501 CTTTTTCCGC GTCTGCTTCA GGCATGACTT GGATGTACAT CGTCCATTTC
551 GGAAACTCGC CGCGTTCGAT GGCTTCsTAT AAGTCGCGCT GATGGCTTTC
601 GCGGTCGTCG GCGATGATTT TGGCGGCTTC TTCGTTGGTC AGGTTTTTAA
651 TGCCTTGTTG GGTGCGGAAA TGGAATTTCA CCAAAAACG CTCGCCTGCT
701 TCGTTCCAGA AGCTGTAGGT ATGCGAACCG AAGCCGTGCA TATGGCGGTA
751 GCCGCGGGG ATGCCGCGGT CGCTCATCAC GATGGTAACT TGGTGAGTG
801 CTTGCGGCAG CAGCGTCCAG AAGTCCCAGT TGTTTGTGGC AGAGCGCATA
851 TTGGTGC GCGG GGTGCGGTTT GACGGCTTTG TTCAGGTCGG GGAACTTACG
901 CGGGTCGCGC AGGAAGAACA CGGGCGTGTT GTTGCCGACC ACATCCCAGT
951 TGCCTTCTTC GGTATAAAAT TTCAAGCAA AACCGCGGAT GTCGCGTTCT
1001 GCATCGGCTG CGCGCGCTTC GCCTGCCACG GTGGTGAAAC GGGCGAACAT
1051 CTCGTTTTTT TTGCCGACTT CGCTGAAGAT TCCTTTGGCG TGCATACGGC
1101 GTTCGGGGAT GACTTCGCGC ACGAAGTCGG CGAGTTTTTC AGTCATCGCT
1151 CTTGTTCCTT TTCTCAGGTT GGTCAAATGG GGGTAAACGG CTTACAGTAC
1201 GATTTGGCGG AAAGCGTATT CGTAACCGGT TTCTTGATTG CAATAAATTT
1251 CTTGAATCGA CATTTTATTT CCCTTTTGTA AAAACTATGG ATGCGACTAT
1301 ACGCCAAGAT TTTGCTATT AA

```

This corresponds to the amino acid sequence <SEQ ID 1378; ORF 506>:

m506.pep

```

1  MAVFDEVGRV AHCGGGVAEQ CLFLRVVHGV EQGARLAEIV VIVLAVVPVC
51  RVAVDQRRF GESGLLLPLA EAVGFVVRQA AXVAVGAALP VAXXAVNXAT
101 RTIDGNLAEV YAQTVALCVG VIEQTRLQHF IXAGADTNE VARCEGGLFH
151 IGEEVFGLAV QLEFAHFNQR IVFFRPNFGQ VKRMIRYFFR VCFRHLDDVH
201 RPFRLAAFD GFXXVALMAF AVVGDDFGGF FVGQVFNALL GAEMEFHPKT
251 LACFVPEAVG MRTEAVHMAV AGGDAVAHH DGNLVQCFQ QRPEVPVVC
301 RAHIGARVAF DGFVQVGELT RVAQEEHGRV VADHIPVAFF GIKFQGTAD
351 VAFICGCAAF ACHGGETGEH LGFFADFAED FGAGVFGDVV RYGKRTERAR
401 TFGVHTAFGD DFAHEVGEFF IQPQILRQQR AARTGGQAVL IVGNRRRAVVH
451 GQMGYRAFFG SHRSCSFSQV GQMGKRLTV RFGGKRIRNR FLDCNKFLES
501 TFYFPFVKTM DATIRQDFRY *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 506 shows 89.2% identity over a 520 aa overlap with a predicted ORF (ORF 506.ng) from *N. gonorrhoeae*:

m506/g506

```

m506.pep      10      20      30      40      50      60
MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDQRRF
|||||:| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g506          10      20      30      40      50      60
MAVFDEVGRVIAHCGGGVVKQSLFLRVVHQVEQGARLAEVVIVLAVVPVCRVAVDQRRF

```

	70	80	90	100	110	120
m506.pep	GESGLLLPLAEAVGFVVRQAA	XVAVGAALPV	AXXAVNXATRT	IDGNLAEVYAQT	VALCVG	
g506	GEVGLLLPLAEAVGFVVRQAA	VVAVGAALSVAL	VAVNRATRT	IDGDLAEVHTQ	AVTLRVG	
	70	80	90	100	110	120
	130	140	150	160	170	180
m506.pep	VIEQTRLQHFIXAGADT	GNEVARCEGGLF	HIGEEVFGIAV	QLEFAHFNQR	IVFFRPNFGQ	
g506	VIEQTGLQHFI	RARADTGN	EVARCEGGLF	HIGEEVFGIAV	QLEFAHFNQR	IVFFRPNFGQ
	130	140	150	160	170	180
	190	200	210	220	230	240
m506.pep	VKRMIRYFFRVC	FRHDLDVHRP	FRKLAAPDGF	XXVALMAFAV	VVGDDFGGF	VGVQVFNALL
g506	VKRMIRHFFG	IGFRHDLDVHRP	PRELAALDGF	VQVALMAFAV	VVGDDFCSF	FFVGVQVFNPLL
	190	200	210	220	230	240
	250	260	270	280	290	300
m506.pep	GAEMEFHPKTL	ACFVPEAVGM	RTEAVHMAVAG	GDAVAHHDGN	LVQCFCGQR	PEVPVVCG
g506	AAEMEFHPKTF	ARFVPEAVGM	RTEAVHMAVAG	NTAVAHHDGN	LVQFGFCGQR	PEVPVVCG
	250	260	270	280	290	300
	310	320	330	340	350	360
m506.pep	RAHIGARVAFD	GVQVGELTR	VAQEEHGRV	VADHIPVAF	FGIKFQGKT	ADVAFCIGCAAF
g506	GTHIGARIAFD	GVQVGEGFAR	VAQEEHGRV	VADHIPVAF	FGIEFQRKT	ADVAFRIGCAAL
	310	320	330	340	350	360
	370	380	390	400	410	420
m506.pep	ACHGGETGEHL	GFFADFAEDF	GAGVFGDV	VRYGKRTER	ARTFGVHTAF	GDDFAHEVGEFF
g506	ACHGGETGEHL	GFFADFAENF	GAGVFGDV	VCYGKRTER	ARTFGVHTAF	GDDFAHEVGEFF
	370	380	390	400	410	420
	430	440	450	460	470	480
m506.pep	IQPQILRQQA	AARTGGQAV	LIVGNRRAV	VHGMGYRA	FGGSHRSCS	SFSQVGQMGGKRLTV
g506	IQPQILRQQA	AARAGGQAV	LIVGNRAV	VHGMGYGA	FGGSHRSCS	SFSQVGQMGGKRLTV
	430	440	450	460	470	480
	490	500	510	520		
m506.pep	RFGGKRIRNR	FLDCNKFLE	STFYFPFVK	TMDATIRQDF	RY	
g506	RFGGKRIRNR	FLDCNKFLE	STFYFPFAK	TMDAIRQDF	RY	
	490	500	510	520		

a506.seq

1	ATGGCGGTAT	TTGATGAAGT	CGGGCGCGTC	GCCCATTGCG	GCGGCGGTGT
51	TGCCGAACAA	TGCCTGTTTC	TGCGCGTCGT	TCATCAGGTT	GAACAGGGCG
101	CGCGGTTGGC	TGAATAAGTC	GTCATCGTCT	TGGCGGTAGT	CCCAAGTGCGC
151	GCGCTCGCGC	TTGATTTTCA	AAGGCGGTTT	GCGCAAGTCG	GGCTGCTGCT
201	GCCATTGGCC	GAAGCTGTTG	GGTTCGTAGT	GCGGCAGGCT	GCGGTAGTTG
251	CCGTGCGGCG	GTCCTTGTCC	GTCGCGCTGG	TTGCTGTGAA	CAGGGCAACG
301	CGGACGGTTG	ACAGGGATTT	GTCGGAAGTT	CACGCCAAAG	CGGTAGCGTT
351	GCGCGTCGGC	GTAATTGAAC	AAACGCGCCT	GCAACATTTT	ATCTGGGCTG
401	GCGCCGACAC	CGGGAACGAG	GTTGCTCGGT	GCGAAGGCGG	ATTGTTCCAC
451	ATCGGCGAAG	AAGTTTTCGG	GATTGCGGTT	CAACTCGAAT	TCGCCCACTT
501	CAATCAGCGG	ATAGTCTTTT	TTCGGCCAAA	CTTTGGTCAA	GTCAAACGGA
551	TGATACGGCA	CTTTTTCGCG	ATCGGCTTCA	GCGATGACTT	GGATGTACAT
601	CGTCCATTTT	GGAAACTCGC	CGCGCTCGAT	GGCTTCGTAC	AGGTGCGGCT

751

```

651 GATGGCTTTC ACGGTCGTCG GCGATGATTT TGGCGGCTTC TTCGTTGGTC
701 AGGTTTTTAA TGCCTTGTTG GGTGCGGAAA TGGAAATTTCA CCCAAAAACG
751 CTCGCTGCT TCGTTCCAGA AGCTGTAGGT ATGCGAACCG AAGCCGTGCA
801 TATGGCGGTA GCCGGCGGGG ATGCCGCGGT CGCTCATCAC GATGGTAACT
851 TGGTGCAGTG CTTGCGGCAG CAGCGTCCAG AAGTCCAGT TGTTTGTGGC
901 AGAGCGCATA TTGGTGCGCG GGTGCGGTTT GACGGCTTTG TTCAGGTCGG
951 GGAACCTACG CGGGTCGCGC AGGAAGAACA CGGGCGTGTT GTTGCCGACC
1001 ACATCCCAGT TGCCTTCTTC GGTATAGAAC TTCAACGCAA AACC CGGAT
1051 GTCGCGTTCT GCATCGGCTG CGCCGCGTTC GCCTGCCACG GTGGTGAAAC
1101 GGGCGAACAT CTCGGTTTTT TTGCCGACTT CGCTGAAGAT TTTGGCGCGG
1151 GTGTATTTGG TGATGTCGTG CGTTACGGTA AACGTACCGA ACGCGCCCGA
1201 ACCTTTGGCG TGCATACGGC GTTCGGGGAT GACTTCGCGC ACGAAGTCGG
1251 CGAGTTTTTC ATTACGCCAC AAATCCTGCG CCAGCAGAGG GCCGCGAGGA
1301 CCGGCGGTCA GGCTGTTTTG ATTGTCGGCA ACAGGCGCGC CGTTGTTTAT
1351 GGTACAGATG GTTACAGGGC ATTTGGAGGT ANTCATCGCT CTTGTTCCCTT
1401 TTCTCAGGTT GGTCAAAT.G GGGGTAAACG GCTTACAGTA CGATTGGCG
1451 GAAAGCGTAT TCGTAACCGG TTTCTTGATT GCAATAAATT TCTTGAATCG
1501 ACATTTTATT TCCCTTTTGT AAAAATATG GATGCGACTA TACGCCAAGA
1551 TTTTCGCTAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 1380; ORF 506.a>:

```

a506.pep
  1 MAVFDEVGRV AHC GGGVAEQ CLFLRVVH QV EQGARLAEIV VIVLAVVPVR
 51 R VAVDFQRRF GEVGLLLPLA EAVGFVVRQA AVVAVGASLS VALVAVNRAT
101 RTVDRDLAEV HAQAVALRVG VIEQTRLQHF IWAGADTGNE VARCEGGLFH
151 I GEEVFGIAV QLEFAHFNQR IVFFRPNFGQ VKRMIRHFFR IGRHDLVDH
201 R PFRKLAALD GFVQVALMAF TVVGDDFGGF FVGQVFNALL GAEMEFHPKT
251 LACFVPEAVG MRTEAVHMAV AGGDAVAHH DGNLVQCFGQ QRPEVPVVC
301 RAHIGARVAF DGFVQVGELT RVAQEEHGRV VADHIPVAFF GIELQRKTAD
351 VAFICGCAAF ACHGGETGEH LGFFADFAED FGAGVFGDVV RYGRTERAR
401 TFGVHTAFGD DFAHEVGEFF IQPQILRQQR AARTGGQAVL IVGNRRAVVH
451 GQMGYRAFGG XHRSCSFSQV QXGGKRLTV RFGGKRIRNR FLDCNKFLES
501 TFYFPFVKTM DATIRQDFRY *

```

m506/a506 94.8% identity in 520 aa overlap

	10	20	30	40	50	60
m506.pep	MAVFDEVGRVAHC GGGVAEQCLFLRVVH QVEQGARLAEIVVIVLAVVPVCRVAVDFQRRF					
a506	MAVFDEVGRVAHC GGGVAEQCLFLRVVH QVEQGARLAEIVVIVLAVVPVRRVAVDFQRRF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m506.pep	GESGLLLPLAEAVGFVVRQAAXVAVGAALPVAXXAVNXATRTIDGNLAEVYAQTVALCVG					
a506	GEVGLLLPLAEAVGFVVRQAAXVAVGASLSVALVAVNRATRTVDRDLAEVHAQAVALRVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m506.pep	VIEQTRLQHFIXAGADTGNEVARCEGGLFHI GEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
a506	VIEQTRLQHFIWAGADTGNEVARCEGGLFHI GEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m506.pep	VKRMIRYFFRVCFRHDLDVHRPFRKLAALDGFXXVALMAFAVVGDDFGGFVVGQVFNALL					
a506	VKRMIRHFFRIGFRHDLDVHRPFRKLAALDGFVQVALMAFTVVGDDFGGFVVGQVFNALL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m506.pep	GAEMEFHPKTLACFVPEAVGMRTAVHMAVAGGDAVAHHDGNLVQCFGQQRPEVPVVC					
a506	GAEMEFHPKTLACFVPEAVGMRTAVHMAVAGGDAVAHHDGNLVQCFGQQRPEVPVVC					
	250	260	270	280	290	300

752

	310	320	330	340	350	360
m506.pep	RAHIGARVAFDGFVQVGELTRVAQEEHGRVVADHIPVAFFGIKFQGKTADVAFICGCAAF					
a506	RAHIGARVAFDGFVQVGELTRVAQEEHGRVVADHIPVAFFGIELQKRTADVAFICGCAAF					
	310	320	330	340	350	360
	370	380	390	400	410	420
m506.pep	ACHGGETGEHLGFFADFAEDFGAGVFGDVVRYGKRTERARTFGVHTAFGDDFAHEVGEFF					
a506	ACHGGETGEHLGFFADFAEDFGAGVFGDVVRYGKRTERARTFGVHTAFGDDFAHEVGEFF					
	370	380	390	400	410	420
	430	440	450	460	470	480
m506.pep	IQPQILRQQRARTGGQAVLIVGNRRRAVVHGMGYRAFGGSHRSCSFQVGMGGKRLTV					
a506	IQPQILRQQRARTGGQAVLIVGNRRRAVVHGMGYRAFGGXHRSCSFQVGMGXGGKRLTV					
	430	440	450	460	470	480
	490	500	510	520		
m506.pep	RFGGKRIRNRFDCNKFLESTFYFPFVKTM DATIRQDFRYX					
a506	RFGGKRIRNRFDCNKFLESTFYFPFVKTM DATIRQDFRYX					
	490	500	510	520		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1381>:

g507.seq

```

1  ATGCTCTTGC CGGCTTTGCA ACAAGGCGGC GGCTTCCTGA GCGGCGGCGG
51  TTTCGGCCTC GTCGGGCAGG TTCAGGGCTT GGTTCCTCTG CTTCAGACGG
101 CCTTTGCGCT CTTCGTGCTT GGCAACGGTT TGTTCCGGCAT GGGCAAGCTG
151 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCCTGCT
201 GGGTTTGGA AAGCAGCGTT AGCGTGGCTT GGACTTCTTC CAATTCGGGC
251 AGACGCTCCT CGTGTTCGGC AACCTGCATC GCCCATTCCT CCAATTCGGT
301 TTGCTTTTCT TCGACCTGCA ACTCGTTTTC CTCAAGCTGC ACGCGGATTT
351 GCTGCTGCTC CTGCGCGATG CGTTGCAACT GCGCCTGCGC TGCCTGCTTG
401 TCGCGTTTCA TCGCTTGGTG CAGGTTTTCG CCGTGGCGGA TTTGTTCTTC
451 CAAACGGGCA ATCTGCTCGC GCAACACGCC GCGTTTGTTC CTCAATTCGT
501 GTACTGCCTG CTGCTGCGAC TGTTCGGCAG TCTGCAAGGC GTGTACTTCG
551 TTATTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1382; ORF 507.ng>:

g507.pep

```

1  MLLPALQGG GFLSGGGFGL VGQVQGLVFL LQTAFALFVL GNRLFQGMGKL
51  LLLQRQFAAD AVCLVLLGLE GSVERGLDFF QFGQTLFVFG NLHRPFRQFG
101 LLFFDLQLVF LKLHADLLLL LPDALQLRLR CLLVAFDALV QVLPVADLFF
151 QTGNLLAQHA AFVAQFVYCL LLRLFGSLQG VYFVI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1383>:

m507.seq

```

1  ATGCTCTTGC TGACTTTGCA ACAAGGCGGC TGCTTCCTGC GCGGCGGCGG
51  TTTCGGCCTC GTCGGGCAGG TTTAAGGCTT GGTTCCTCTG TTTCAGACGA
101 CCTTTGCGCT CTTCGTGCTT GGCAATCGTT TGTTCCGGCAT GGGCAAGCTG
151 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCCTGCT
201 GGGTTTGGA AAGCAGCGTT AGCGTGGCTT GGGCTTCTTC CAATTCGGGC
251 AGACGCTCCT CGTGTTCGGC AACCTGCATC GCCCATTCCT CCAGCTCGGT
301 TTGTTTTTCT TCGACCTGCA ACTCGTTTTC TTCAAGCTGC ACGCGGATTT
351 GCTGCTGCTC TTGATGAATG CGTTGTA ACT GCGCCTGCGC TGCCTGCTTG
401 TCGCGTTTCA TCGCTTGGTG CAGGTTTTCG TGATGGCGGA TTTGTTCTTC
451 CAAACGGGCA ATCTGCTCGC GCAACACGCC GCGCTTGTTC CTCAATTCAT
501 GCACTGCCTG CTGCTGCGAC TGTTCGGCAG TCTGCAAGGC GTGTACTTCG
551 TCGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1384; ORF 507>:

m507.pep

```

1  MLLLTLLQGG CFLRGGGFGF VGQVXGLVFL FQTTFALFVL GNRLFQGMGKL

```


753

51 LLLQRQFAAD AVCLVLLGLE GGVERGLGFF QFGQTLLVFG NLHRPFRQLG
 101 LFFFDLQLVF FKLHADLLLL LMNALXRLRL CLLVAFDALV QVLLMADLFF
 151 QTGNLLAQHA ALVAQFMHCL LLRLFGSLQG VYFVV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 507 shows 87.0% identity over a 185 aa overlap with a predicted ORF (ORF 507.ng) from *N. gonorrhoeae*:

m507/g507

	10	20	30	40	50	60
m507.pep	MLLLTLQQGGCFLRGGGFGFVGVQVXGLVFLFQTTFALFVLGNRLFGMGKLLLLQRQFAAD					
	: :					
g507	MLLPALQQGGFSLGGGFLVGVQVGLVFLLOTAFALFVLGNLFGMGKLLLLQRQFAAD					
	10	20	30	40	50	60
m507.pep	AVCLVLLGLEGGVERGLGFFQFGQTLLVFGNLHRPFRQLGLFFFDLQLVFFKLHADLLLL					
	: : :					
g507	AVCLVLLGLEGSVERGLDFFQFGQTLFVFGNLHRPFRQFGLLFFDLQLVFLKLHADLLLL					
	70	80	90	100	110	120
m507.pep	LMNALXRLRLRCLLVAFDALVQVLLMADLFFQTGNLLAQHAALVAQFMHCLLLRLFGSLQG					
	: : : :					
g507	LPDALQLRLRCLLVAFDALVQVLPVADLFFQTGNLLAQHAAFVAQFVYCLLLRLFGSLQG					
	130	140	150	160	170	180
m507.pep	VYFVV					
	:					
g507	VYFVI					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1385>:

a507.seq

1	ATGCTCTTGC	TGGCTTTGCA	ACAAGGCGGC	AGCTTCCTGC	GCGGCGGCGG
51	TTTCGGCTTC	GTCAGGCAGA	TTCAGGGCTT	GGTTTTCCTG	TTTCAGACGA
101	CCTTTGCGCT	CTTCGTGCTT	GGCAACGGTT	TGTCGGCAT	GGGCAAGCTG
151	CTGCTGCTTC	AACGCCAGTT	CGCGGCGGAT	GCGGTTTGCC	TCGTCCTGCT
201	GGGTTTGGA	GGCGGCATTG	AGTGTGGCTT	GGGTTTCTTC	CAATTGCGGC
251	AGACGCTCTT	CGTGTTCCGC	AACCTGCATC	GCCCATTCCG	CCAATTCGGT
301	TTGCTTTTCT	TCCGCCTGCA	ACTCGTTTTT	TTCAAGCTGC	ACGCGGATTT
351	GCTGCTGCTC	CTGATGGATG	CGCTGCATCT	GCGCCTGCGC	CGCCTGCTTG
401	TCGCGTTTCG	TGCGTTGGTG	CAGGTTTTGC	TGATGGCGGA	TTTGTTCTTC
451	CAAACGGGCA	ATCTGTTTCG	GCAACACGCC	GCGTTTGTG	CCCAATTCGT
501	GCACCGCCTG	CTGCTGCGAC	TGTTCCGGCAG	TCTGCAAGGC	GTGTACTTCG
551	TCGTTTAA				

This corresponds to the amino acid sequence <SEQ ID 1386; ORF 507.a>:

a507.pep

1	MLLLALQQGG	SFLRGGGFGF	VRQIQGLVFL	FQTTFALFVL	GNLFGMGKL
51	LLLQRQFAAD	AVCLVLLGLE	GGIECGLGFF	QFGQTLFVFG	NLHRPFRQFG
101	LLFFRLQLVF	FKLHADLLLL	LMDALHLRLR	RLVAFDALV	QVLLMADLFF
151	QTGNLFAQHA	AFVAQFVHRL	LLRLFGSLQG	VYFVV*	

m507/a507 89.7% identity in 185 aa overlap

	10	20	30	40	50	60
m507.pep	MLLLTLQQGGCFLRGGGFGFVGVQVXGLVFLFQTTFALFVLGNRLFGMGKLLLLQRQFAAD					
	: :					
a507	MLLLALQQGGSFLRGGGFGFVRQIQGLVFLFQTTFALFVLGNLFGMGKLLLLQRQFAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120

754

```

m507.pep  AVCLVLLGLEGGVERGLGFFQFGQTLFVFGNLHRPFRQLGLFFFDLQLVFFKLHADLLLL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a507       AVCLVLLGLEGGIECGLGFFQFGQTLFVFGNLHRPFRQFGLLFFRLQLVFFKLHADLLLL
          70      80      90      100     110     120

          130     140     150     160     170     180
m507.pep  LMNALXLRRLRCLLVAFDALVQVLLMADLFFQTGNLLAQHAALVAQFMHCLLLRLFGSLQG
          ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a507       LMDALHLRLRLRLVAFDALVQVLLMADLFFQTGNLFAQHAAFAVQFVHRLLLRLFGSLQG
          130     140     150     160     170     180

m507.pep  VYFVVX
          |||||
a507       VYFVVX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1387>:

```

g508.seq
1  ATGGTAGCGT TTGGCGTTGA TCAGGGCCTC CTGCTGCTGC AACAGGGCGG
51 TTTGGGTGGC GGCTGAAGC TGCGGCAGCT TGGTTTGACG GGTTTGACG
101 CGGGCGTATT GCTCCCTGCC CTGTTCTCTGA ATCTGCGCGA GTTTTCTCTG
151 CACGGCGATG TATCTTTCGT CCAGCGTGTG TACGGTTTCG GTCAACTCGT
201 CGAGCTTGAT GTGCTGCTCG TCGTTTTGGA ACTCGGTTTC ATAGGCGAGG
251 GCAAGCTCTT GCCGGCGTTC CTGCCAGTCC AGGGTTTGCT GTTCGAGCCG
301 GCGGATTGTC TGCCGGTAGT TTTGTTTTTG CGGGTTGAGT TTGTGGACGG
351 CGACTTCGGC AAGCCCGTAT TGGCGGTTGG CTTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGGCCTTG CTGCTCTTGG CGGCTGTGCG CGGTGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAAGTA GCGATGTCGT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1388; ORF 508.ng>:

```

g508.pep
1  MVAFGVDQGL LLLQQGGLGG GLKLRQLGLQ GLYAGVLLPA LFLNLRFFFL
51 HGDVFFVQRV YGFGQLVELD VLLVVLELGF IGEGKLLPAF LPVQGLLFEP
101 GDLLPVVLF L RVEFVDGDFG KPVLA VGFQQ GKLRLFQTAL LLLAAVRGGL
151 LLVFEFGGGF LQSSDVV

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1389>:

```

m508.seq
1  ATGGTAGCGT TTGGCGTTGA TCAGGGCTTC CTGCTGCTGC AACAGGGCGG
51 TTTGGGTGGC GGCTGAAGC TGCGGCAGCT TGGTTTGACG GGTTTGCACT
101 TTAGCGTATT GCTCCCTGCC CTGTTCTCTGA ATCTGCGCGA GTTTCTCTTG
151 CACAACAATA TATCTTTCGT CCAAGGTCTG TACGGCTTCG CTTAATTCTT
201 CAAGCTTGAT GTGCTGCTCG TCGTTTTGGA ACTCGGTTTC ATAGGCGAGG
251 GCAAGCTCTT GCTGGCGTTC CTGCCAGTCG AGGGTTTGCT GTTCAAGCTG
301 GCGGATTGTC TGCCGGTAGT TTTGTTTTTG CTGGTTGAGT TTGTGGACGG
351 CGACTTCGGC AAGCCCGTAT TGGCGGTTGG CTTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGGCCTTG CTGCTCTTGG CGGCTGTGCG CGGTGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAAGTA ACGATGTCGT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1390; ORF 508.ng>:

```

m508.pep
1  MVAFGVDQGF LLLQQGGLGG GLKLRQLGLQ GLHFSVLLPA LFLNLRFFLL
51 HNNIFFVQGL YGFAXFFKLD VLLVVLELGF IGEGKLLAF LPVEGLLFKL
101 GDLLPVVLF L LVEFVDGDFG KPVLA VGFQQ GKLRLFQTAL LLLAAVRGGL
151 LLVFEFGGGF LQNDVV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 508 shows 86.8% identity over a 167 aa overlap with a predicted ORF (ORF 508.ng) from *N. gonorrhoeae*:

m508/g508

755

	10	20	30	40	50	60
m508.pep	MVAFGVDQGGFLLQQGGGLGGGLKLRQLGLQGLHFSVLLPALFLNLRFFLLHNNIFFVQGL					
g508	MVAFGVDQGGFLLQQGGGLGGGLKLRQLGLQGLYAGVLLPALFLNLRFFLLHGDVFFVQRV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m508.pep	YGFAXFFKLDVLLVVLELGFIGEGKLLLAFLPVEGLLFLKLGDLLPVVLFLLVEFVDGDFG					
g508	YGFQQLVELDVLLVVLELGFIGEGKLLPAFLPVQGLLFEPGDLLPVVLFLLRVEFVDGDFG					
	70	80	90	100	110	120
	130	140	150	160		
m508.pep	KPVLA VG FQ QG KLR L FQTALLLLAAVRGGLLVFEFGGGFLQGN DVV					
g508	KPVLA VG FQ QG KLR L FQTALLLLAAVRGGLLVFEFGGGFLQSS DVV					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1391>:

```
a508.seq
1  ATGGTAGCGT TTGGCGTTGA TCAGGGCTTC CTGCTGCTGC AACAGGGCGG
51  TTTGGGTGGC GGCCTGAAGC TGCGGCAGCT TGGTTTGCAG GGTTTGTACG
101 CGGGCGTATT GTTCCCTACC CTGCTCCTGA ATCTGCGCGA GTTCTCCTG
151 TACGACAATA TATTCTTCGT CCAAACCTCG TACGGCTTCG CTCAACTCTT
201 CGAGCTTGAT GTGCTGCTCG TCGTTTGGGA ACTCGGTTTC ATAGGCGAGG
251 GCAAGCTCTT GCTGGCGTTC CTGCCAATCG AAGGTTTGT GTTCAAGCTG
301 GGCAATTTGC TGTGGTAGT TTTGTTTTTG CTGGTTGAGC TTGTGGACGG
351 CGACTTCGGC AAGCCCGTAT TGGCGGTTGG CTTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGACCTTG CTGCTCTTGG CGGCTGTGCG CGGCGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAATG GCGATGTCGT
501 CTGA
```

This corresponds to the amino acid sequence <SEQ ID 1392; ORF 508.a>:

```
a508.pep
1  MVAFGVDQGF LLLQQGGGLGG GLKLRQLGLQ GLYAGVLFPT LLLNLRFFLL
51  YDNIFFVQTL YGFAQLFELD VLLVVLELGF IGEGKLLLAFL LPIEGLLFLK
101 GNLLLVVFL LVELVDGDFG KPVLA VG FQ QG KLR L FQTALLLLAAVRGGL
151 LLVFEFGGGF LQNGDVV*
```

m508/a508 88.6% identity in 167 aa overlap

	10	20	30	40	50	60
m508.pep	MVAFGVDQGGFLLQQGGGLGGGLKLRQLGLQGLHFSVLLPALFLNLRFFLLHNNIFFVQGL					
a508	MVAFGVDQGGFLLQQGGGLGGGLKLRQLGLQGLYAGVLFPTLLNLRFFLLYDNIFFVQTL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m508.pep	YGFAXFFKLDVLLVVLELGFIGEGKLLLAFLPVEGLLFLKLGDLLPVVLFLLVEFVDGDFG					
a508	YGFAQLFELDVLVVLELGFIGEGKLLLAFLPIEGLLFLKLGNNLLVVLFLLVELVDGDFG					
	70	80	90	100	110	120
	130	140	150	160		
m508.pep	KPVLA VG FQ QG KLR L FQTALLLLAAVRGGLLVFEFGGGFLQGN DVVX					
a508	KPVLA VG FQ QG KLR L FQTALLLLAAVRGGLLVFEFGGGFLQNG DVVX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1393>:

g509.seq

756

```

1   atggtcgctg tatgtgatga acgggctgta cagcggacgt tgggtggccca
51  attcgcgcaa caaggcggct tgtttttgct cttcgttcag gctgtttag
101 tcttccaagc ctgcgtgttg gaaaagctcg gcaaccacat cggcgtgttt
151 gcctgcgtgt tggcgcaggt cgagcggcat catgtggaag ccgaacacgg
201 acacggaacg gatgaggtct gccaaacggc cttcggcaag caggcggctg
251 ccgttgtcga taagggaacg ttgcaatttt ttcaaatacat cgagaaattt
301 ttgggcccga gcataaggct cgagaaagcc gaatttgcag cccatgccca
351 aaccgagcga gcgcgctttg cccatagcgc gcgccataat gtaggcaatg
401 gcgcggcggt aagggttcttc ggtgcgggcg atttcttcgt caggcgagag
451 ggctgccagt gccattacgt cgtcgttgac tttgacgcgg cggatggaaa
501 gcggcagttc gcggtaaagt ttgtcgagtt cgtgcggta aaaacggaac
551 acggcatcgg cgtggcggcg gaaggcaaag cgcagggttt cgccagaaac
601 aaacggattg ccgtcgcggg cgccgccgat ccagccgccg attttaagga
651 tattcggaac gcggacatcg ggataggccg tctgaaagtc gtgtccatc
701 ttgcggtaga gtttgggcag ggcttcaaaa aagctcatcg ggaagatgga
751 cacgccgttg ttgatttcgt cgttgacgct gagtttgtgg cggcgcgttt
801 cgtcgttctg ccacaagccc agaagcacgg tgtcgatttc gcggcgcagc
851 cgtgccagcg cgtcggcatt ggtgcagcgt tcgcgttgcg gcagcagcgc
901 gcggatgcgg cggttgaaat tcaaaacggg ttggcgttgc acttcggctg
951 ggtgcgcggg caaaacggcg gtaacggacg tattgtccaa ctgccgctgc
1001 accgatttgc cgtcggcttt ccccgctttg agcctgcgga cggttccgt
1051 caggctgcct tctgctgcgt tgtggccggc atcttcgtgg atttggcggc
1101 ggcgttcgtg gtgcacgtct tcggcgatat tcagaatctg ggcgaaacagc
1151 ccgcaggcaa gcgtcagatc gtaggtctgc cgttcgtcca attgcggcaa
1201 tactttttca atcaatgccg cgtgtcgtc ggaagtggac aagagtttga
1251 ccgttttcgac aaccaacggc gaggttcttc cgtgcaggag gttgaacagg
1301 gactgtttca aaaattccgc gtcgcgcgc aaagccgcgt ccttcggatt
1351 gttcaggata tgcagttgca tgattttcct ctcattgccg taaatactgt
1401 aaatgtacct caaatgccgc atccgtgcca aaccgttcac actttaacca
1451 ctcattgtcc gaaatgccgt ctgaagttag acgccgcccg acggcggcgt
1501 tacaatcgcc cgcaactgtt tttttccgaa catcatcatg accgcgaccg
1551 aacacgacaa cgacgacgca ctctgctgc ggtacagccg ccacatcctc
1601 ttggacgaaa tcggcatcga agggcagcag aagctttccg ccgcgcatac
1651 tttggtcgtc ggctgcggcg gattgggcgc cgcgcgccct gccctatctc
1701 gccgcctcgg gggtcggcac gctga

```

This corresponds to the amino acid sequence <SEQ ID 1394; ORF 509.ng>:

g509.pep

```

1   MVAVCDERAV ORTLVAQFAQ QGGLEFLLFVQ AVVVVFQACVL EKLGNHIGVF
51  ACVLAQVERH HVEAEHGHGT DEVCQTAFGK QAAAVVDKGT LQFFQIIIEKF
101 LGRSIRLEKA EFAAHAQTER ARFAHSARHN VGNGAAVRFF GAGDFFVRRRE
151 GCQCHYVVVD FDAADGKRQF AVKFVEFAAV KTEHGIGVAA EGKAQGFARN
201 KRIAVAAAD PAADFKDIRN ADIGIGRLKV VFHLAVEFGQ GFKKAHREDG
251 HAVVDFVUDA EFVAARFAGL PQAQKHGVDF AAQPCQRVGI GAAAFALRQQR
301 ADAAVEIQNG LALHFGRVRG QNGGNGRIVQ LPLHRFAVGF PRFEPADGFR
351 QAAFCCVVAG IFVDLAAAFV VHVFGDIQNL GEQPAGKRQI VGLPFVQLRQ
401 YFFNQCRVVV GSGQEFDRFD NQRRGFFVQE VEQGLFQKFR VRRQSRVLRI
451 VQDMLHDFP LIAVNTVNVP QMPHPCQTVH TLTHVTPKCR LKLNAARRRR
501 YNRPQLFFSE HHHRDRDRTRQ RRRTPAAVQP PHPLGRNRHR RAAEAFRRAY
551 FGRRLLRRIGR RRPCISPPIR GSAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1395>:

m509.seq

```

1   ATGGTCGCTG TATGTGATAA ACGGGCTGTA CAGAGGACGT TGATGGCTCA
51  ATTCGCGCAA CAGGGCGGTT TGTTTTGTCT CTTCGTTCAG GCGGTTGTAG
101 TCTTCCAAGC CTGCGTGTGT GAAAAGCTCG GCAACCACAT CGGCGTGTTC
151 GCCTGCGTGT TGGCGCAAGT CGAGCGGCAT CATGTGAAAG CCGAACACGG
201 ATACGGAACG GATGAGGTCT GCCAAACGGC CTTGCGCAAG CAGACGGCTG
251 CCGTTGTGCA TAAGGGAACG TTGCAATTTT TTCAAATCAT CCAGAACTC
301 TTGTGCCGAA GCATAAGGCT CGAGAAAGCC GAATTTGCAG CCCATACCCA
351 AACCGAGCGC GCGCGCTTTG CCCATAGCGC GCGCCATAAT GTAGGCGATG
401 GCGCGGCGGT AGGGTTCTTC GGCGCGGGCG ATTTCTTCGT CGGGCGATTT
451 GTCGGACAAC GCCGTTACAT CGCCGTTGAC TTTGACGCGG CGGATGGAGA
501 GCGGCAGTTC GCGGTAGAGT TTGTCGAGTT CGCCGCGATA GAAGCGGAAC

```

757

```

551 ACGGCATCGG CGTGGCGGCG GAAGGCAAAG CGCAGGGTTT CGGCAGAAAC
601 AAACGGATTG CCGTCGCGGT CGCCGCCGAT CCAGCCGCCG ATTTTGAGGA
651 TGTCCGGAAC GCGGACGCCG GGATAGGCCG TCTGAAAGTC GTGTTCCATC
701 TTGCGGTAGA GCTTGGGCAG GGCTTCGAAA AAGCTCATCG GGAAGATGGA
751 CACGCCGTTG TTGATTTCGT CGTTGACGCT GAGTTTGTGG CGGCGCGTTT
801 CGCTGGTCTG CCACAAGCCC AGCAGGATAG TGTCGATTtC GCgGCGCAGC
851 CGTGCCAGCG CGTCGGCATT GGTGCAGCGT TCgCGTTGCG GCAACAGTGC
901 GCGGATGCGG CGGTTGAAGC TTAAGACGGT TTGGCGTTGC ACTTCGGTCG
951 GGTGCGCGGT CAAAACGGCG GTAACGGACG TATTGTCCAA CTGCCGCTGC
1001 ACCGATTTGC CGTCGGCTTT CCCCCTTTG AGCCTGCGGA CGGTTTCCGT
1051 CAGGCTGCC'T TCCGCGCCGC CGCGTCCGGC TTCTTCGTGG ATTTGGCGGC
1101 GCGGTTCTGT GTGCACGTCT TCGGCGATGT TCAAATCTG GGCGAACAGG
1151 CCGCAGGCCA AGGTTAAATC GTGGGTTTGT TGTTCTGTTT ATTGCGGCAA
1201 TACTTTTTCA ATCAATGCCG CGCTGTCGTC GGAAGTGGAC AAGAGTTTGA
1251 CTGTTTCGAC AACCAACGGC GAGGCTTCTT CGTGCAGGAG GTTGAACAGG
1301 GATTGTTTCA GAAATTCCGC GTCCGCCGCC AAAGCCGCGT CCTTTGGATT
1351 GTTCAGAATA TGCAGTTGCA TGATTTTTCT CTCTCGTCTG CCGTAAATAT
1401 TGTAATGTA CCCCAAATGC CGCATCCGTG CCAAACCGTT CACACTTTAA
1451 CCGCCCGTGT CCCGAAATGC CGTCTGAAGT TGAACGCCGC CCGACGGCAG
1501 CGTTACAATC GCCCGCAACT GTTTTtTTCC GAACATCATC ATGACCACGA
1551 CCGAACACGA CAACGACGAT GCATTCTGTC TCGGTACAG CCGCCACATC
1601 CTCTTGACG AAATCGGCAT CGAAGGGCAG CAGAACTTT CCGCCGCGCA
1651 TATTTTGGTC GTCGGCTGCG GCGGTTTGGG TGCCGCCGCA CT.GCCCTAC
1701 CTTGCCGCTT CGGGTGTCGG CACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1396; ORF 509>:

```

m509.pep
1  MVAVCDKRAV QRTLMAQFAQ QGGLFLLFVQ AVVVVFQACVL EKLGNHIGVF
51 ACVLAQVERH HVKAEHGYGT DEVCQTAFGK QTAAVVDKGT LQFFQIIQKL
101 LCRSIRLEKA EFAAHTQTER ARFAHSARHN VGDGAAVGFF GAGDFFVGRF
151 VGQRRYIAVD FDAADGERQF AVEFVEFAAI EAEHGIGVAA EGKAQGFGRN
201 KRIAVAVAAD PAADFEDVRN ADAGIGRLKV VFHLAVELGQ GFKAHREDG
251 HAVVDFVDA EFVAARFAGL PQAQDSDVDF AAQPCQRVGI GAAFALRQQC
301 ADAAVEAXDG LALHFGVRG QNGNGRIVQ LPLHRFAVGF PRFEPADGFR
351 QAAFRAAASG FFVDLAAAFV VHVFGDVQNL GEQAAGQGXI VGLLFVQLRQ
401 YFFNQCRVV GSGQEFDCF NQRRGFFVQE VEQGLFQKFR VRRQSRVLWI
451 VQNMQLHDFS LSSAVNIVNV PQMPHPCQTV HTLTARVPKC RLKLNARRQ
501 RYNRPQLFFS EHHHDHRT RRCIPAAVQ PPHPLGRNRH RRAAETFRRA
551 YFGRRLRRFG CRRTXPTLPL RVSAR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 509 shows 87.8% identity over a 575 aa overlap with a predicted ORF (ORF 509.ng) from *N. gonorrhoeae*:

```

m509/g509
          10      20      30      40      50      60
m509.pep  MVAVCDKRAVQRTLMAQFAQQGGLFLLFVQAVVVVFQACVLEKLGNHIGVFACVLAQVERH
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g509      MVAVCDERAVQRTLVAQFAQQGGLFLLFVQAVVVVFQACVLEKLGNHIGVFACVLAQVERH
          10      20      30      40      50      60

          70      80      90      100     110     120
m509.pep  HVKAEHGYGTDEVCQTAFGKQTAAVVDKGTLQFFQIIQKLLCRSIRLEKAEFAAHTQTER
          ||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g509      HVEAEHGHGTDEVCQTAFGKQAAAVVDKGTLQFFQIEKFLGRSIRLEKAEFAAHAQTER
          70      80      90      100     110     120

          130     140     150     160     170     180
m509.pep  ARFAHSARHNVDGAAVGFFGAGDFFVGRFVGQRRYIAVDFDAADGERQFAVEFVEFAAI
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g509      ARFAHSARHNVGNAAVRFFGAGDFFVRREGCQCHYVVVDFDAADGKRQFAVKFVEFAAV
          130     140     150     160     170     180

```

	190	200	210	220	230	240
m509.pep	EAEHGIGVAAEGKAQGGFRNKRIAVAVAADPAADFEDVRNADAGIGRLKVVFHLAVELGQ					
	::	:		:		:
g509	KTEHGIGVAAEGKAQGGFARNKRIAVAVAADPAADFDIRNADIGIGRLKVVFHLAVEFGQ					
	190	200	210	220	230	240
	250	260	270	280	290	300
m509.pep	GFEKAHREDGHAVVDFVVDAAEFVAARFAGLPQAQQDSVDFAAQPCQRVGIGAAAFALRQQC					
	:			:		
g509	GFKKAHREDGHAVVDFVVDAAEFVAARFAGLPQAQKHGVDFAAQPCQRVGIGAAAFALRQQR					
	250	260	270	280	290	300
	310	320	330	340	350	360
m509.pep	ADAAVEAXDGLALHFGRVRGQNGNGRIVQLPLHRFAVGFPFRFEPADGFRQAAAFRAAASG					
	:					::
g509	ADAAVEIQNGLALHFGRVRGQNGNGRIVQLPLHRFAVGFPFRFEPADGFRQAAAFCCVVG					
	310	320	330	340	350	360
	370	380	390	400	410	420
m509.pep	FFVDLAAAFVHVHFGDVQNLGEEAAGQGXIUGLLFVQLRQYFFNQCRVVGSGQEFD					
	:	:				
g509	IFVDLAAAFVHVHFGDIQNLGEEPAQKRQIVGLPFVQLRQYFFNQCRVVGSGQEFDRFD					
	370	380	390	400	410	420
	430	440	450	460	470	480
m509.pep	NQRRGFFVQEVEQGLFQKFRVRRQSRVLWIVQNMQLHDFSLSSAVNI VNPQMPHPCQTV					
			:			
g509	NQRRGFFVQEVEQGLFQKFRVRRQSRVLRIQDMQLHDFPLI-AVNTVNPQMPHPCQTV					
	430	440	450	460	470	
	490	500	510	520	530	540
m509.pep	HTLTARVPKCRCLKLNAARRQRYNRPQLFFSEHHHDHDRTRQRRICIPAAVQPPHPLGRNRH					
	::	:		:		
g509	HTLTTHVPKCRCLKLNAARRRRYNRPQLFFSEHHHDHDRTRQRRRTPAAVQPPHPLGRNRH					
	480	490	500	510	520	530
	550	560	570			
m509.pep	RRAAETFRRAYFGRRLRRRFGCRRTCPTLPLRV SAR					
	:					
g509	RRAAEAFRRAYFGRRLRRRIGRRRRCPI SPPRG SAR					
	540	550	560	570		

```
a509.seq
1  ATGGTGCCTG  TATGTGATGA  ACGGACTGTA  CAGTGGACGT  TGATGGCTCA
51  ATTCGCGCAA  CAGGGCGGCT  TGTTTTTGCT  CTTCTGTGAG  GCTGTTGTAG
101 TCTTCCAAGC  TCGCGTGTG  GAAAAGCTCG  GCCAACCAT  CGGCGTGTTT
151 GCCTGCGTGT  TGGCGCAGGT  CGAGCGGCAT  CATGTGGAAG  CCGAACACGG
201 ATACGGAACG  GATGAGGTCT  GCCAACCGGC  CTTCGGCAAG  CAGGCGGCTG
251 CCGTTGTCTG  TAAGGGAATG  TTGCAATTTT  TTCAAATCAT  CGAGAAATTC
301 TTGTGCCGAA  GCATAAGGCT  CGAGAAAGCC  GAATTGTGAC  CCCATACCCA
351 AACCGGACGC  GCGCGCTTTG  CCCATAGCGC  CGCCATAAAT  TAGGCAATG
401 GCGCGACGGT  AGGGTTCTTC  GGCGCGGGCG  GTTTCCTTCG  CGGGCGATTT
451 GTCGGACAAC  GCCATCACAT  CGCCGTTGAC  TTTGACGCGG  CGGATGGAGA
501 GCGGCAGTTC  GCGGTAGAGT  TTGTCGAGTT  CGCCACGGTA  AAAACGGAA
551 ACGGATCCGG  CGTGCGGCG  GAAGGCAAAA  CGCAAGGTTT  CGGCAGAAAC
601 GAACGGATTG  CCGTCGCGGT  CGCCGCCGAT  CGACCGCCG  ATTTTGAGGA
651 TGTCCGGAAC  GCGGACATCG  GGATAGGCCG  TCTGAAAGTC  GTGTTCCATC
701 TTGCGGTAGA  GCTTGGGCAG  GGCTTCAAAA  AAGCTCATCG  GAAAGATGGA
751 CACGCCGTTG  TTGATTTCGT  CGTTGACGCT  GAGTTTGTGG  CGGCGCGTTT
801 CGCTGGTCTG  CCACAAGCCC  AGCAGGATAG  TGTGATTTC  GCGGCGCAGT
851 CGTGCCAGCG  CGTCGGCATT  GGTACAGCGT  TCGCGTTGCG  CGAGCAGCGG
```

a509.pap

1	MVAVCDERTV	QWTLMAQFAQ	QGGLFLLFVE	<u>AVVVFQACVL</u>	EKLGNHIGVF
51	ACVLAQVERH	HVEAEHGYGT	DEVCTQAFGK	QAAAVVDKGM	LQFFQIIEKF
101	LCRSIRLEKA	EFAAHTQTER	ARFAHSARHN	VGNGATVGFF	GAGGFFVGRF
151	VGQRHHIAVD	FDAADGERQF	AVEFVEFATV	KTEHGIGVAA	EGKTKQGFGR
201	ERIAVAVAAD	PAADFEDVRN	ADIGIGRLKV	VFHLAVELGQ	GFKKAHRKDG
251	HAVDVFFVDA	EFVAARFAGL	PQAQQDSVDF	AAQPCQRVGI	GTAFALRQQR
301	ADAAVEIQDG	LALHFGRVRG	QNGGNGRIVQ	LPLHREAVGF	PRFEPADGFR
351	<u>QAAFRAAASG</u>	<u>FFVDLAAAFV</u>	VHVFQDVQNL	GEQAAGQG*I	VGLLFVQLRQ
401	YFFNQCRAVV	SGSGQEDFRD	NQRQGFVQVE	VEQGLFQKFR	VRRQSRVLWI
451	VQNMQLHDFS	LIAVNTVNVF	QMPHPCQTVH	TLTARVPKCR	LKLNAARRQR
501	YNRPMQLFXSE	HXHDHTRTRQ	RRCIPAAVQP	PHPLGRNWRH	RAAETFRRAY
551	FGRRLRRFGC	RXPCPISPLP	ASAR*		

	10	20	30	40	50	60
m509.pep	MVAVCDKRAVQRTLMAQFAQQGGLFLLFVQAVVVFQACVLEKLGNHIGVFACVLAQVERH					
a509	: :					
	10	20	30	40	50	60
m509.pep	70	80	90	100	110	120
	HVKAEHGYGTDEVCQTAFGKQTAAVVDKGTLQFFQIIQKLLCRSIRLEKAEEFAAHTQTER					
a509	:					
	70	80	90	100	110	120
m509.pep	130	140	150	160	170	180
	ARFAHSARHNVGDGAAGVFFGAGDFVGRFVGQRRYIAVDFDAADGERQFAVEFVEFAAI					
a509						
	130	140	150	160	170	180
m509.pep	190	200	210	220	230	240
	EAEHGIGVAAEGKAQGFGRNKRIAVAVAADPAADFEDVRNADAGIGRLKVVFHLAVELGQ					
a509	: :					
	190	200	210	220	230	240
m509.pep	250	260	270	280	290	300
	GFKAHREDGHAVVDFVVDAAEFVAARFAGLPQAQQDSVDFAAQPCQRVGIGAAAFALRQQC					
a509	: :					
	250	260	270	280	290	300
m509.pep	310	320	330	340	350	360
	GFKKAHRKDGHAVVDFVVDAAEFVAARFAGLPQAQQDSVDFAAQPCQRVGIGTAFALRQQR					

760

m509.pep	ADAAVEAXDGLALHFGRVRGQNGNGRIVQLPLHRFAVGFPRFEPADGFRQAAFRAAASG
a509	ADAAVEIQDGLALHFGRVRGQNGNGRIVQLPLHRFAVGFPRFEPADGFRQAAFRAAASG
	310 320 330 340 350 360
m509.pep	FFVDLAAAFVVHVFGDVQNLGEQAAGQGXIVGLLFVQLRQYFFNQCRVVGSGQEFDCFD
a509	FFVDLAAAFVVHVFGDVQNLGEQAAGQGXIVGLLFVQLRQYFFNQCRVVGSGQEFDRFD
	370 380 390 400 410 420
m509.pep	NQRRGFFVQVEVEQGLFQKFRVRRQSRVLWIVQNMQLHDFSLSSAVNIVNVPQMPHPCQTV
a509	NQRRGFFVQVEVEQGLFQKFRVRRQSRVLWIVQNMQLHDFSLI-AVNTVNVPQMPHPCQTV
	430 440 450 460 470 480
m509.pep	HTLTARVPKCRKLKNAARRQRYNRPQLFFSEHHHDHTRQRRICIPAAVQPPHPLGRNRH
a509	HTLTARVPKCRKLKNAARRQRYNRPQLFXSEHHHDHTRQRRICIPAAVQPPHPLGRNWH
	480 490 500 510 520 530
m509.pep	RRAAETFRRAYFGRRLRRFGCRRTXPTLPLRV SARX
a509	RRAAETFRRAYFGRRLRRFGCRXPCISP LPASARX
	540 550 560 570

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1399>:

```

g510.seq
1  atgccttcgc ggacaccgca gggaaaaagg ggattattcct gccccaaagcg
51 ggatagtgcc ttttgccagg cgttgtccat atcggttatt ttacgcgcaa
101 aatcgccgat tgccaaatcg ccgccgttca gggaggtttt caataggctcg
151 tggacgacgt tgagcgcggc cataatgacg atttttctgc tgccgcgac
201 gcggccgcct tcgcggatgg ctccggcttt gccgttgagc attccgactg
251 cctgcaacag tgtgtctttt tcttctgccg gcgtgttgac agtcagccgg
301 ggcgtgcatg acttcgatgt agacttgctc gatgttcac ctttaactct
351 tattgctgcg tttcctgccg ttgggggagg cgcgctgccg gtgcgctga

```

This corresponds to the amino acid sequence <SEQ ID 1400; ORF 510.ng>:

```

g510.pep
1  MPSRTPQGKR GYSCPKRDSA FWQALSISVI LRAKSPIAKS PPFREVFNRS
51  WTTLSAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTVSR
101 GVHDFDVLDF DVHPLILIAA FPAVGGGALP VR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1401>:

```

m510.seq
1  ATGCCTTCGC GGACACCGCA GGGnAAAAGG GGTATTCTCT GCGCCAAGCG
51  GGATAGTGCT TTTTGCCAGG CGTTGTCCAT ATCGGCTATT TTACGCGCAA
101 AATCGCCGAT TGCCAAATCG CCGCCGTTC AAGGAGTTT CAACAGGTCG
151 TGGACGACGT TGAGCGCGGC CATAATGACG ATTTTTCGCG GTCCGCGAC
201 GCGTCCGCCT TCGCGGATGG CTTCGGCTTT GCCGTTGAGC ATTCGACTG
251 CCTGCAACAG TGTGTCTTTT TCTTCTGCCG GCGTGTGAC GGTACGCCG
301 GCGGTGCAW ACTTCsAtGT GGAATTGTTG GATGTTTCAT CTTTAATCCT
351 TATTGCTGCG TTTCCTGCCA TTGGGGGAGG CGCGCTGCCA GTGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1402; ORF 510>:

```

m510.pep
1  MPSRTPQGKR GYSCAKRDSA FWQALSISAI LRAKSPIAKS PPFREVFNRS
51  WTTLSAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTVSR
101 GVXDFXVDLF DVHPLILIAA FPAIGGGALP VR*

```

Computer analysis of this amino acid sequence gave the following results:

761

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 510 shows 96.2% identity over a 132 aa overlap with a predicted ORF (ORF 510.ng) from *N. gonorrhoeae*:

m510/g510

	10	20	30	40	50	60
m510.pep	MPSRTPQGKRGYSCAKRDSAFAWQALSISAILRAKSPIAKSPPFREVFNRSWTTLSAAIMT					
	:					
g510	MPSRTPQGKRGYSCPKRDSAFAWQALSISVILRAKSPIAKSPPFREVFNRSWTTLSAAIMT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m510.pep	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRGVXDFXVDLFDVHPLILIAA					
	:					
g510	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRGVHDFDVLFDVHPLILIAA					
	70	80	90	100	110	120
	130					
m510.pep	FPAIGGGALPVRX					
	:					
g510	FPAVGGGALPVRX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1403>:

a510.seq

1	ATGCCTTCGC	GGACACCGCA	GGGAAAAAGG	GGTTATTCCT	CGGCCAAGCG
51	GGATAGTGCT	TTTTGGCAGG	CGTTGTCCAT	ATCGGCTATT	TTACGCGCAA
101	AATCGCCGAT	TGCCAAATCG	CCGCCGTTCA	GGGAGGTTT	CAACAGGTCG
151	TGGACGACGT	TGAGCGCGGC	CATAATGACG	ATTTTTTCGC	TGTCCGCGAC
201	GCGTCCGCCT	TCGCGGATGG	CTTCGGCTTT	GCCGTTGAGC	ATTCCGACTG
251	CCTGCAACAG	TGTGTCTTTT	TCTTCTGCCG	GCGTGTGAC	GGTCAGCCGG
301	G.CGTGCATG	ACTTCGATGT	GGACTTGTTT	GATGTTTCATC	CTTTAATCCT
351	TATTGCTGCG	TTTCTTGCCG	TTGGGGGAGG	CGCGCTGCCA	GTGCGCTGA

This corresponds to the amino acid sequence <SEQ ID 1404; ORF 510.a>:

a510.pep

1	MPSRTPQGKR	GYSCAKRDSA	FWQALSISAI	LRAKSPIAKS	PPFREVFNR
51	WTTLSAAIMT	IFSLSATRPP	SRMASALPLS	IPTACNSVSF	SSAGVLTVSR
101	XVHDFDVLDF	DVHPLILIAA	FPAVGGGALP	VR*	

m510/a510 97.0% identity in 132 aa overlap

	10	20	30	40	50	60
m510.pep	MPSRTPQGKRGYSCAKRDSAFAWQALSISAILRAKSPIAKSPPFREVFNRSWTTLSAAIMT					
	:					
a510	MPSRTPQGKRGYSCAKRDSAFAWQALSISAILRAKSPIAKSPPFREVFNRSWTTLSAAIMT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m510.pep	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRGVXDFXVDLFDVHPLILIAA					
	:					
a510	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRXVHDFDVLFDVHPLILIAA					
	70	80	90	100	110	120
	130					
m510.pep	FPAIGGGALPVRX					
	:					
a510	FPAVGGGALPVRX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1405>:

g512.seq

1	atgaaagtgc	ttgttttagg	tgcgggtggt	gccggcgat	cctccgtgtg
---	------------	------------	------------	-----------	------------

51	gtatctggca	gaggccggac	atgaagtaac	ggtcatcgac	cgcaccgagg
101	gtgtggcgat	ggaaaccagt	tttgccaatg	caggccagct	ttcttacggc
151	tataccacgc	cttgggtctgc	acccggtatt	ccgaccaaag	cactgaaacg
201	gctgtttaaa	agccatccgc	ctttactgtt	ccgccctgac	ggcggcctgt
251	atcaaatcga	atggctgtgg	cggatgtctg	aaaactgcac	ggcaacgcgc
301	tatcaaatca	ataaagagcg	catggtcagg	atttccgaat	acagccgtga
351	aatgttccgc	cgttttgaag	cgaaaccga	catgaatttt	cgaaggacgca
401	aaaaagggac	gttgacagatt	ttccgccaaa	ccgaagaagt	cgaagcggca
451	aaacaagaca	ttgccgtttt	ggaacgctac	ggcgtgccgt	accgccgtct
501	gaagcccgaa	gaatgcgcag	aattcgagcc	tgcgttgcca	cgcgttaccg
551	ccaaaattgt	cggcggctctg	cacctgcctg	cggatgcgac	cggcgactgc
601	cgectcttca	ccgaaaacct	gtacaaattg	tgtcaagaga	agggggtacg
651	gtttctacttc	aaccaaacca	tcagccgcac	cgaccacaac	gggctgcgca
701	tcaaagccgt	tgaacctgaaa	caggcggtt	tgaaccagat	gccgttgtct
751	gcgcgtctcg	ctgcttcagc	aggactgtgt	tggcgagtt	ggatctcaat
801	ctgcccat	atcccgctcaa	aggctattcc	ttga	

This corresponds to the amino acid sequence <SEQ ID 1406; ORF 512.ng>:

g512.pep

1	<u>MKVLVLGAGV</u>	AGVSSVWYLA	EAGHEVTVID	RTEGVAMETS	FANAGQLSYG
51	YTTTPWAAPGI	PTKALKRLFK	SHPLLFRPD	GGLYQIEWLW	RMLQNCTATR
101	YQINKERMVR	ISEYSREMFR	RFEAQTDMNF	EGRKKGTLQI	FRQTEEEVEAA
151	KQDIAVLRY	GVPPYRLKPE	ECAEFEPALA	RVTAKIVGGL	HLPADATGDC
201	RLFTENLYKL	CQEKGVRFYF	NQTSIRIDHN	GLRIKAVETK	QGGLKQMPLS
251	ARSAASAGLC	WRSWISICPF	IPSKAIP*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1407>:

m512.seq (partial)

```

1      .GTTTTGGAAC GCTACGGCGT GCCGTACCGC CGTCTGAAAC CCGAAGAATG
51     TGCAGAATTT GAGCCTGCGC TGGCACGCGT TACCGCCAAA ATTGCCGGCG
101    GCCTGCACCT GCCTGCAGAT GCGACGGCG ACTggCGCCT CTTCACTGAA
151    AACCTATACA AATTGTGTCA GGAAAAGGGC GTACGGTTTC ATTTCAACCA
201    AAACATCAGC CGCATCGAC ACAACGGGCT GCGCATCAA ACCGTTGAAA
251    CCAACAGGG CGGTTTGAAG CAGATGCCGT TGCTGCGCG CTCGGTTGCT
301    TACGACAGGAC GGGTTTGGCG CAGTTGGATC TCAATCTGCC CATTATCCC
351    GTCAAAGGCT ATTCCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1408; ORF 512>:

m512.pep (partial)

```

1  ..VLERYGVPIYR RLKPEECAEF EPALARVTAK IAGGLHLPAD ATGDWRLFTE
51  NLYKLCQKEG VRFHFNQNIS RIDHNGLRIK TVETKQGGLK QMPLSARSA
101  SAGRFWRSWI SICPFIPSKA IP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 512 shows 93.4% identity over a 122 aa overlap with a predicted ORF (ORF 512.ng) from *N. gonorrhoeae*:

m512/g512

```

                                10      20      30
m512.pep                      VLERYGVPYRRLKPEECAEFEPALARVTAK
                                |||||
g512      TDMNFEGRKKGTLQIFRQTEEVEAAKQDIAVLERYGVPYRRLKPEECAEFEPALARVTAK
              130      140      150      160      170      180

                                40      50      60      70      80      90
m512.pep      IAGGLHLPADATGDWRLFTENLYKLCQEKGVRFHFNQNISRIDHNGLRIKTVETKQGGLK
              |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g512      IVGGLHLPADATGDCRLFTENLYKLCQEKGVRFYFNQTISRIDHNGLRIKAVETKQGGLK
              190      200      210      220      230      240

                                100      110      120
m512.pep      QMPLSARSVASAGRFWRSWISICPFIPSKAIP
              |||||||:|||||
g512      QMPLSARSAASAGLCWRSWISICPFIPSKAIP

```

763

250

260

270

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1409>:

```
a512.seq
  1  ATGAAAGTGC TTGTTTTAGG TGCTGGTGTT GCCGGCGTAT CTTCCGCGTG
 51  GTATCTGGCA GAGGCAGGAC ATGAAGTAAC GGTTCATCGAC CGCGCCGAGG
101  GCGTGGCGAT GGAACCAGT TTTGCCAACG CAGGCCAGCT TTCTTACGGC
151  TATACCACGC CTTGGGCTGC ACCCGGTATT CCGACCAAAG CACTGAAATG
201  GCTGTTTAAA AGCCATCCGC CTTTGCTGTT TCGCCCCGAC GGCAGCCTGT
251  ATCAAATCGA ATGGCTGTGG CAGATGCTGC AACACTGCAC GGCAGCGCGC
301  TATCAAATCA ATAAAGAGCG CATGGTCAGG ATGTCCGAAT ACAGCCGTGA
351  AATGTTCCGC CGTTTTGAAG CGCAAACCGG CATGAATTTT GAGGGACGCA
401  AAAAAGGGAC GTTGCAGATT TTCCGCCAAA CCAAAGAAGT CGAAGCGGCA
451  AAACAAGACA TTGCCGTTTT GGAACGCTAC GGCCTGCCGT ACCGCCGTCT
501  GAAGCCCGAA GAATGCGCAG AATTCGAGCC TGCCTGGCA CGCGTTACCG
551  CAAAATTGCG CGGCGGCGCT CACCTGCCCC CAGACGCGAC CGGCGACTGC
601  CGCCTCTTCA CTGAAAACCT GTACAAATTG TGTCAAGAAA AGGGCGTACG
651  GTTTCATTTT AACCAAACCA TCAGCCGCAT CGACCACAAC GGGCTGCGCA
701  TCAAAACCGT TGAACGAAA CAGGGCGGTT TGAAGCAGAT GCCGTTGTCT
751  GCGCGCTCGG CTGCTTCAGC AGGACGGTTT TGGCGCAAGT GGATCTCAAT
801  CTGCCGATTT ATCCCGTCAA AGGCTATTCC TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1410; ORF 512.a>:

```
a512.pep
  1  MKVLVLGAGV AGVSSAWYLA EAGHEVTVID RAEGVAMETS FANAGQLSYG
 51  YTTPWAAPGI PTKALKWLFK SHPPLFRPD GSLYQIEWLW QMLQHCTAAR
101  YQINKERMVR MSEYSREMFR RFEAQTMNF EGRKKGTLOI FRQTKVEEAA
151  KQDIAVLERY GVPYRLKPE ECAEFEPALA RVTAKIAGGL HLPADATGDC
201  RLFTENLYKL CQEKGVRFHF NQTISRIDHN GLRIKTVETK QGGLKQMPLS
251  ARSAASAGRF WRKWISICRF IPSKAIP*
```

m512/a512 95.9% identity in 122 aa overlap

```
m512.pep                                10      20      30
                                VLERYGVVPYRLKPEECAEFEPALARVTAK
a512                                |||||
                                130      140      150      160      170      180
                                TGMNFEGRKKGTLOIFRQTKVEEAAKQDIAVLERYGVVPYRLKPEECAEFEPALARVTAK

                                40      50      60      70      80      90
m512.pep                                IAGGLHLPADATGDWRLFTENLYKLCQEKGVRFHFNQNISRIDHNGLRIKTVETKQGGLK
a512                                |||||
                                IAGGLHLPADATGDCRLFTENLYKLCQEKGVRFHFNQNISRIDHNGLRIKTVETKQGGLK
                                190      200      210      220      230      240

                                100      110      120
m512.pep                                QMPLSARSVASAGRFWRWSISICPFIPSKAIPX
a512                                |||||:|||||:|||||
                                QMPLSARSAASAGRFWRKWISICRFIPSKAIPX
                                250      260      270
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1411>:

```
g513.seq
  1  ATGGGTTCGG CGCCGAACGC CGCCGCCGCC GCCGAAGTGA AACACCCTGT
 51  TTCGCAAGGT ATGATTCAAA TGCTGGGCGT GTTGTCGAT ACCATCATCG
101  TTTGTTCTTG CACCGCCTTC ATCATCTTGA TTTACCAACA GCCTTATGGC
151  GATTTGAGCG GTGCGGCGCT GAcgcAGGCG GCGATTGTCA GCCAAGTGGG
201  GCAATGGGGC GCGGGTTTCC TCGCCGTCAT CCTGTTTATG TTTGCCTTTT
251  CCACCGTTAT CGGCAACTAT GCCTATGCCG AGTCCAACGT CCAATTCATC
301  AAAAGCCATT GGCTGATTAC CGCCGTTTTT CGTATGCTGG TTTTGGCGTG
351  GGTCTATTTT GGC GCGGTTG CCAATGTGCC TTTGGTCTGG GATATGGCGG
401  ATATGGCGAT GGGCATCATG GCGTGGATCA ACCTCGTCGC CATCCTGCTG
451  CTCTCGCCat TGGCGTTTAT GCTGCTGCGC GATTACACCG CCAAGCTGAA
```

501 AATGGGCAAA GACCCCGAGT TCAAACTTTc cgAACATCCG GGCCTGAAAC
 551 GCCGCATCAA ATCCGATGTT TGGTAA

This corresponds to the amino acid sequence <SEQ ID 1412; ORF 513.ng>:

g513.pep

1 MGSAPNAAAA AEVKHPVSQG MIQMLGVFVD TIIVCSCTAF IILIYQQPYG
 51 DLSGAALTQA AIVSQVGQWG AGFLAVILFM FAFSTVIGNY AYAESNVQFI
 101 KSHWLITAVF RMLVLAWVYF GAVANVPLVW DMADMAMGIM AWINLVAILL
 151 LSPLAFMLLR DYTAKLKM GK DPEFKLSEHP GLKRRIKSDV W*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1413>:

m513.seq

1 ATGGGTTCCG CGCCGAACGC CGCCGCCGCC GCCGAAGTGA AACACCCTGT
 51 TTCGCAAGGT ATGATTCAA TGCTGGGCGT GTTTGTCTGAT ACCATCATCG
 101 TTTGTTCTTG CACCGCCTTC ATCATCTTGA TTTACCAACA GCCTTATGGC
 151 GATTTGAGCG GTGCGGCGCT GAcgcAGGCG GCGATTGTCA GCCAAGTGGG
 201 GCAATGGGGC GCGGGTTTCC TCGCCGTCAT CCTGTTTATG TTTGCCTTTT
 251 CCACCGTTAT CGGCAACTAT GCCTATGCCG AGTCCAACGT CCAATTCATC
 301 AAAAGCCATT GGCTGATTAC CGCCGTTTTT CGTATGCTGG TTTTGGCGTG
 351 GGTCTATTTC GGCGCGGTTG CCAATGTGCC TTTGGTCTGG GATATGGCGG
 401 ATATGGCGAT GGGCATCATG GCGTGGATCA ACCTCGTCGC CATCCTGCTG
 451 CTCTCGCCat TGGCGTTTAT GCTGCTGCGC GATTACACCG CCAAGCTGAA
 501 AATGGGCAAA GACCCCGAGT TCAAACTTTc cgAACATCCG GGCCTGAAAC
 551 GCCGCATCAA ATCCGATGTT TGGTAA

This corresponds to the amino acid sequence <SEQ ID 1414; ORF 513>:

m513.pep

1 MGSAPNAAAA AEVKHPVSQG MIQMLGVFVD TIIVCSCTAF IILIYQQPYG
 51 DLSGAALTQA AIVSQVGQWG AGFLAVILFM FAFSTVIGNY AYAESNVQFI
 101 KSHWLITAVF RMLVLAWVYF GAVANVPLVW DMADMAMGIM AWINLVAILL
 151 LSPLAFMLLR DYTAKLKM GK DPEFKLSEHP GLKRRIKSDV W*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 513 shows 99.5% identity over a 191 aa overlap with a predicted ORF (ORF 513.ng) from *N. gonorrhoeae*:

m513/g513

	10	20	30	40	50	60
m513.pep	MGSAPNAAAAAEVKHPVSQGM IQMLGVFVD TIIVCSCTAF IILIYQQPYGDLSGAALTQA					
g513	MGSAPNAAAAAEVKHPVSQGM IQMLGVFVD TIIVCSCTAF IILIYQQPYGDLSGAALTQA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m513.pep	AIVSQVGQWGAGFLAVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYF					
g513	AIVSQVGQWGAGFLAVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m513.pep	GAVANVPLVWDMADMAMGIMAWINLVAILLSPLAFMXLRD Y TAKLKM GK DPEFKLSEHP					
g513	GAVANVPLVWDMADMAMGIMAWINLVAILLSPLAFMLLRD Y TAKLKM GK DPEFKLSEHP					
	130	140	150	160	170	180
	190					
m513.pep	GLKRRIKSDVW					
g513	GLKRRIKSDVW					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1415>:

a513.seq

765

```

1  ATGAACGAGA ACTTTACCGA ATGGCTGCAC GGCTGGGTCG GCGCCATCAA
51  CGATCCGATG TGGTCATACT TGGTTATNT GCTTTGGGT ACGGGGCTTT
101 TCTTCACCGT AACCACGGGC TTTGTCCAAT TCCGCCTGTT CGGGGCGAGC
151 ATCAAAGAAA TGCTCGGCGG CCGCAAACAG GGGGACGACC CTCACGGCAT
201 CACGCCGTTT CAGGCATTG TAACCGGCCT TGCCAGCCGC GTGGGCGTGG
251 GCAATATCGC GGGCGTGGCC ATCGCCATCA AAGTCGGCGG ACCGGGCGCG
301 GTGTTTTGGA TGTGGGTAAC CGCCTTAATC GGTATGAGTT CGGCGTTTGT
351 CGAATCTTCG CTGGCGCAGC TCTTTAAAGT CCGCGACTAC GACAACCACC
401 ATTTCCGGGG CGGCCCTGCC TACTACATCA CTCAAGGGCT GGGGCAGAAA
451 TGGCTGGGCG TGTTGTTGCG CCTGAGCCTG ATTTTCTGTT TCGGCTTGT
501 GTTTGAAGCG GTTCAGACCA ATACCATTGC CGATACCGTC AAAGCGGCGT
551 GGGGTTGGGA GCCTCATTAT GTCGGCGTCG CCCTGGTGAT TTTAACCGCG
601 CCGATTATCT TCGGCGGCAT CAGGCGCATA TCTAAAGCGG CGGAAATCGT
651 CGTCCCCCTG ATGGCGGTTT TGTACCTCTT TATCGCGCTT TTCATCATTT
701 TGACCAATAT TCCGATGATT CCGGACGTGT TCGGTGAGAT TTTTTCGGGC
751 GCGTTCAAAT TCGACGCGGC AGCAGGCGGC TTA CTGCGGCG GTCTGATTTC
801 GCAAACGATG ATGATGGGCA TCAAACGCGG CCTGTATTCC AACGAGGCGG
851 GTATGGGTTC CGCGCCGAAC GCCGCCGCGG CCGCCGAAGT GAAACACCCCT
901 GTTTCGCAAG GTATGATTCA AATGCTGGGC GTGTTTGTCT ATACCATCAT
951 CGTTTGTCT TGCACCGCCT TCATCATCTT GATTTACCAA CAGCCTTACG
1001 GCGATTGAG CGGTGCGGCG CTGACGCAGG CGGCGATTGT CAGCCAAGTG
1051 GGGCAATGGG GCGCGGGCTT CCTCGCGCTC ATCCTGTTTA TGTTTGCTTT
1101 TTCCACCGTT ATCGGCAACT ATGCCTATGC CGAGTCCAAC GTCCAATTCA
1151 TCAAAGCCA TTGGCTGATT ACCGCCGTTT TCCGTATGCT GGTTTTGGCG
1201 TGGGTCTATT TCGGCGCGGT TGCCAATGTG CTTTGTGCTT GGGATATGGC
1251 GGATATGGCG ATGGGCATTA TGGCGTGGAT CAACCTTGTC GCCATCCTGC
1301 TGCTCTCGCC CTTGGCGTTT ATGCTGCTGC GCGATTACAC CGCCAAGCTG
1351 AAAATGGGCA AAGACCCCGA GTTCAAACCT TCCGAACATC CGGGCCTGAA
1401 ACGCCGTATC AAATCCGACG TTTGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1416; ORF 513.a>:

```

a513.pep
1  MNENFTEWLH GWVGAINDPM WSYLVYXLLG TGLFFTVTG EVQFRLFGRS
51  IKEMLGGRKQ GDDPHGITPF QAFVTGLASR VGVGNIAGVA IAIKVGPGPA
101 VFWMWVTALI GMSSAFVESS LAQLFKVRDY DNHHFRGGPA YYITQGLGQK
151 WLGVLFALSL IFCFGEVFEA VQNTIADTV KAAWGWEPHY VGVALVILTA
201 PIIFGGIRRI SKAAEIVVPL MAVLYLFIAL FIILTNPIMI PDVFGQIFSG
251 AFKFDAAGG LLGLISQTM MMGIKRGLYS NEAGMGSAPN AAAAAEVKHP
301 VSQGMQMLG VFVDTIIVCS CTAFIILYQ QPYGDLGAA LTQAAIVSQV
351 QQWAGFLAV ILFMFAFSTV IGNYAYAESN VQFIKSHWLI TAVFRMLVLA
401 WVYFGAVANV PLVWDMADMA MGIMAWINLV AILLSPPLAF MLLRDYTAKL
451 KMGKDPEFKL SEHPGLKRRI KSDVW*

```

m513/a513 100.0% identity in 191 aa overlap

```

m513.pep
10 20 30
MGSAPNAAAAAEVKHPVSQGMQMLGVFVD
|||||

a513
260 270 280 290 300 310
DAAAGLLGLISQTM MMGIKRGLYSNEAGMGSAPNAAAAAEVKHPVSQGMQMLGVFVD

40 50 60 70 80 90
TIIIVCSCTAFIILYQ QPYGDLGAA LTQAAIVSQVQWAGFLAVILFMFAFSTVIGNY
|||||

a513
320 330 340 350 360 370
TIIIVCSCTAFIILYQ QPYGDLGAA LTQAAIVSQVQWAGFLAVILFMFAFSTVIGNY

100 110 120 130 140 150
AYAESNVQFIKSHWLI TAVFRMLVLAWVYFGAVANVPLVWDMADMA MGIMAWINLVAILL
|||||

a513
380 390 400 410 420 430
AYAESNVQFIKSHWLI TAVFRMLVLAWVYFGAVANVPLVWDMADMA MGIMAWINLVAILL

160 170 180 190
LSPLAFMLLRDYTAKL KMGKDPEFKLSEHPGLKRRIKSDVWVX
|||||

```

a513 LSPLAFMLLRDY TAKLMGKDPEFKLSEHPGLKRRIKSDVWX
 440 450 460 470

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1417>:

g515.seq
 1 atggttcaaa tacaggttgt gcgcgcgcc gccgttgccc gtggtctgca
 51 ttccgagttt gcgcgcgctg taactgccga ggaaatagcc ttcgacaatg
 101 ccgttttgaa tcacgaagcg cggcgcggtg gcaacacctt ccgcatcaaa
 151 atagctgctg cggaaagagc gggggatgtg cggttcttcg cgcaggttga
 201 ggaaatcggg caggactttt ttgccgatgc tgcgatcag gaaactgctt
 251 tggcggtaga gcgcgcgcc ggagagtgtg ccgacgaggt gtccgatcag
 301 cccgcccga acggtggtat cgaagaggac ggggtagctg cctgtcggga
 351 tgctgcggct gccgagtcgg cgaagatgc gccgggcggc ggtttgaccg
 401 atggtttcgg ggctgtccat atccggatgg cggcaggcgg aatcgtacca
 451 gtatgcgcgc tgcattccgt ttctcgtcgc gccgacgacg ctgcaggaaa
 501 tgctgtggtg cgtgctttgc cgggtgtcgg caaaaccgtg ggtgttgccg
 551 taaacgtatt ggtactgtcc ggtttgacc gccgcgcctt cggagttttc
 601 gatgcggctg tccgtgtcca acgctgcctg ttcgcattgt ttgccaagc
 651 cgacggcggc ttccgtatcc aaatcccat cgtggtaaa gtcggggtcg
 701 ccgatgtgtt gcgccatcaa ctccgggtcg gcaagtccgg cgcaaccgtc
 751 ttcggcggtg tggcgggcga tgcgcggcgc gccgcggacg gtgtcgcgca
 801 gggcttggtt ggagaagtcg gcggtgccgg cgcggccttt gcgtttgccg
 851 acgtaaacgg taatgtccag cgatttgtcc tgctggaact cgatttgttc
 901 gatttcgccc aagcgcacgc tgacgctttg tccgagcgat tcgctgaagt
 951 cggttcggc gccggtcgcg cccgctgctt ttgccagtc gagcgtcgg
 1001 cggcagaggt cgaggagttc ggaagcgggt tggttgaaca gcataacaat
 1051 ctttcttggg ggagcgttgt gccattttaa

This corresponds to the amino acid sequence <SEQ ID 1418; ORF 515.ng>:

g515.pep
 1 MVQIQVRAA GVARGLHSEF ARAVTAEIEA FDNAVLNHEA RRGNTFRIK
 51 IAAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERRA GECADDEVSDQ
 101 PARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
 151 VVALHSVFVG GDDAAGNAV V RALPVCCKTV GVAVNVLVLS GLHRRAFGVF
 201 DAAVRVQRCL FALFCQADGG FRIQIPFVK VGVADVLRHQ LGVGKSGATV
 251 FGGVAGDVGG GADGVAQGLF GEVGGAGAAF AFADVNGNVQ RFVLLLELDLF
 301 DFAQAHADAL SERFAEVGFG GGRARCFCQV ERAAAEVEEF GSGVVEQHNN
 351 LSWSVVAF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1419>:

m515.seq (partial)
 1 ..GGAAGAGCG GGGGATGTGC GTTCTTCGCG CAGGTTGAGG AAATCGGGCA
 51 GGACTTTTCT GCCGATGCTG TCGATCAGGA AACTGCTTTG GCGGTAGAGC
 101 GCGCCGCCGG AGAGTGCGCC GACGAGGTGT CCGATAAGAC CGCCGAAAC
 151 GGTGGTATCG AAGAGGACGG GGTAGCTGCC TGTCGGGATG CTGCGGCTGC
 201 CGAGTCGGCG CAAAGTGC GGCGCGCGG TTTGACCGAT GGTTCGGGG
 251 CTGTCCATAT CCGGATGGCG GCAGGCGGAA TCGTACCAGT AGTCGCGCTG
 301 CATGCCGTTT TCGTCGGCGG CAACGACGCT GCAGGAAATG CTGTGGTGCG
 351 TGCCCTGCGG GTGTGCGGCA AAACCGTGGG TGTGCGCGTA AACGTATTGG
 401 TAATGGCCGG TTTGCACCGC CGCGCCTTCG GAGTTTTCGA TCGCTCATC
 451 CTCGTTACAG GCGGCTTGTT CGCATTGTTT TGCCAAGCCG ACGCGGCTK
 501 CCGTATCCAA ATCCCATTCG TGGTAAAGGT CGGGGTCGCC GATGTGTTTT
 551 GCCATCAGAC AGGCATCGGC AAGTCCGCG CAACCGTCTT CGGCGGTGTG
 601 GCGGGCGATG TCGATGGCGG CTTTGACGGT GTCTTGACAG GCTTTTTCGG
 651 AGAAGTCGGC AGTACTGGCG CGGCCTTTGC GTTTGCCGAC GTAAACGGTA
 701 ATGTCCAGCG ACTTGTCTCG CTGGAACTCG ATTTGTTsGA TTTsGCCAG
 751 CCGCACGCTG ACGCTTTGTC CCAATGATTC GCTGAAATCG GCTTCGGCGG
 801 CGGTTGCGCC CGTCGCTTTT GCCAAGTCGA GCGTGC GGCG GCAGAGGTG
 851 AGGAGTTCGG AAGCGGTGTG GTTgAACAGC ATAGAAATCT TTCTTGATGA
 901 TGCTTTCGGG CATTTTAA

This corresponds to the amino acid sequence <SEQ ID 1420; ORF 515>:

m515.pep (partial)

767

```

1  .GKSGGCAFFA QVEEIGQDFS ADAVDQETAL AVERAAGECA DEVSDKTARN
51  GGIEEDGVAA CRDAAAESA QSAAGGGLTD GFGAVHIRMA AGGIVPVVAL
101 HAVFVGGNDA AGNAVVRALP VCGKTVGVAV NVLVMAGLHR RAFGVFDALI
151 LVQGGFLFALF CQADGGXRIQ IPFVVKVGVA DVFCHQTGIG KSGATVFGGV
201 AGDVDGGFDG VLQGGFGEVG STGAFAFAD VNGNVQRLVL LELEDLXDXAQ
251 PHADALSQXF AEIGFGGGCA RRFCQVERAA AEVEEFGSGV VEQHRNLSXX
301 CFAAF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 515 shows 85.9% identity over a 304 aa overlap with a predicted ORF (ORF 515.ng) from *N. gonorrhoeae*:

m515/g515

```

                                10      20      30
m515.pep                      GKSGGCAFFAQVEEIGQDFSADAVDQETALA
                                ::|  |||||  |||||  |||||  |||||  |||||
g515                          AEEIAFDNAVLNHEARRGGNTFRIKIAAERAGDVRFFAQVEEIGQDFFADAVDQETALA
                                30      40      50      60      70      80

                                40      50      60      70      80      90
m515.pep                      VERAAGECADEVSDKTARNGGIEEDGVAACRDAAAESAQSAAGGGLTDGFGAVHIRMAA
                                |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g515                          VERAAGECADEVSDQPARNGGIEEDGVAACRDAAAESAQSAAGGGLTDGFGAVHIRMAA
                                90     100     110     120     130     140

                                100     110     120     130     140     150
m515.pep                      GGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTVGVAVNVLMAGLHRRRAFGVFDALIL
                                |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g515                          GGIVPVVALHSVFVGGDDAAGNAVVRALPVCCKTVGVAVNVLVLSGLHRRRAFGVFDAAVR
                                150     160     170     180     190     200

                                160     170     180     190     200     210
m515.pep                      VQGGFLFALFCQADGGXRIQIPFVVKVGVAADVDFCHQTGIGKSGATVFGGVAGDVDGGFDG
                                ||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g515                          VQRCFLFALFCQADGGFRIQIPFVVKVGVAADVLRHQLGVGKSGATVFGGVAGDVGGGADGV
                                210     220     230     240     250     260

                                220     230     240     250     260     270
m515.pep                      LQGGFGEVGSTGAFAFADVNGNVQRLVLELEDLXDXAQPHADALSQXFAEIGFGGGCGAR
                                ||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g515                          AQGLFGEVGGAGAAFAFADVNGNVQRFVLELEDLFDFAQAHADALSERFAEVGFGGGRAR
                                270     280     290     300     310     320

                                280     290     300
m515.pep                      RFCQVERAAAEEVEFGSGVVEQHRNLSXXCFAAF
                                |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g515                          CFCQVERAAAEEVEFGSGVVEQHNNLSWWSVAF
                                330     340     350

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1421>:

a515.seq

```

1  ATGGTTCAAA TAAAGGTTGT GCGCGCCGCC GCGGTTGCC GTGGTCTGCA
51  TTCCGAGTTT GCGCGCGCTG TAACTGCTGA GGAAATAGCC TTCGACAATG
101 CCGTTTGAAT TCACGAAGCG CGGTGCGGTG GCAACGCCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCTCCGCC GGAGAGTGC GCGACGAGGT GTCCGATAAG
301 ACCGCCCCGA ACGGTGGTAT CGAAGAGGAC GGGGTAGTTG CCTGTGCGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GGCGGGCGGC GGTTTGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CGGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATGCCGT TTTCGTGCGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CGGTGTGCGG CAAAACCGTA GGTGTTGCCG

```

551	TAAACGTATT	GGTAATGGCC	GGTTTGACC	GCCGCGCCTT	CGGAGTTTTT
601	GATGCGCTCA	TCCTCGTTCA	GGGCGGCTTG	TTCGATTGT	TTTGCCAAGC
651	CGACGGCGGC	TTCCGTATCC	AAATCCCATT	CGTGGTAAAG	GTCGGGGTCG
701	CCGATGTGTT	GCGCCATCAA	CTCGGGTCTG	GCAAGTCCGG	CGCAACCGTC
751	TTCGGCGGTG	TGGCGGGCGA	TGTCNNNNGC	GCGCGGACG	GTGTCGCGCA
801	GGGCTTGTTC	GGAGAAATCG	CGCGTGCCGG	CGCGGCCTTT	CGGTTTGCCG
851	ACGTAAACGG	TAATGTCCAG	CGACTTGTCC	TGCTGAAACT	CGATTTGTTC
901	GATTTGCCCC	AGCCGCACGC	TGACGCTTTG	TCCCAATGAT	TCGCTGAAAT
951	CGGCTTCGGC	GGCGGTTGCG	CCCCTCGCTT	TTGCCAAGTC	GAGCGTGCGG
1001	CGGCAGAGGT	CGAGGAGTTC	GGAGCGGTG	TGGTTGAACA	GCATAGAAAT
1051	CTTTCTTGAT	GATGCTTTGC	GGCATTTTAA		

a515.pep

1	MVQIKVVRAA	GVARGLHSEF	ARAVTAEIEA	FDNAVLNHEA	RCGGNAFRIK
51	IAAAERAGDV	RFFAQVEEIG	QDFFADAVDQ	ETALADVERSA	GECADEVSDK
101	TARNNGIEED	GVVACRDAAA	AESAQSAAGG	GLTDGFGAVH	IRMAAGGIVP
151	VVALHAVFVG	GNDAAAGNAV	RALPVCCKTV	GVAVNVLVMA	GLHRRAGFVG
201	<u>DALILVQGG</u> L	<u>FALEFCQAD</u> GG	FRIQIPFVVK	VGVAADVLRHQ	LGVGKSGATV
251	FGGAGQDVXX	GADGVAQGLF	GEIGAGAAAF	AFADVNGNVQ	RLVLLKLDLF
301	DFAQPHADAL	SQ*FAEIGFG	GGCARRFCQV	ERAAAEVEEF	SGSVVEQHRN
351	LS**CFAAF*				

[illegible]

g515-1.seq

1 ATGGTTCAAA TACAGGTTGT GCGCGCCGCC GGC GTTGCCC GTGGTCTGCA


```

51  TTCCGAGTTT GCGCGCGCTG TAACTGCCGA GGAAATAGCC TTCGACAATG
101 CCGTTTTGAA TCACGAAGCG CGGCGCGGTG GCAACACCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCGCCGCC GGAGAGTGTG CCGACGAGGT GTCCGATCAG
301 CCCGCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGCTG CCTGTCGGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GCGGGGCGGC GGTTTGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CCGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATTCCGT TTTCTGCGGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CGGTGTGCGG CAAAACCGTG GGTGTGCGCG
551 TAAACGTATT GGTAGTGTCC GGTTTGCACC GCGCGCCTT CGGAGTTTTC
601 GATGCGGCTG TCCGTGTCCA ACGCTGCCTG TTCGCATTGT TTTGCCAAGC
651 CGACGGCGGC TTCCGTATCC AAATCCCATT CGTGTTAAAG GTCGGGGTCG
701 CCGATGTGTT GCGCCATCAA CTCGGGGTCG GCAAGTCCGG CGCAACCGTC
751 TTCGGCGGTG TGGCGGGCGA TGTCGGCGGC GCGCGGACG GTGTCGCGCA
801 GGGCTTGTTT GGAGAAGTCG GCGGTGCGCG CGCGGCCTTT GCGTTTGCCG
851 ACGTAAACGG TAATGTCCAG CGATTGTGCC TGCTGGAACG CGATTGTGTC
901 GATTTGCGCC AAGCGCACGC TGACGCTTTG TCCGAGCGAT TCGCTGAAGT
951 CCGCTTCGGG GCGGTGCGCG CCCGTGCTT TTGCCAAGTC GAGCGTGCGG
1001 CGGCAGAGGT CGAGGAGTTC GGAAGCGGTG TGGTTGAACA GCATAACAAT
1051 CTTTCTTGTT GGAGCGTTGT GGCATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1424; ORF 515-1.ng>:

g515-1.pep

```

1  MVQIQVVRAA GVARGLHSEF ARAVTAEIEA FDNAVLNHEA RRGGNTFRIK
51  IAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERAA GECADDEVSDQ
101 PARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHSVFVG GNDAAAGNAV RALPVCCKTV GVAVNVLVVS GLHRRAFGVF
201 DAAVRVQRCL FALFCQADGG FRIQIPFVVK VGVADVLRHQ LGVGKSGATV
251 FGGVAGDVGG GADGVAQGLF GEVGGAGAAF AFADVNGNVQ RFLVLELDLF
301 DFAQAHADAL SERFAEVGFG GGRARCFQCV ERAAAEVEEF GSGVVEQHNN
351 LSWWSVVAFF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1425>:

m515-1.seq

```

1  ATGGTTCAAA TACAGGTTGT GCGCGCCGCC GCGGTTGCCC GTGGTCTGCA
51  TACCGAGTTT GCGCGCGCTG TAACTGCTGA GGAAATAGCC TTCGACAATG
101 CCGTTTTGAA TCACGAAGCG CGGTGCGGTG GCAACGCCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCGCCGCC GGAGAGTGTG CCGACGAGGT GTCCGATAAG
301 ACCGCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGCTG CCTGTCGGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GCGGGGCGGC GGTTTGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CCGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATGCCGT TTTCTGCGGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTGC CGGTGTGCGG CAAAACCGTG GGTGTGCGCG
551 TAAACGTATT GGTAAATGCC GGTTTGCACC GCGCGCCTT CGGAGTTTTC
601 GATGCGCTCA TCCTCGTTCA GGGCGGCTTG TTCGCATTGT TTTGCCAAGC
651 CGACGGCGGC TTCCGTATCC AAATCCCATT CGTGTTAAAG GTCGGGGTCG
701 CCGATGTGTT TTGCCATCAG ACAGGCATCG GCAAGTCCGG CGCAACCGTC
751 TTCGGCGGTG TGGCGGGCGA TGTCGATGGC GGCTTTGACG GTGCTTGTGA
801 GGGCTTTTTT GGAGAAGTCG GCAGTACTGG CGCGGCCTTT GCGTTTGCCG
851 ACGTAAACGG TAATGTCCAG CGACTTGTCG TGCTGGAACG CGATTGTGTC
901 GATTTGCGCC AGCCGCACGC TGACGCTTTG TCCCAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1426; ORF 515-1>:

m515-1.pep

```

1  MVQIQVVRAA GVARGLHTEF ARAVTAEIEA FDNAVLNHEA RCGGNAFRIK
51  IAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERAA GECADDEVSDK
101 TARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHSAFVG GNDAAAGNAV RALPVCCKTV GVAVNVLVMA GLHRRAFGVF
201 DALLVQGGGL FALFCQADGG FRIQIPFVVK VGVADVFC HQ TGIGKSGATV
251 FGGVAGDVGG GFDGVLQGF GEVSTGAAF AFADVNGNVQ RLVLELDLF
301 DFAQPHADAL SQ*

```

m515-1/g515-1 91.7% identity in 312 aa overlap

```

          10      20      30      40      50      60
g515-1.pep  MVQIQVVRAAGVARGLHSEFARA VTAEIEAFD NAVLNHEARRGGNTFRIKIAAAERAGDV
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m515-1      MVQIQVVRAAGVARGLHTEFARA VTAEIEAFD NAVLNHEARCGGNAFRIKIAAAERAGDV
          10      20      30      40      50      60

```

770

	70	80	90	100	110	120
g515-1.pep	RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDQPARNGGIEEDGVAACRDAAA					
m515-1	RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDKTARNGGIEEDGVAACRDAAA					
	70	80	90	100	110	120
g515-1.pep	AESAQSAAGGLTDGFGAVHIRMAAGGIVPVVALHSVFVGGNDAAGNAVVRALPVCCKTV					
m515-1	AESAQSAAGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV					
	130	140	150	160	170	180
g515-1.pep	GVAVNVLVVSGLHRRAFGVFDAAVRVQRCLFALFCQADGGFRIQIPFVVVKVGVADVLRHQ					
m515-1	GVAVNVLVMAGLHRRAFGVFDALILVQGGFLALFCQADGGFRIQIPFVVVKVGVADVFCHQ					
	190	200	210	220	230	240
g515-1.pep	LGVGKSGATVFGGVAGDVGGGADGVAQGLFGEVGGAGAAFAFADVNGNVQRFLVLELDF					
m515-1	TGIGKSGATVFGGVAGDVDDGGFDVLQGGFGEVGGSTGAFAFADVNGNVQRLVLELDF					
	250	260	270	280	290	300
g515-1.pep	DFAQAHADALSERFAEVGFGGGRARCFQVERAAAEVEEFGSGVVEQHNNLSWWSVVAFX					
m515-1	DFAQPHADALSQX					
	310	320	330	340	350	360

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1427>:

a515-1.seq

```

1  ATGGTTCAAA TAAAGTTGT GCGCGCCGCC GCGCTTGCCC GTGGTCTGCA
51  TTCCGAGTTT GCGCGCGCTG TAACTGCTGA GGAAATAGCC TTCGACAAATG
101 CCGTTTTGAA TCACGAAGCG CGGTGCGGTG GCAACGCCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCTCCGCC GGAGAGTGCG CCGACGAGGT GTCCGATAAG
301 ACCGCCCCGA ACGGTGTGAT CGAAGAGGAC GGGGTAGTTG CCTGTCGGGA
351 TGCTGCGGCT GCCGAGTCCG CGCAAAGTGC GCGCGGCGGC GGTTCGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CCGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATGCCGT TTTCGTCGCG GGCAACGACG CTGCAGGAAA
501 TGCTGTGTTG CGTGCTTTGC CGGTGTGCGG CAAAACCGTA GGTGTGCGCG
551 TAAACGTATT GGTAATGGCC GGTTCGACC GCGCGCCTT CGGAGTTTTC
601 GATGCGCTCA TCCTCGTTCA GGGCGGCTTG TTGCGATTGT TTTGCCAAGC
651 CGACGGCGGC TTCCGTATCC AAATCCCATC CGTGGTAAAG GTCGGGGTGC
701 CCGATGTGTT GCGCCATCAA CTCGGGGTCG GCAAGTCCGG CGCAACCGTC
751 TTCGGCGGTG TGCGGGCGCA GTGCGGCGGC GCGCGGACG GTGTCGCGCA
801 GGGCTTGTTG GGAGAAATCG GCGGTGCCGG CCGGCCTTT GCGTTTGCCG
851 ACGTAAACGG TAATGTCCAG CGACTTGTC TGCTGAAACT CGATTGTGTC
901 GATTTCGCCC AGCCGCACGC TGACGCTTTG TCCCAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1428; ORF 515-1.a>:

a515-1.pep

```

1  MVQIKVVRAA GVARGLHSEF ARAVTAEEIA FDNVNLNHEA RCGGNAFRIK
51  IAAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERSA GECADDEVSDK
101 TARNGGIEED GVVACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHAVFVG GNDAAGNAV RALPVCCKTV GVAVNVLVMA GLHRRAFGVF
201 DALILVQGG FALFCQADGG FRIQIPFVVK VGVADVLRHQ LGVGKSGATV
251 FGGVAGDVGG GADGVAQGLF GEIGGAGAAF AFADVNGNVQ RLVLLKLDLF
301 DFAQPHADAL SQ*

```

m515-1/a515-1 94.9% identity in 312 aa overlap

	10	20	30	40	50	60
a515-1.pep	MVQIKVVRAAGVARGLHSEFARAVTAEEIAFDNAVNLNHEARCGGNAFRIKIAAAERAGDV					
m515-1	MVQIQVVRAAGVARGLHTEFARAVTAEEIAFDNAVNLNHEARCGGNAFRIKIAAAERAGDV					
	10	20	30	40	50	60
a515-1.pep	RFFAQVEEIGQDFFADAVDQETALAVERSAGECADEVSDKTARNGGIEEDGVVACRDAAA					

```

m515-1      RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDKTARNGGIEEDGVAACRDAAA
              70          80          90          100          110          120

a515-1.pep   AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV
              130          140          150          160          170          180
|||||
m515-1      AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV
              130          140          150          160          170          180

a515-1.pep   GVAVNVLMAGLHRRAFGVFDALILVQGGFLFALFCQADGGFRIQIPFVVKVGVADVLRHQ
              190          200          210          220          230          240
|||||
m515-1      GVAVNVLMAGLHRRAFGVFDALILVQGGFLFALFCQADGGFRIQIPFVVKVGVADVLRHQ
              190          200          210          220          230          240

a515-1.pep   LGVGKSGATVFGGVAGDVGGGADGVAQGLFGEIGGAGAAFAFADVNGNVQRLVLLKLDLF
              250          260          270          280          290          300
|:|||||
m515-1      TGIGKSGATVFGGVAGDVGGGADGVAQGLFGEIGGAGAAFAFADVNGNVQRLVLLKLDLF
              250          260          270          280          290          300

a515-1.pep   DFAQPHADALSQX
              310
|||||
m515-1      DFAQPHADALSQX
              310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1429>:

```

g516.seq
1  atgttggtcc gtaaaacgac cgccgccggt ttggcgccaa ccttgatact
51  gaacggctgt acgatgatgt tgcgggggat gaacaacccg gtcagccaaa
101 caatcacccg caaacacggt gacaaagacc aaatccgcgc cttcgggtgtg
151 gttgccgaag acaatgcccc attggaaaag ggcagcctgg tgatgatggg
201 cgggaaatac tggttcgccg tcaatcccga agattcggcg aagctgacgg
251 gccttttgaa ggccgggttg gacaagccct tccaaatagt tgaggatacc
301 ccgagctatg cccgccacca agccctgccc gtcaaattcg aagcgcccgg
351 cagccagaat ttcagtaccg gaggtctttg cctgcgctat gataccggca
401 gacctgacga catcgccaag ctgaaacagc ttgagtttaa agcgggtcaa
451 ctcgacaatc ggaccattta cgcgcgtgct gtatccgcca aaggcaaata
501 ctacgccacg ccgcaaaaac tgaacgccga ttatcatttt gagcaaagt
551 tgcccgccga tatttattat acggttactg aaaaacatac cgacaaatcc
601 aagctgtttg gaaatatctt atatacgccc cccttggtga tattggatgc
651 ggcggccgcg gtgctggtct tgcctatggc tctgattgca gccgcgaatt
701 cctcagacaa atga

```

This corresponds to the amino acid sequence <SEQ ID 1430; ORF 516.ng>:

```

g516.pep
1  MLFRKTTAAV LAATLILNGC TMMLRGMNPN VSQTITRKHV DKDQIRAFGV
51  VAEDNAQLEK GSLVMMGGKY WFAVNPEDSA KLTGLLKAGL DKPFQIVEDT
101 PSYARHQALP VKFEAPGSQN FSTGGLCLRY DTGRPDIAK LKQLEFKAVK
151 LDNRTIYTRC VSAKGKYYAT PQKLNADYHF EQSVPADIYY TVTEKHTDKS
201 KLFGNILYTP PLLILDAAAA VLVLPMALIA AANSSDK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1431>:

```

m516.seq
1  ATGTTGTTCC GTAAACGAC CGCCGCCGTT TTGGCGGCAA CCTTGATGCT
51  GAACGGCTGT ACCTTGATGT TGTGGGGAAT GAACAACCCG GTCAGCGAAA
101 CAATCACCCG CAAACACGTT GACAAAGACC AAATCCGC GCCTTCGGTGTG
151 GTTGCCGAAG ACAATGCCCA ATTGGAAAAG GGCAGCCTGG TGATGATGGG
201 CGGAAAATAC TGGTTCGTCG TCAATCCCGA AGATTCCGCG AAGCTGACGG
251 GCATTTTGAA GGCAGGGCTG GACAAACCCT TCCAAATAGT TGAGGATACC
301 CCGAGCTATG CTCGCCACCA AGCCCTGCCG GTCAAACCTG AATCGCCTGG
351 CAGCCAGAAAT TTCAGTACCG AAGGCCTTTG CCTGCGCTAC GATACCGACA
401 AGCCTGCCGA CATGCCAAG CTGAAACAGC TCGGGTTTGA AGCGGTCAAA
451 CTCGACAATC GGACCATTTA CACGCGCTGC GTATCCGCCA AAGGCAAATA

```

772

```

501 CTACGCCACA CCGCAAAAAC TGAACGCCGA TTACCATTTT GAGCAAAGTG
551 TGCCTGCCGA TATTTATTAC ACGGTTACTG AAGAACATAC CGACAAATCC
601 AAGCTGTTTG CAAATATCTT ATATACGCC CCCTTTTGA TACTGGATGC
651 GCGGGCGCG GTACTGGCCT TGCCTGCGGC GGCTCTGGGT GCGTCTGTGG
701 ATGCCGCCCC CAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1432; ORF 516>:

```

m516.pep
  1 MLFRKTTAAV LAATLMLNGC TLMLWGMNPN VSETITRKHV DKDQIRAFGV
  51 VAEDNAQLEK GSVLMMGGKY WFFVNPEDSA KLTGILKAGL DKPFQIVEDT
 101 PSYARHQALP VKLESPGSQN FSTEGCLCLRY DTDKPADIAK LKQLGFCAVK
 151 LDNRTIYTRC VSAKGKYYAT PQKLNADYHF EQSVPADIYY TVTEHTDKS
 201 KLFANILYTP PFLILDAAGA VLALPAAALG AVVDAARK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 516 shows 90.0% identity over a 231 aa overlap with a predicted ORF (ORF 516.ng) from *N. gonorrhoeae*:

```

m516/g516
      10      20      30      40      50      60
m516.pep MLFRKTTAAVLAATLMLNGCTLMLWGMNPNVSETITRKHVDKDQIRAFGVVAEDNAQLEK
g516      MLFRKTTAAVLAATLILNGCTMMLRGMNPNVSQTITRKHVDKDQIRAFGVVAEDNAQLEK
      10      20      30      40      50      60
      70      80      90     100     110     120
m516.pep GSVLMMGGKYWFFVNPEDSAKLTGILKAGLDKPFQIVEDTPSYARHQALPVKLESPGSQN
g516      GSVLMMGGKYWFAVNPEDSAKLTGLLKAGLDKPFQIVEDTPSYARHQALPVKFEAPGSQN
      70      80      90     100     110     120
      130     140     150     160     170     180
m516.pep FSTEGCLCLRYDTDKPADIAKLKQLGFCAVKLDNRTIYTRCVSAKGKYYATPQKLNADYHF
g516      FSTGGLCLRYDTGRPDDIAKLQLEFKAVKLDNRTIYTRCVSAKGKYYATPQKLNADYHF
      130     140     150     160     170     180
      190     200     210     220     230     239
m516.pep EQSVPADIYYTVTEHTDKSKLFANILYTPPFLILDAAGAVLALPAAALGAVVDAARK
g516      EQSVPADIYYTVTEKHTDKSKLFGNILYTPPLLILDAAGAVLALPMAIAAANSSDK
      190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1433>:

```

a516.seq
  1 ATGTTGTTC GATAAACGAC CGCCGCCGTT TTGGCGGCAA CCTTGATGTT
  51 GAACGGCTGT ACGGTAATGA TGTGGGGTAT GAACAGCCCG TTCAGCGAAA
 101 CGACCGCCCG CAAACACGTT GACAAGGACC AAATCCGCGC CTTCGGTGTG
 151 GTTGCCGAAG ACAATGCCCA ATTGGAAAAG GGCAGCCTGG TGATGATGGG
 201 CGGGAAATAC TGGTTCGTCTG TCAATCCTGA AGATTCGGCG AAGCTGACGG
 251 GCATTTTGAA GGCCGGGTTG GACAAGCAGT TTCAAATGGT TGAGCCCAAC
 301 CCGCGCTTTG CCTACCAAGC CCGCCGGTTC AAATCGAAT CGCCCGCCAG
 351 CCAGAATTTC AGTACCGAAG GCCTTTGCCT GCGCTACGAT ACCGACAGAC
 401 CTGCCGACAT CGCCAAGCTG AAACAGCTTG AGTTTGAAGC GGTGGAAGT
 451 GACAATCGGA CCATTTACAC GCGCTGCGTC TCCGCCAAAG GCAAATACTA
 501 CGCCACACCG CAAAACTGA ACGCCGATTA TCATTTTGAG CAAAGTGTGC
 551 CTGCCGATAT TTATTACACG GTTACGAAAA AACATACCGA CAAATCCAAG
 601 TTGTTTGAAA ATATTGCATA TACGCCACAC ACGTTGATAC TGGATGCGGT
 651 GGGCGCGGTG CTGGCCTTGC CTGTCGCGGC GTTGATTGCA GCCACGAATT
 701 CCTCAGACAA ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1434; ORF 516.a>:

a516.pep

773

```

1  MLFRKTTAAV LAATLMLNGC TVMMWGMNSP FSETTARKHV DKDQIRAFGV
51 VAEDNAQLEK GSLVMMGGKY WFFVNPEDSA KLTGILKAGL DKQFQMVPEPN
101 PRFAYQALPV KLESPASQNF STEGLCLRYD TDRPADIAKL KQLEFEAVEL
151 DNRTIYTRCV SAKGKYATP QKLNADYHFE QSVADIYYT VTKKHTDKSK
201 LFENIAYTPT TLILDAVGAV LALPVAALIA ATNSSDK*

```

m516/a516 86.1% identity in 238 aa overlap

```

              10      20      30      40      50      60
m516.pep      MLFRKTTAAVLAATLMLNGCTLMLWGMNPNVSETITRKHVDKDQIRAFGVVAEDNAQLEK
              |||||:|||||:| |||:|||||
a516           MLFRKTTAAVLAATLMLNGCTVMMWGMNSPFSETTARKHVDKDQIRAFGVVAEDNAQLEK
              10      20      30      40      50      60

              70      80      90      100     110     120
m516.pep      GSLVMMGGKYWFFVNPEDSAKLTGILKAGLDKPFQIVEDTPSYARHQALPVKLESPGSQN
              |||||:|||||:| |||:|:|:|:|
a516           GSLVMMGGKYWFFVNPEDSAKLTGILKAGLDKQFQMVPEPNRFA-YQALPVKLESPASQN
              70      80      90      100     110

              130     140     150     160     170     180
m516.pep      FSTEGCLCLRYDTPDKPADIAKLQLGFEAVKLDNRTIYTRCVSAKGKYATPQKLNADYHF
              |||||:|||||:| |||:|||||
a516           FSTEGCLCLRYDTPDRPADIAKLQLEFEAVELDNRTIYTRCVSAKGKYATPQKLNADYHF
120           130     140     150     160     170

              190     200     210     220     230     239
m516.pep      EQSVPADIYYTVTEHTDKSKLFANILYTPPFLILDAAGAVLALPAAALGAVVDAARKX
              |||||:|||||:| |||:|||||:| |||:|:|:|
a516           EQSVPADIYYTVTKHTDKSKLFENIAYTPTTLILDAVGAVLALPVAALIAATNSSDKX
180           190     200     210     220     230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1435>:

```

g517.seq
1  atgcatcggg tttcagacgg cattggagtg tcagtcgtgt tctgccgatt
51 cgtaggcttc gacgattttt tgcaccagag gatgccggac aacgtcttcg
101 ccggtgaagg tatggaaata cagtcctgcc acgccgtgca gttctcacg
151 tgcgtctttc aatcccgatt tgatgttttt gggcaggtcg atttggtctg
201 tgtcgccggt aatgacggct ttcgcgccga agccgatgcg ggtcaggaa
251 attttcattt gttcgggctt ggtgttttgc gttcgtcga ggatgatgta
301 tgcgccgttg agcgtcctgc cgcgcatata ggcgagcggg gcgatttcaa
351 tcaggccttt ttcaatcagc ttggttacac ggtcaaagcc catcagggtca
401 tagagggcat cataaagcgg acggaggtag gggtcgactt tttgggtcag
451 gtctccgggc aggaagccca gtttctcacc ggcttcgacg gcaggccgaa
501 ctaa

```

This corresponds to the amino acid sequence <SEQ ID 1436; ORF 517.ng>:

```

g517.pep
1  MHRVSDGIGV SVVFCRFVGF DDFLHQMPD NVFAGEGMEI QSCHAVQFLT
51 CVFQSRFDVF GQVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV
101 CAVERPAAHI GERGDFNQAF FNQLGYTVKA HQVIEGIIKR TEVGVDFLGQ
151 VSGQEAQFLT GFDGRPN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1437>:

```

m517.seq
1  ATGCATCGGG TTTCAGACGG CATTGGAATG TCAGTCGTGT TCTGCCGATT
51 CGTAGGCTTC GACGATTTT TGCACCAAAG GATGCCGGAC AACGCTCTCG
101 CCGGTAAAGG TGTGAAATA CAGCCCTTCC ACCTTGTCGA GTTCTCACG
151 CGCATCTTTT AATCCCATT TGATGTTTTT GGGCAGGTCG ATTTGGCTGG
201 TGTCGCCGGT AATGACGGCT TTCGCGCCGA AGCCGATGCG GGTCAGGAAC
251 ATTTTCATTT GTTCGGGCGT GGTGTTTTGC GCTTCGTCGA GGATGATGTA
301 TGCGCCGTTG AGCGTCCTGC CGCGCATATA GGCGAGCGGG GCGATTTCOA
351 TCAGGCCTTT TTCAATCAGC TTGGTTACAC GGTCAAAGCC CATCAGGTCA
401 TAGAGGGCAT CATAAAGCGG ACGAAGGTAG GGATCGACTT TCTGGGTCAG

```

774

451 GTCTCCGGGC AGGAAGCCCA GTTCTCGCC GGCTTCGACG GCTGgGCGCA
501 CTAA

This corresponds to the amino acid sequence <SEQ ID 1438; ORF 517>:

m517.pep
1 MHRVSDGIGM SVVFCRFVGF DDFLHQMPD NVFAGKGVEI QPFHVQFLT
51 RIFXSRFDVF GQVDLAGVAG NDGFRAEADA QGEHFHFLFGR GVLRFVEDDV
101 CAVERPAAHI GERGDFNQAF FNQLGYTVKA HQVIEGIIKR TKVGIDFLGQ
151 VSGQEAQFLA GFDGWAH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 517 shows 92.7% identity over a 164 aa overlap with a predicted ORF (ORF 517.ng) from *N. gonorrhoeae*:

m517/g517

	10	20	30	40	50	60
m517.pep	MHRVSDGIGMSVVFCRFVGFDLHQMPDNVFAKGVEIQPFHVQFLTRIFXSRFDVF					
	: : : : :					
g517	MHRVSDGIGSVVVFCRFVGFDLHQMPDNVFAEGMEIQSCHAVQFLTCVFQSRFDVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m517.pep	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF					
	: : : : :					
g517	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF					
	70	80	90	100	110	120
	130	140	150	160		
m517.pep	FNQLGYTVKAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLAGFDGWAH					
	: : : : :					
g517	FNQLGYTVKAHQVIEGIIKRTVEGVDFLGQVSGQEAQFLTGFDGRPN					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1439>:

a517.seq

1 ATGCATCGGG TTTCAGACGG CATTGGAATG TCAGTCGTGT TCTGCCGATT
51 CGTAGGCTTC GACGATTTTT TGCACCAAAG GATGCCGGAC AACGTCTTCG
101 CCGGTAAGG TGTGGAAATA CAGCCCTTCC ACGCCGTGCA GTTCTCACG
151 CGCATCTTTT AATCCCGATT TGATGTTTTT GGGCAGGTCG ATTTGGCTGG
201 TGTCGCCGGT AATGACGGCT TTCGCGCCGA AGCCGATGCG GGTCAGGAAC
251 ATTTTCATTT GTTCGGGCGT GGTGTTTTGC GCTTCGTCGA GGATGATGTA
301 TCGCGCGTTG AGCGTCCTGC CGCGCATATA GCGGAGCGGG GCAATCTCAA
351 TCAGACCTTT TTCAATCAGC TTGGTGACAC GGTCTGAAGCC CATCAGGTCA
401 TAGAGGCGAT CATAAAGCGG ACGAAGGTAG GGATCGACTT TCTGGGTCAG
451 GTCACCGGGC AGAAAACCCA GTTCTCGCC GGCTTCGACG GCAGGCCGCA
501 CTAA

This corresponds to the amino acid sequence <SEQ ID 1440; ORF 517.a>:

a517.pep

1 MHRVSDGIGM SVVFCRFVGF DDFLHQMPD NVFAGKGVEI QPFHAVQFLT
51 RIF*SRFDVF GQVDLAGVAG NDGFRAEADA QGEHFHFLFGR GVLRFVEDDV
101 CAVERPAAHI GERGNLNQTF FNQLGDTVEA HQVIEGIIKR TKVGIDFLGQ
151 VTGQKTQFLA GFDGRPH*

m517/a517 93.4% identity in 167 aa overlap

	10	20	30	40	50	60
m517.pep	MHRVSDGIGMSVVFCRFVGFDLHQMPDNVFAKGVEIQPFHVQFLTRIFXSRFDVF					
	: : : : :					
a517	MHRVSDGIGMSVVFCRFVGFDLHQMPDNVFAKGVEIQPFHAVQFLTRIFXSRFDVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m517.pep	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF					
	: : : : :					
a517	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGNLNQTF					

775

	70	80	90	100	110	120
m517.pep	130	140	150	160		
	FNQLGYTVKAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLAGFDGWAHX					
a517	130	140	150	160		
	FNQLGDTVEAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLAGFDGRPHX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1441>:

```

g518.seq
1   atgacgtttt cggcgggcaaa gctcaacatt tcggcactga tgttgtgtct
51  ttcggcagga atgaccgttt tactttccgc ttttttactg ctccgaccgg
101 aaggcagcat cttattcaac cattttttca gcataaatat tctgaccgga
151 agagcggcat ctccacgggc aaccgtgttc agactgcata aggcggtagc
201 attccacaag atgccgaaaa ccataagcaa aatgcgtaga aactacgccg
251 tccgaatcac gccgcctcct cggcgggcaa cgcttcatta taacagattg
301 ccccttaaaa aatcagaccc tgcttttgtg gcggagtctg aaatttga

```

This corresponds to the amino acid sequence <SEQ ID 1442; ORF 518.ng>:

```

g518.pep
1   MTFSAAKLNI SALMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
51  RAASPRATVF RLHQAVRFHK MPKTISKMRN NYAVRITPPP RAATLHYNRL
101 PLKKSDFAFV AESEI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1443>:

```

m518.seq
1   ATGACGTTTT CGGCGGCAAA GCTCAACATT TCGGCACGGA TGTGTGTCT
51  TTCGGCAGGA ATGACGTTTT TACTTCCGC TTTTACTG CTCCGACCGG
101 AAGGCAGCAT CTTATTCAAC CATTTTTTCA GCATAAATAT TCTGACCCGA
151 AGAGCGGCAT CTCCACAGGC AACCGTGTTT AGACGGCATC AGGCGCGGTT
201 TGCAAGATGC CGTACCATAA ACAAAGGCG TAGAACTAC GCCGTCCGAA
251 TCACGCCGCC CTCGCG.GCG GCAACGCGTC ATTATAACAG ATTGCCCTCC
301 GCGGCAGGCT TAGTGCGGCG GGAGCGCCGC CGTTGCGCAG TAATATTGTC
351 TAACGGGAGG AAAAAATCAG ACCCTGCTTT TGTGGCAGAG TCTGAAATTT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 1444; ORF 518>:

```

m518.pep
1   MTFSAAKLNI SARMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
51  RAASPQATVF RRHQARFARC RTINKRRRNY AVRITPPSXA ATRHYNRLPS
101 AAGLVRERRR RCAVILSNR KKSDPAFVAE SEI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 518 shows 74.1% identity over a 135 aa overlap with a predicted ORF (ORF 518.ng) from *N. gonorrhoeae*:

```

m518/g518

m518.pep      MTFSAAKLNISARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPQATVF
g518          MTFSAAKLNISALMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPQATVF
               10      20      30      40      50      60

m518.pep      RRHQA-RFARC-RTINKRRRNYAVRITPPSXAATRHYNRLPSAAGLVRERRRCAVILSN
g518          RLHQAVRFHKMPKTISKMRNRYAVRITPPRAATLHYNRLPL-----
               70      80      90     100

m518.pep      120      130
g518          GRKKSDPAFVAESEI
               |||||
g518          --KKSDPAFVAESEI
               110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1445>:

```
a518.seq
1  ATGACGTTTT CGGCGGCAAA GCTCAACATT TCGGCACGGA TGTGTGTCT
51  TTCGGCAGGA ATGACCGTTT TACTTTCCGC TTTTCTACTG CTCCGACCGG
101 AAGGCAGCAT CTTATTCAAC CATTTTTTCA GCATAAATAT TCTAACCCGA
151 AGAGCGGCAT CTCCACGGGC AACCGTGTC AGACGGCATC AGGCGGTACG
201 ATCCGCAAG ATGCCGACCA TAAACAAAAG GCGTAGAAAC TACGCCGTCC
251 GAATCACGCC GTCCTCG.CG GCGGCAACGC GTCATTATAA CAGATTGCCC
301 TCC.....
351 .....AAAAAAT CAGACCCTGC TTTGTGGCA GAGTCTGAAA
401 TTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1446; ORF 518.a>:

```
a518.pep
1  MTFSAAKLNI SARMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
51  RAASPRATVF RRHQAVRFRK MPTINKRRRN YAVRITPSSX AATRHYNRLP
101 S..... .KKSDPAFVA ESEI*
```

m518/a518 79.9% identity in 134 aa overlap

	10	20	30	40	50	60
m518.pep	MTFSAAKLNISARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPOATVF					
a518	MTFSAAKLNISARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPRATVF					
	10	20	30	40	50	60
	70	80	90	100	110	119
m518.pep	RRHQAVRFRK MPTINKRRRN YAVRITPSSX AATRHYNRLP SAAGLVRRERRRCAVILSNG					
a518	RRHQAVRFRK MPTINKRRRN YAVRITPSSX AATRHYNRLP S-----					
	70	80	90	100		
	120	130				
m518.pep	RKKSDPAFVAESEIX					
a518	-KKSDPAFVAESEIX					
		110				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1447>:

```
g519.seq
1  atggaatttt tcattatcctt gttggcagcc gtcgcccgttt tcggcttcaa
51  atcctttgtc gtcacccccc agcaggaagt ccacgttgctc gaaaggctcg
101 ggcgtttcca tcgcgccctg acggccggtt tgaatatattt gattcccttt
151 atcgaccgcg tcgcctaccg ccattcgctg aaagaaatcc ctttagacgt
201 acccagccag gtctgcatca cgcgcgataa tacgcaattg actgttgacg
251 gcatcatcta tttccaagta accgatccca aactcgcctc atacggttcg
301 agcaactaca ttatggcaat taccagctt gcccaaacga cgtgcgttc
351 cgttatcggtt cgtatggagt tggacaaaac gtttgaagaa cgcgacgaaa
401 tcaacagtac cgtcgtctcc gccctcgatg aagccgcccg ggcttggggg
451 gtgaaagtcc tccgttacga aatcaaggat ttggttccgc cgcaagaaat
501 ccttcgcgca atgcaggcac aaattaccgc cgaacgcgaa aaacgcgccc
551 gtattgccga atccgaaggc cgtaaaatcg aacaaatcaa ccttgccagt
601 ggtcagcgtg aagccgaaat ccaacaatcc gaaggcgagg ctgaggtcgc
651 ggtcaatgcg tccaatgccc agaaaaatcg ccgcatcaac cgcgccaaag
701 gcgaagcgga atccctgcgc cttgttgccg aagccaatgc cgaagccaac
751 cgtcaaattg ccgcccctt tcaaacccta agcggggcgg atgcggtcaa
801 tctgaagatt gcgggacaat acgttaccgc gttcaaaaat cttgccaaag
851 aagacaatac gcggattaag cccgccaagg ttgccgaaat cgggaaccct
901 aattttcggc ggcataaaaa attttcgcca gaagcaaaaa cggccaaata
951 a
```

This corresponds to the amino acid sequence <SEQ ID 1448; ORF 519.ng>:

```
g519.pep
1  MEFFIILLAA VAVFGFKSFV VIPQQEVHVV ERLGRFHRAL TAGLNILIPF
51  IDRVAYRHSI KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
```


777

101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
 151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
 201 GQREAEIQQS EGQAQAVNA SNAEKIARIN RAKGEAESLR LVAEANAEN
 251 RQIAAALQTQ SGADAVNLKI AGQYVTAFKN LAKEDNTRIK PAKVAEIGNP
 301 NFRRHEKFSP EAKTAK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1449>:

m519.seq (partial)
 1 ..TCCGTTATCG GCGTATGGA GTTGGACAAA ACGTTTGAAG AACGCGACGA
 51 AATCAACAGT ACTGTTGTTG CGGCTTTGGA CGAGGCGGCC GGGgCTTgGG
 101 GTGTGAAGGT TTTGCGTTAT GAGATTAAAG ACTTGGTTCC GCCGCAAGAA
 151 ATCCTTCGCT CAATGCAGGC GCAAATTACT GCCGAACGCG AAAAACGCGC
 201 CCGTATCGCC GAATCCGAAG GTCGTAAAAT CGAACAAATC AACCTTGCCA
 251 GTGGTCAGCG CGAAGCCGAA ATCCAACAAT CCGAAGGCGA GGCTCAGGCT
 301 GCGGTCAATG CGTCAAATGC CGAGAAAATC GCCCGCATCA ACCGCGCCAA
 351 AGGTGAAGCG GAATCCTTGC GCCTTGTTCG CGAAGCCAAT GCCGAAGCCA
 401 TCCGTCAAAT TGCCGCGGCC CTTCAAACCC AAGGCGGTGC GGATGCGGTC
 451 AATCTGAAGA TTGCGGAACA ATACGTCGCT GCGTTCAACA ATCTTGCCAA
 501 AGAAAGCAAT ACGCTGATTA TGCCCGCCAA TGTTGCCGAC ATCGGCAGCC
 551 TGATTCTGTC CGGTATGAAA ATTATCGACA GCAGCAAAAC CGCCAAaTAA

This corresponds to the amino acid sequence <SEQ ID 1450; ORF 519>:

m519.pep (partial)
 1 ..SVIGRMELDK TFEERDEINS TVVAALDEAA GAWGVKVLRY EIKDLVPPQE
 51 ILRSMQAQIT AEREKRARIA ESEGRKIEQI NLAGQREAE IQQSEGEAQA
 101 AVNASNAEKI ARINRAKGEA ESLRLVAEAN AEAIRQIAAA LOTQGGADAV
 151 NLKIAEQYVA AFNNLAKESN TLIMPANVAD IGSLISAGMK IIDSSKTAK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 519 shows 87.5% identity over a 200 aa overlap with a predicted ORF (ORF 519.ng) from *N. gonorrhoeae*:

m519/g519

m519.pep				10	20	30
				SVIGRMELDKTFEERDEINSTVVAALDEAA		
g519	YFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIGRMELDKTFEERDEINSTVVSALDEAA					
	90	100	110	120	130	140
m519.pep		40	50	60	70	80
		GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLAGQREAE				
g519		GAWGVKVLRYEIKDLVPPQEILRAMQAQITAEREKRARIAESEGRKIEQINLAGQREAE				
		150	160	170	180	190
m519.pep		100	110	120	130	140
		IQQSEGEAQA AVNASNAEKIARINRAKGEAESLRLVAEANA AEAIRQIAAALQTQGGADAV				
g519		IQQSEGEAQA AVNASNAEKIARINRAKGEAESLRLVAEANA EANRQIAAALQTQSGADAV				
		210	220	230	240	250
m519.pep		160	170	180	190	200
		NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL-ISAGMKIIDSSKTAK				
g519		NLKIAEQYVTAFKNLAKEDNTRIKPAKVAEIGNPNFRRHEKFSP EAKTAK				
		270	280	290	300	310

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1451>:

a519.seq
 1 ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
 51 ATCCTTTTGT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
 101 GGCGTTTCCA TCGCGCCCTG ACGGCCGTT TGAATATTTT GATTCCCTTT
 151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTAGACGT

778

```

201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TCGGTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAAATCG AACAAATCAA CCTTGCCAGT
601 GGTGAGCGCG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAATGCGG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GCGGGTGC GGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCCGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAAT TATCGACAGC AGCAAAACCG CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1452; ORF 519.a>:

```

a519.pep
1  MEFFIILLAA VVVFQKSFV VIPQQEVHVV ERLGRFHRAL TAGLNILIPF
51  IDRVAIRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIYFQV TDPKLASYGS
101 SNYIMAITQL AQTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAIAI
251 RQIAAALQTO GGADAVNLKI AEQYVAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

m519/a519 99.5% identity in 199 aa overlap

```

m519.pep
10 20 30
SVIGRMELDKTFEERDEINSTVVAALDEAA
|||||:|||||
a519 YFOVTDPKLASYGSSNYIMAITQLAQTLRSVIGRMELDKTFEERDEINSTVVSALDEAA
90 100 110 120 130 140

m519.pep
40 50 60 70 80 90
GAWGVKVLRYEIKDLVPPQEILRSMAQITAEREKRARIAESEGRKIEQINLASGQREAE
|||||:|||||
a519 GAWGVKVLRYEIKDLVPPQEILRSMAQITAEREKRARIAESEGRKIEQINLASGQREAE
150 160 170 180 190 200

m519.pep
100 110 120 130 140 150
IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAIAIRQIAAALQTGGADAV
|||||:|||||
a519 IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAIAIRQIAAALQTGGADAV
210 220 230 240 250 260

m519.pep
160 170 180 190 200
NLKIAEQYVAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
|||||:|||||
a519 NLKIAEQYVAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
270 280 290 300 310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1453>:

```

g519-1.seq
1  ATGGAATTTT TCATTATCTT GTTGGCAGCC GTCGCCGTTT TCGGCTTCAA
51  ATCCTTTGTC GTCATCCCCC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GGCGTTTCCA TCGCGCCCTG ACGGCCGTTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGCGATAA TACGCAATTG ACTGTTGACG
251 GCATCATCTA TTTCCAAGTA ACCGATCCCA AACTCGCCTC ATACGGTTTCG
301 AGCAACTACA TTATGGCAAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGTAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG GGCTTGGGGT
451 GTGAAAGTCC TCCGTTACGA AATCAAGGAT TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCGCA ATGCAGGCAC AAATTACGCG CGAACGCGAA AAACGCGCCC
551 GTATTGCCGA ATCCGAAGGC CGTAAAATCG AACAAATCAA CCTTGCCAGT
601 GGTGAGCGTG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCCAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GCGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GCGGGGCGG ATGCGGTCAA

```

779

801 TCTGAAGATT GCGGAACAAT ACGTAGCCGC GTTCAACAAT CTTGCCAAAG
 851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
 901 ATTTCTGCCG GCATGAAAT TATCGACAGC AGCAAAACCG CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 1454; ORF 519-1.ng>:

g519-1.pep

1 MEFFIILLAA VAVFGFKSFV VIPQQEVHV ERLGRFHRAL TAGLNILIPF
 51 IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIYFQV TDPKLASYGS
 101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
 151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
 201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAEAI
 251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
 301 ISAGMKIIDS SKTAK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1455>:

m519-1.seq

1 ATGGAATTTT TCATTATCTT GTTGGTAGCC GTCGCCGTTT TCGGTTTCAA
 51 ATCCTTTGTT GTCATCCAC AACAGGAAGT CCACGTTGTC GAAAGGCTGG
 101 GCGTTTCCA TCGCGCCCTG ACGGcCGGTT TGAATATTTT GATTCCCTTT
 151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTAGACGT
 201 ACCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
 251 GCATCATCTA TTTCCAAGTA ACCGACCCA AACTCGCCTC ATACGGTTCG
 301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
 351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
 401 TCAACAGTAC TGTGTGTCG GCTTTGGACG AGGCGGCCGG GGCTTGGGGT
 451 GTGAAGGTTT TGCGTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
 501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC CGAACGCGAA AAACGCGCCC
 551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
 601 GGTACGCGCG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
 651 GGTCAATGCG TCAATGCGG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
 701 GTGAAGCGGA ATCCTTGCGC CTGTGTGCGG AAGCCAATGC CGAAGCCATC
 751 CGTCAAATTG CCGCGCCCT TCAAACCAA GGCGGTGCGG ATGCGGTCAA
 801 TCTGAAGATT GCGGAACAAT ACGTCGCTGC GTTCAACAAT CTTGCCAAAG
 851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
 901 ATTTCTGCCG GTATGAAAT TATCGACAGC AGCAAAACCG CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 1456; ORF 519-1>:

m519-1.

1 MEFFIILLVA VAVFGFKSFV VIPQQEVHV ERLGRFHRAL TAGLNILIPF
 51 IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIYFQV TDPKLASYGS
 101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVA ALDEAAGAWG
 151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
 201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAEAI
 251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
 301 ISAGMKIIDS SKTAK*

m519-1/g519-1 99.0% identity in 315 aa overlap

	10	20	30	40	50	60
g519-1.pep	MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL					
m519-1	MEFFIILLVAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL					
	10	20	30	40	50	60
g519-1.pep	KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
m519-1	KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
	70	80	90	100	110	120
g519-1.pep	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQAQITAERE					
m519-1	RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE					
	130	140	150	160	170	180
g519-1.pep	KRARIAESEGRKIEQINLASGQREAEIQSEGEAQAAVNASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEGRKIEQINLASGQREAEIQSEGEAQAAVNASNAEKIARINRAKGEAESLR					
	190	200	210	220	230	240
g519-1.pep						
m519-1						

780

```

m519-1      KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
              190      200      210      220      230      240

              250      260      270      280      290      300
g519-1.pep  LVAEANAEAIRQIAAALQTGGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              |||||
m519-1      LVAEANAEAIRQIAAALQTGGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              250      260      270      280      290      300

              310
g519-1.pep  ISAGMKIIDSSKTAKX
              |||||
m519-1      ISAGMKIIDSSKTAKX
              310

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1457>:

```

a519-1.seq
1  ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
51  ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GGCGTTTCCA TCGCGCCCTG ACGCGCGGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCTACCG CCATTCGCTG AAAGAAATCC CTTTAGACGT
201 ACCGACCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCTC ATACGTTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TCGGTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAGCGCG AAGCCGAAAT CCAACAATCC GAAGCGGAGG CTCAGGCTGC
651 GGTCAATGCG TCAATGCCG AGAAAATCGC CGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCGCCCT TCAAACCCAA GGCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCCGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAT TATCGACAGC AGCAAAACCG CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1458; ORF 519-1.a>:

```

a519-1.pep.
1  MEFFIILLAA VVVFQKSFV VIPQEVHV ERLGRFHRAL TAGLNILIPF
51  IDRVAYRHSI KEIPLDVPSQ VCITRDNTQL TVDGIYFQV TDPKLASYGS
101 SNYIMAITQL AQTTLRVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEGRKIEQINLAS
201 QREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAEAI
251 RQIAAALQQT GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

m519-1/a519-1 99.0% identity in 315 aa overlap

```

              10      20      30      40      50      60
a519-1.pep  MEFFIILLAAVVVFQKSFVVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSI
              |||||
m519-1      MEFFIILLVAVAVFGKSFVVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSI
              10      20      30      40      50      60

              70      80      90      100     110     120
a519-1.pep  KEIPLDVPSQVCITRDNTQLTVDGIYFQVTDPKLASYGSSNYIMAITQLAQTTLRVIG
              |||||
m519-1      KEIPLDVPSQVCITRDNTQLTVDGIYFQVTDPKLASYGSSNYIMAITQLAQTTLRVIG
              70      80      90      100     110     120

              130     140     150     160     170     180
a519-1.pep  RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQQAQITAERE
              |||||
m519-1      RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQQAQITAERE
              130     140     150     160     170     180

              190     200     210     220     230     240
a519-1.pep  KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
              |||||

```

```

m519-1      KRARIAESEGRKIEQINLASGQREAEIQQSEGEAAVNASNAEKIARINRAKGEAESLR
              190      200      210      220      230      240

              250      260      270      280      290      300
a519-1.pep  LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              |||||
m519-1      LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              250      260      270      280      290      300

              310
a519-1.pep  ISAGMKIIDSSKTAKX
              |||||
m519-1      ISAGMKIIDSSKTAKX
              310

```

Expression of ORF 519

The primer described in Table 1 for ORF 519 was used to locate and clone ORF 519. ORF 519 was cloned in pET and pGex vectors and expressed in E.coli as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 4A shows the results of affinity purification, and Figure 4B shows the expression in E.coli. Purified Nis-fusion protein was used to immunize mice whose sera were used for ELISA (positive result), FACS analysis (Figure 4C), western blot (Figure 1E), and a bactericidal assay (Figure 4D). These experiments confirm that 519 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 519 are provided in Figure 8. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996; *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 519 and the amino acid sequence encoded thereby as provided herein.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1459>:

```

g520.seq
1  atgcctgcgc ttctttcaat acgtcgggca aacgcgctgc ctttttcgcg
51  catttcggaa aggatgaagt tgctgggtgcc gttaataatg ccggcgatgg
101 atttaatcct gtttgccgcc aaaccttcgc gcacggcttt gatgattggg
151 ataccgcccg ctactgccgc ttcaaattgg acgatgacgt tttgtttttc
201 cgccagcggg aagatttcgt tgccgtattc ggcgagcagt tttttgttgg
251 cggtaacgat gtgtttgccg ttttcaatgg ctttcaacac cgcttctttg
301 gcaatgcccg tgccgcccga caattcgacc aagacatcga cgtctttacg
351 cgcgaacagt tcgaacggat cttttgacaa gggcggggcga cgggcccatt
401 ttggcgggct ttttcttcgc ttaagtcgca catggcagaa atacggattt
451 cgcgcccaca gcggcgggaa atttctctcg cgttgtcccg caacacggca
501 gccgcaccgc cgccgaccgt acctaacgct aaaagaccga tgtttactgg
551 cttcattgtg tctccttgta agccgactga aatgtaaata ttga

```

This corresponds to the amino acid sequence <SEQ ID 1460; ORF 520.ng>:

```

g520.pep
1  MPALLSIRRA NALPFSRISE RMKLLVPLIM PAMDILILFAA KPSRTALMIG
51  IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FSMAFNATSL
101 AMPVPPNNST KTSTSLRANS SNGSFDKGG RADFGLFLR LSRTWQKYGF
151 RAPSGGKFPL RCPATRQPHR RRPYLSLKDR CLLASLCLLV SRLKCKY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1461>:

```

m520.seq
1  ATGCCTGCGC TTCTTTCAGT ACATCG.GCA AACGCGCTGC CTTTTTCGCG
51  CATTTCGGrk AGGATGAAGT TGCTGGTGCC GTTAATAATG CCGGCGATGG
101 ATTTAATCCT GTTTGCCGCC AAACCTTCGC GCAGGGCTTT GATGATTGGG
151 ATACGCCCCG CTACTGCCGC TTCAAATTGG ACGATGACGT TTTGTTTTTC
201 CGCCAGCGGG AAGATTTCGT TGCCGTATTG GCGAGCAGT TTTTGTGTTG
251 CGGTAACGAT GTGTTTGCCG TTTTCAATGG CTTTCAACAC CGCATCTTTG

```

782

```

301  GCAATGCCGG TACCGCCGaa CAATTCGACG ACGACATCGA CGTCTTCACG
351  TGCGACCAAGT TCGAACGGAT CTTTGACAAA GGCTGc.CGG ACGGGCAGGT
401  TTGTCGGGCT TTTTCTTCAC TCAAATCGCA CACGGCAGAA ATACGGATTT
451  CGCGCCCCAA GCGACGGGAA ATTTCTCCG CGTTGTcscG CAACACGGCA
501  GCCGTACCGC CGCCGACCGT ACCCAAACCT AAAAGACCGA TGTTTACTGG
551  CTTCATTGTG TCTCCTTGTA AGCCGACTGA AATGTAAATA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1462; ORF 520>:

```

m520.pep
  1  MPALLSVHXA NALPFSRISX RMKLLVPLIM PAMDILFAA KPSRRALMIG
 51  IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FSMAFNTASL
101  AMPVPPNNST TTSTSSRATS SNGSLTKAXR TGRFVGLFLH SNRTRQKYGF
151  RAPSDGKFPP RCXATROPYR RRPYPNLKDR CLLASLCLLV SRLKCKY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 520 shows 87.3% identity over a 197 aa overlap with a predicted ORF (ORF 520.ng) from *N. gonorrhoeae*:

```

m520/g520

      10      20      30      40      50      60
m520.pep  MPALLSVHRANALPFSRISXRMKLLVPLIMPAMDILFAAKPSRRALMIGIPPATAASNW
          |||||::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g520       MPALLSIRANALPFSRISERMKLLVPLIMPAMDILFAAKPSRTALMIGIPPATAASNW
          10      20      30      40      50      60

      70      80      90     100     110     120
m520.pep  TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATS
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g520       TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTKTSTSLRANS
          70      80      90     100     110     120

      130     140     150     160     170     180
m520.pep  SNGSLTKAARTGRFVGLFLHSNRTRQKYGFRAPSDGKFPPRCXATROPYRRRPYNLKDR
          |||: ||:| : | |||: :| ||||| ||| || ||||: |||| :|||
g520       SNGSFDKGGRRADFGGLFLRLSRTWQKYGFRAPSGGKFPLRCPATROPHRRRPYLSLKDR
          130     140     150     160     170     180

      190
m520.pep  CLLASLCLLVSRKCKY
          ||||| ||||| ||||| |||||
g520       CLLASLCLLVSRKCKY
          190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1463>:

```

a520.seq
  1  ATGCCTGCGC TTCTTTCAGT ACATCGG.CA AACGCGCTGC CTTTTTCGCG
 51  CATTTTCGGAG AGGATGAAGT TGCTGGTGCC GTTAATAATG CCGGCGATGG
101  ATTTAATCCT GTTTGCCGCC AAACCTTCGC GCAGGGCTT GATGATTGGG
151  ATACCGCCCC CTACTGCCGC TTCAAATTGG ACGATGACGT TTTGTTTTC
201  CGCCAGCGGG AAGATTTCTG TGCCGTATTC GGCGAGCAGT TTTTGTGTTG
251  CGGTAACGAT GTGTTTGCCG TTTTCAATGG CTTTCAACAC CGCATCTTTG
301  GCAATGCCGG TACCGCCGAA CAATTCGACG ACGACATCGA CGTCTTCACG
351  TGCGACCAAGT TCGAACGGAT CTTTGACAAA GGCTG..CGG ACGGGCAGGT
401  TTGTCGGGCT TTTTCTTCAC TCAAATCGCA CACGGCAGAA ATACGGATTT
451  CGCGCCCCAA GCGACGGGAA ATTTCTCCG CGTTGTCCG CAACACGGCA
501  GCCGTACCGC CGCCGACCGT ACCCAAACCT AAAAGACCGA TGTTTACTGG
551  CTTCATTGTG TCTCCTTGTA AGCCGACTGA AATGTAAATA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1464; ORF 520.a>:

```

a520.pep
  1  MPALLSVHRX NALPFSRISE RMKLLVPLIM PAMDILFAA KPSRRALMIG
 51  IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FSMAFNTASL
101  AMPVPPNNST TTSTSSRATS SNGSLTKAXR TGRFVGLFLH SNRTRQKYGF

```

783

151 RAPSDGKFPP RCPATRQPYR RRPYPNLKDR CLLASLCLLV SRLKCKY*

m520/a520 98.0% identity in 197 aa overlap

	10	20	30	40	50	60
m520.pep	MPALLSVHXANALPFSRISXRMKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNW					
a520	MPALLSVHRXNALPFSRISERMKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNW					
	10	20	30	40	50	60
	70	80	90	100	110	120
m520.pep	TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATS					
a520	TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m520.pep	SNGSLTKAXRTGRFVGLFLHSNRTRQKYGFRAPSDGKFPPRCXATRQPYRRRPYNLKDR					
a520	SNGSLTKAXRTGRFVGLFLHSNRTRQKYGFRAPSDGKFPPRCPATRQPYRRRPYNLKDR					
	130	140	150	160	170	180
	190					
m520.pep	CLLASLCLLVSRLLKCKYX					
a520	CLLASLCLLVSRLLKCKYX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1465>:

g520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTTGCTTGC CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC TTCTTTGGCA ATGCCCGTGC
251 CGccgAACAA TTCGACGACG ACATCGACGT CTTTACGCGC GACCAGTtCG
301 AACGGATCTT TGACAAAGGC GCGGACGGG CAGATTGGC GGGCTTTTTT
351 TTCGCTTAAG TCGCACATGG CAGAAATACG GATTTCGCGC CCCAAGCGGC
401 GGGAAATTC CTCTGCGTTG TCCCGCAACA CGGCAGCCG ACCGCCGCCG
451 ACCgTACCTA AGCCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1466; ORF 520-1.ng>:

g520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCFASGK
51  ISLPYSASSE LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSLRATSS
101 NGSLLTKAADG QIWRAFSSLK SHMAEIRISR PKRREISSAL SRNTAAAPP
151 TVPKPKRPMF TGFIVSPCKP TEM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1467>:

m520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTTGCTTGC CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC ATCTTTGGCA ATGCCGGTAC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTACGTGTC GACCAGTTCG
301 AACGGATCTT TGACAAAGGC TGCGGACGGG CAGGTTGTCT GGGCTTTTTT
351 TTCACCTCAA TCGCACACGG CAGAAATACG GATTTCGCGC CCCAAGCGAC
401 GGGAAATTC CTCCGCGTTG TCCCGCAACA CGGCAGCCGT ACCGCCGCCG
451 ACCGTACCCA AACCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1468; ORF 520-1>:

m520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCFASGK
51  ISLPYSASSE LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSSRATSS

```

784

101 NGSLTKAADG QVCRAFSSLK SHTAEIRISR PKRREISSAL SRNTAAVPPP
151 TVPKPKRPMF TGFIVSPCKP TEM*

g520-1/m520-1 97.1% identity in 173 aa overlap

	10	20	30	40	50	60
g520-1.pep	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTCFCSASG	KISLPYSASSF	
m520-1	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTCFCSASG	KISLPYSASSF	
	10	20	30	40	50	60
	70	80	90	100	110	120
g520-1.pep	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSLR	ATSSNGSLTKA	ADGQIWRASF	SSLK
m520-1	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSSR	ATSSNGSLTKA	ADGQVCRAFSS	SLK
	70	80	90	100	110	120
	130	140	150	160	170	
g520-1.pep	SHMAEIRISRPKR	REISSALSRNTA	AAVPPPTVPKPK	RPMFTGFI	VSPCKPTEMX	
m520-1	SHTAEIRISRPKR	REISSALSRNTA	AAVPPPTVPKPK	RPMFTGFI	VSPCKPTEMX	
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1469>:

a520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCAAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTT GTTTTCCGC CAGCGGAAG
151 ATTCGTTGCG CGTATTCGGC GAGCAGTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC ATCTTTGGCA ATGCCGTAC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTCACGTGC GACCAAGTCG
301 AACGGATCTT TGACAAAGGC TCGGACGGG CAGGTTTGTG GGGCTTTTTC
351 TTCACTCAAA TCGCACACGG CAGAAATACG GATTTCGCGC CCCAAGCGAC
401 GGGAAATTC CTCCGCGTTG TCCCGCAACA CGGCAGCGGT ACCGCCGCGG
451 ACCGTACCCA AACCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1470; ORF 520-1.a>:

a520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTCFCSASGK
51  ISLPYSASSF LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSSRATSS
101 NGSLTKAADG QVCRAFSSLK SHTAEIRISR PKRREISSAL SRNTAAVPPP
151 TVPKPKRPMF TGFIVSPCKP TEM*

```

m520-1/a520-1 100.0% identity in 173 aa overlap

	10	20	30	40	50	60
a520-1.pep	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTCFCSASG	KISLPYSASSF	
m520-1	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTCFCSASG	KISLPYSASSF	
	10	20	30	40	50	60
	70	80	90	100	110	120
a520-1.pep	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSSR	ATSSNGSLTKA	ADGQVCRAFSS	SLK
m520-1	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSSR	ATSSNGSLTKA	ADGQVCRAFSS	SLK
	70	80	90	100	110	120
	130	140	150	160	170	
a520-1.pep	SHTAEIRISRPKR	REISSALSRNTA	AAVPPPTVPKPK	RPMFTGFI	VSPCKPTEMX	
m520-1	SHTAEIRISRPKR	REISSALSRNTA	AAVPPPTVPKPK	RPMFTGFI	VSPCKPTEMX	
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1471>:

g521.seq

```

1  ATGAAATCAA AACTCCCCTT AATCCTAATC AACCTTTCCC TGATTTCAG
51  CCCATTGGGT GCGAATGCGG CAAAATCTA TACCTGCACA ATCAACGGAG
101 AAACCGTTTA CACCACCAAG CCGTCTAAAA GCTGCCACTC AACCGATTG

```


785

```

151 CCCCCAATCG GCAACTACAG CAGCGAACGC TATATCCTGC CCCAACTCC
201 CGAACCGGCA CCATCACCGT CAAACGGCGG ACAGGCTGTC AAATATAAAG
251 CCCC GGTC AAACAGTATCC AAGCCGGCAA AATCCAATAC GCCGCCTCAA
301 CAAGCACCTG TAAATAACAG CAGACGCTCC ATTCTcgaag caGaattaag
351 cAatgaacgc aaagccctGa ctGaAGCCCA AAAAATGTTA TCACAagcac
401 gtCtGGCAAA AGGCGgcaAC AtcaaCCatc aaaAaatcaa cgcattgtaa
451 AGCAATGTTt tggacAGACA GCAAAATaTC Caagcactgc aaaGAgAATt
501 GGGACGTATG TAA

```

This corresponds to the amino acid sequence <SEQ ID 1472; ORF 521.ng>:

```

g521n.pep
  1 MKSKLPLILI NLSLISSPLG ANAAKIYTCT INGETVYTTK PSKSCHSTD
 51 PPIGNYSSER YILPQTPEPA PPSNGGQAV KYKAPVKTVS KPAKSNTTPQ
101 QAPVNSRRS ILEAELSNER KALTEAQKML SQARLAKGN INHQKINAL*
151 SNVLD RQONI QALQRELGRM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1473>:

```

m521.seq
  1 ATGAAATCAA AACTCCTCTT AATCCTAATC AACTTTTCCC TGATTTC AAG
 51 CCCATTGGGT GCGAATGCGG CCAAAATCTA sACCTGCACA ATCAACGGAG
101 AAACCGTTTA CACCAsCAAG CCGTCCAAAA GCTGCCACTC AACCGATTG
151 CCCCCAATCG GCAACTACAG CAGCGAACGC TATATCCCGC CCCAAACGCC
201 CGAACCGGTA TCATCACCGT CAAACGGCGG ACwGGTTGTC AAATATAAAG
251 CCCC GGTC AAACAGTATCC AAGCCGGCAA AATCCArTAC GCCGCCGCCG
301 CAACAAGCAC CCTCAAACAA CAGCAGACGC TCCATTCTCG AAACAGAATT
351 GAGCAACGAA CGCAAAGCAT TGGTTGAAGC CCAAAAAATG TTATCACAAG
401 CACGTCTGGC AAAGGGCGGC AACATCAACC ATCAAGAAAT AAATGCATTA
451 CAAAGCAATG TATTGGACAG GCAGCAAAAT ATTCAAGCCC TGCAAAGGGA
501 ACTGGGGCGT ATGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1474; ORF 521>:

```

m521.pep
  1 MKSKLLLILI NFSLISSPLG ANAAKIXTCT INGETVYTXK PSKSCHSTD
 51 PPIGNYSSER YIPPQTPEPV SSPSNGGXVV KYKAPVKTVS KPAKSXTPPP
101 QQAPSNNRR SILETELSNE RKALVEAQKM LSQARLAKGG NINHQEINAL
151 QSNVLD RQON IQALQRELGR M*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 521 shows 90.6% identity over a 171 aa overlap with a predicted ORF (ORF 521.ng) from *N. gonorrhoeae*:

```

m521/g521

          10      20      30      40      50      60
m521.pep  MKSKLLLILINFLISSPLGANAAKIXTCTINGETVYTXKPSKSCHSTDLPPIGNYSSER
          ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g521       MKSKLPLILINLSLISSPLGANAAKIYTCTINGETVYTTKPSKSCHSTDLPPIGNYSSER
          10      20      30      40      50      60

          70      80      90      100     110     120
m521.pep  YIPPQTPEPVSSPSNGGXVVKYKAPVKTVSKPAKSXTPPPQQAPSNNRRSILETELSNE
          || ||||| : ||||| : ||||| ||||| ||||| ||||| ||||| |||||
g521       YILPQTPEPAPSPSNGGQAVKYKAPVKTVSKPAKSNTTP-QQAPVNSRRSILEAELSNE
          70      80      90      100     110

          130     140     150     160     170
m521.pep  RKALVEAQKMLSQARLAKGGINHQEINALQSNVLD RQONI QALQRELGRMX
          ||||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
g521       RKALTEAQKMLSQARLAKGGINHQKINALXSNVLD RQONI QALQRELGRMX
          120     130     140     150     160     170

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1475>:

```

a521.seq
  1 ATGAAATCAA AACTCCCCTT AATCCTAATC AACTTTTCCC TGATTTC AAG

```

786

```

51  CCCATTGGGT  GCGAATGCGG  CCAAATCTA  CACCTGCACA  ATCAACGGAG
101 AAACCGTTTA  CACCACCAAG  CCGTCCAAA  GCTGCCTCTC  AACCGATTG
151 CCCCCAATCG  GCAACTACAG  CAGCGAACGC  TATATCCCGC  CCCAAACATC
201 CGAACCGACA  CCATCACCGT  CAAACGGCGG  ACAGGCTGTC  AAATATAAAG
251 CCCCAGGTCAA  AACAGTATCC  AAGCCGGCAA  AATCCAATAC  GCCGCCGCCG
301 CAACAAGCAC  CCTCAAACAA  CAGCAGACGC  TCCATTCTCG  AAACAGAATT
351 GAGCAACGAA  CGCAAAGCAT  TGGTTGAAGC  CCAAAAAATG  TTATCACAAAG
401 CACGTCTGGC  AAAAGGCGGC  AACATCAACC  ATCAAGAAAT  CAACGCATTG
451 CAAAGCAATG  TATTGGACAG  GCAGCAAAT  ATCCAAGCAC  TGCAAAGAGA
501 ATTGGGACGT  ATGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1476; ORF 521.a>:

```

a521.pep
1  MKSKLPLILI  NFSLISSPLG  ANAAKIYTCT  INGETVYTTK  PSKSCLSTDL
51  PPIGNYSSER  YIPPQTSEPT  PSPSNGGQAV  KYKAPVKTVS  KPAKSNTPPP
101 QQAPSNNRR  SILETELSNE  RKALVEAQKM  LSQARLAKGG  NINHQEINAL
151 QSVLDRQON  IQALQRELGR  M*

```

m521/a521 94.2% identity in 171 aa overlap

	10	20	30	40	50	60
m521.pep	MKSLLLLILINFSLISSPLGANAAKIXTCTINGETVYTXKPSKSCHSTDLPPIGNYSSER					
a521	MKSKLPLILINFSLISSPLGANAAKIYTCTINGETVYTTKPSKSCLSTDLPPIGNYSSER					
	10	20	30	40	50	60
	70	80	90	100	110	120
m521.pep	YIPPQTPEPVSSPSNGGXVVKYKAPVKTVSKPAKXTPPPQQAPSNNRRSILETELSNE					
	: :					
a521	YIPPQTSEPTSPSNGGQAVKYKAPVKTVSKPAKSNTPPPQQAPSNNRRSILETELSNE					
	70	80	90	100	110	120
	130	140	150	160	170	
m521.pep	RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDROQNIQALQRELGRMX					
a521	RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDROQNIQALQRELGRMX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1477>:

```

g522.seq
1  atgactgagc  cgaaacacga  aacgccgacg  gaagagcagg  ttgccgcgcg
51  caaaaaagca  aaagccaaaa  tccgcaccat  ccgcatttgg  gcgtgggtca
101 ttttggcggt  gctcgcttca  accgccctgc  tctcccaatg  cgcgatgtcc
151 aaaccgcagg  caaaacagaa  aattgtcgag  tcttgcataa  aaaatattcc
201 gtttgcgtga  aaatggcaga  acgatttgaa  agcgcgcggc  ttggatgcgg
251 acaatacccg  tctcgccgct  gactactgca  aatgtatgtg  ggagcagcct
301 ttggacggat  tgagcgagaa  acagatcagc  tccttcggca  aactcgggtc
351 acaagaacag  cttgacctgc  tcggcggcgc  aaacgcgttt  gaaactcgag
401 acaaacaatg  tgtcgcggat  ttgaaagccg  attga

```

This corresponds to the amino acid sequence <SEQ ID 1478; ORF 522.ng>:

```

g522.pep
1  MTEPKHETPT  EEQVAARKKA  KAKIRTIRIW  AWVILALLAS  TALLSQCAMs
51  KPQAKQKIVE  SCMKNIPFAE  KWQNDLKARG  LDADNTRLAV  DYCKCMWEQP
101 LDGLSEKQIS  SFGKLGAQEQ  LDLLGGANAF  ETRDKQCVAD  LKAD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1479>:

```

m522.seq
1  ATGACTGAGC  CGAAACACGA  AATGCTGACG  AAAGAGCAGG  TTGCCGCGCG
51  CAAAAAAGCA  AAAGCCAAAA  TCCGCACCAT  CCGCATTGGA  GCGTGGGTCA
101 TTTTGGCGTT  GCTCGCTTTA  ACCGCCCTGC  TCTCCCAATG  CGCGATGTCC
151 AAACCGCAGG  CAAAACAGAA  AATTGTCGAG  TCTTGCCTGA  AGAATATTCC
201 GTTTGCCGAA  AAATGGCAAA  ACGATTGCG  GGCCCGCGGT  TTAGATTCAA
251 ACAATACCCG  CCTCGCCGTC  GACTACTGCA  AATGTATGTG  GGAGCAGCCT

```

787

301 TTGGACAGAT TGAGCGAGAA ACAGATTAGA TCCTTCGGCA AACTCGGCGC
 351 ACAAGAACAG CTTGACCTGC TCGGCGGCGC AAATGCCTTT GAAGCACGTG
 401 ACAAGCAGTG TGTGCGCGAT TTGAAATCAG AATAA

This corresponds to the amino acid sequence <SEQ ID 1480; ORF 522>:

m522.pep

1 MTEPKHEMLT KEQVAARKKA KAKIRTIRIW AWVILALLAL TALLSQCAMSKPQAKQKIVE
 51 KPQAKQKIVE SCVKNIPFAE KWQNDLRARG LDSNNTRLAV DYCKCMWEQP
 101 LDRLSEKQIR SFGKLGAQEQ LDLLGGANAF EARDKQCVAD LKSE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 522 shows 91.0% identity over a 144 aa overlap with a predicted ORF (ORF 522.ng) from *N. gonorrhoeae*:

m522/g522

	10	20	30	40	50	60
m522.pep	MTEPKHEMLTKEQVAARKKAKAKIRTIRIWAWVILALLALTALLSQCAMSKPQAKQKIVE					
	:					
g522	MTEPKHETPTEEQVAARKKAKAKIRTIRIWAWVILALLASTALLSQCAMSKPQAKQKIVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m522.pep	SCVKNIPFAEKWQNDLRARGLDSNNTRLAVDYCKCMWEQPLDRLSEKQIRSFGLGAQEQ					
	: : :					
g522	SCMKNIPFAEKWQNDLKARGLDADNTRLAVDYCKCMWEQPLDGLSEKQISSFGLGAQEQ					
	70	80	90	100	110	120
	130	140				
m522.pep	LDLLGGANAFEARDKQCVADLKSEX					
	: : :					
g522	LDLLGGANAFETRDKQCVADLKAD					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1481>:

a522.seq

1 ATGACTGAGC CGAAACACGA AATGCCGACG GAAGAGCAGG TTGCCGCGCGG
 51 CAAAAAAGCA AAAGCCAAAA TCCGCACCAT CCGCATTTGG GCATGGGTCA
 101 TTTTGGCGTT GCTCGCTTCA ACCGCCCTGC TCTCCCAATG CGCGATGTCC
 151 AAACCGCAGG CAAAACAGAA AATTGTCGAG TCTTGCGTGA AGAATATTCC
 201 GTTTGCCGAA AAATGGCAAA ACGATTTGCG GGCCCGCGGT TTAGATTCAA
 251 ACAATACCCG CCTTACCGTC GACTACTGCA AATGTATGTG GGAGCAGCCT
 301 TTGGACAGAT TGAGCGAGAA ACAGATTAGT TCCTTCGGCA AACTCGGCGC
 351 ACAAGAACAG CTTGACCTGC TCGGCGGCGC AAATGCCTTT GAAACGCGAG
 401 ACAAGCAGTG TGTGCGCGAT TTGAAATCAG AATAA

This corresponds to the amino acid sequence <SEQ ID 1482; ORF 522.a>:

a522.pep

1 MTEPKHEMPT EEQVAARKKA KAKIRTIRIW AWVILALLAS TALLSQCAMSKPQAKQKIVE
 51 KPQAKQKIVE SCVKNIPFAE KWQNDLRARG LDSNNTRLTV DYCKCMWEQP
 101 LDRLSEKQIS SFGKLGAQEQ LDLLGGANAF ETRDKQCVAD LKSE*

m522/a522 95.8% identity in 144 aa overlap

	10	20	30	40	50	60
m522.pep	MTEPKHEMLTKEQVAARKKAKAKIRTIRIWAWVILALLALTALLSQCAMSKPQAKQKIVE					
	:					
a522	MTEPKHEMPTTEEQVAARKKAKAKIRTIRIWAWVILALLASTALLSQCAMSKPQAKQKIVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m522.pep	SCVKNIPFAEKWQNDLRARGLDSNNTRLAVDYCKCMWEQPLDRLSEKQIRSFGLGAQEQ					
	:					
a522	SCVKNIPFAEKWQNDLRARGLDSNNTRLTVDYCKCMWEQPLDRLSEKQISSFGLGAQEQ					
	70	80	90	100	110	120

788

```

                130      140
m522.pep      LDLLGGANAFEARDKQCVDLKSEX
                |||||
a522          LDLLGGANAFETRDKQCVDLKSEX
                130      140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1483>:

```

g523.seq
1  atgactgtat ggtttggtgc cgctgttgcc gtcttaatca tcgaattatt
51  gacgggaacg gtttatcttt tggtgttcag cgcggtttg gcgggttcgg
101 gcatcgcta cgggctgact ggcagcacgc ctgccgccgt cttgaccgcc
151 gcactgcttt ccgcgctggg catttggttc gtacatgcca aaaccgccgt
201 gggaaaagtt gaaacggatt catatcagga tttggatacc ggaaaatatg
251 ccgaaatcct ccgatacaca ggcggcaacc gttacgaagt tttttatcgc
301 ggtacgcact ggcaggcgca aaatacgggg caggaagtgt ttgaaccggg
351 aacgcgcgcc ctcacgtcc gcaaagaagg taaccttctt atcatcgcaa
401 acccttaa

```

This corresponds to the amino acid sequence <SEQ ID 1484; ORF 523.ng>:

```

g523.pep
1  MTVWFVAAVA VLIIELLTGT VYLLVVSAA AGSGIAYGLT GSTPAAVLTA
51  ALLSALGIWF VHAKTAVGKV ETDSYQDLDT GKYAEILRYT GGNRYEVFYR
101 GTHWQAQNTG QEVFEPGTRA LIVRKEGNLL IIANP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1485>:

```

m523.seq (partial)
1  ..GCCGTCCTAA TCATCGAATT ATTGACGGGA ACGGTTTATC TTTTGGTTGT
51  nAGCGCGGCT TTGGCGGGTT CGGGCATTGC TTACGGGCTG ACCGGCAGTA
101 CGCCTGCCGC CGTCTTGACC GncGCTCTGC TTTCCGCGCT GGGTATTnG
151 TTCGTACACG CCAAACCGC CGTTAGAAAA GTTGAAACGG ATTCATATCA
201 GGATTTGGAT GCCGACAAT ATGTCGAAAT CCTCCGACAC ACAGGCGGCA
251 ACCGTTACGA AGTTTTtTAT CGCGGTACGc ACTGGCAGGC TCAAAATACG
301 GGGCAAGAAG AGCTTGAACC AGGAACTCGC GCCCTCATTG TCCGCAAGGA
351 AGGCAACCTT CTTATTATCA CACACCCTTA

```

This corresponds to the amino acid sequence <SEQ ID 1486; ORF 523>:

```

m523.pep (partial)
1  ..AVLIIELLTG TVYLLVVSAA LAGSGIAYGL TGSTPAAVLT XALLSALGIX
51  FVHAKTAVRK VETDSYQDL D AGQYVEILRH TGGNRYEVFY R GTHWQAQNT
101 GQEELEPGTR ALIVRKEGNL LIITHP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF523 shows 91.3% identity over a 126 aa overlap with a predicted ORF (ORF 523.ng) from *N. gonorrhoeae*:

m523/g523

```

                10      20      30      40      50
m523.pep      AVLIIELLTGTVYLLVVSAA LAGSGIAYGLTGSTPAAVLTXALLSALGIXF
                |||||
g523          MTVWFVAAVAVLIIELLTGTVYLLVVSAA LAGSGIAYGLTGSTPAAVLTAALLSALGIWF
                10      20      30      40      50      60

                60      70      80      90      100     110
m523.pep      VHAKTAVRKVETDSYQDL DAGQYVEILRH TGGNRYEVFYRGTHWQAQNTGQEELEPGTRA
                ||||| ||||| ||||| :||| :||| :||| :||| :||| :||| :||| :|||
g523          VHAKTAVGKVETDSYQDLDTGKYAEILRYTGGNRYEVFYRGTHWQAQNTGQEVFEPGTRA
                70      80      90      100     110     120

                120
m523.pep      LIVRKEGNLLIITHP
                |||||

```

789

g523 LIVRKEGNLLIIANPX
130

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1487>:

a523.seq
1 ATGACTGTAT GGTTTGTGTC CGCTGTTGCC GTCTTAATCA TCGAATTATT
51 GACGGGAACG GTTTATCTTT TGGTTGTCAG CGCGGCTTTG GCGGGTTCGG
101 GCATTGCTTA CGGGCTGACC GGCAGCACGC CTGCCGCCGT CTTGACCGCC
151 GCTCTGCTTT CCGCGCTGGG TATTTGGTTC GTACACGCCA AAACCGCCGT
201 GGGAAAAGTT GAAACGGATT CATATCAGGA TTTGGATGCC GGGCAATATG
251 CCGAAATCCT CCGGCACGCA GCGGCAACC GTTACGAAGT TTTTATCGC
301 GGTACGCACT GGCAGGCTCA AAATACGGGG CAAGAAGAGC TTGAACCAGG
351 AACGCGCGCC CTAATCGTCC GCAAGGAAGG CAACCTTCTT ATCATCGCAA
401 AACCTTAA

This corresponds to the amino acid sequence <SEQ ID 1488; ORF 523.a>:

a523.pep
1 MTVWFVAAVA VLIIELLTGT VYLLVVSAA LAGSGIAYGLT GSTPAAVLTA
51 ALLSALGIWF VHAKTAVGKV ETDSYQDLDA GQYAEILRHA GGNRYEVFVR
101 GTHWQAQNTG QEELEPGTRA LIVRKEGNLL IIAKP*

m523/a523 94.4% identity in 126 aa overlap

	10	20	30	40	50
m523.pep	AVLIIELLTGTVYLLVVSAAAGSGIAYGLTGSTPAAVLTXALLSALGIXF				
a523	MTVWFVAAVAVLIIELLTGTVYLLVVSAAAGSGIAYGLTGSTPAAVLTAALLSALGIWF				
	10	20	30	40	50
	60	70	80	90	100
m523.pep	VHAKTAVRKVETDSYQDLDAQYVEILRHAGGNRYEVFVRGTHWQAQNTGQEELEPGTRA				
a523	VHAKTAVGKVETDSYQDLDAQYAEILRHAGGNRYEVFVRGTHWQAQNTGQEELEPGTRA				
	70	80	90	100	110
	120				
m523.pep	LIVRKEGNLLIIITHPX				
a523	LIVRKEGNLLIIAKPX				
	130				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1489>:

g525.seq
1 atgaagtacg tccggttatt tttcctcggc acggcactcg ccggcactca
51 agcggcggtt gccgaaatgg ttcaaactga aggcggcagc taccgcccgc
101 tttatctgaa aaaagatacc ggcttgatta aagtcaaacc gttcaaactg
151 gataaatatc ccgttaccaa tgccgagttt gccgaatttg tcaacagcca
201 cccccaatgg caaaaaggca ggatcggttc caaacaggca gaaccgcgtt
251 acctgaagca ttggatgaaa aacggcagcc gcagctatgc gccgaaggcg
301 ggcgaattga aacagccggt taccaatatt tcctgggttg ccgccaacgc
351 ctattgcgcc gcacaaggca aacgcctgcc gaccatcgac gaatgggaat
401 ttgccggact tgcttcgcc acgcagaaaa aacggctcaa acgaaccggg
451 ctacaaccgc actattctcg attggtatgc cgacggcgga cggaaaggcc
501 tgcacgatgt cggcaaagca ccgcccgaac tactgggggtg tttatgatat
551 gcacgggctg a

This corresponds to the amino acid sequence <SEQ ID 1490; ORF 525.ng>:

g525.pep
1 MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKDDT GLIKVKPFKL
51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWMK NGSRSYAPKA
101 GELKQPVTNI SWFAANAYCA AQQKRLPTID EWEFAGLASA TQKKRLKRT
151 LQPHYSRLVC RRRTERPARC RQSTARTTGV FMICTG *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1491>:

790

```

m525.seq
  1  ATGAAGTATG TCCGGTTATT TTWCCTCGGC GCGGCACTCG cCrrCACTCA
 51  ArCGGCGGCT GcCGAAATGG TTCAAATCGA AGGCGGCAGc TACCGCCCrC
101  TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
151  GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTTG TCAACAGCCA
201  CCCCCAATGG CAAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251  ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGc GCCGAAGgCG
301  GgCGAATTAA AACAACCGGT AACCAATGTT TCCTGGwTTG CCGCCAaCGC
351  CTAtTGC GCCAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401  TTGCCGGACT TGCTTCCGCC ACGCAGAAAA A.CGGCTCAA ACGAACCCGG
451  CTACAACCGC ACTATTCTCG ATTGGTATGC CGACGGCGGA CGGAAAGGCC
501  TGCACGATGT CGGCA.AAGG CCGCCCGAAC TACTGGGGCG TTTATGATAT
551  GCACGGGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1492; ORF 525>:

```

m525.pep
  1  MKYVRLFXLG AALAXTQXAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
 51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101  GELKQPVNTV SWXAANAYCA AQGKRLPTID EWEFAGLASA TQKXRLKRTR
151  LQPHYSRLVC RRRTERPARC RXKAARTTGA FMICTG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 525 shows 94.1% identity over a 186 aa overlap with a predicted ORF (ORF 525.ng) from *N. gonorrhoeae*:

```

m525/g525
      10      20      30      40      50      60
m525.pep  MKYVRLFXLGAALAXTQXAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
g525      MKYVRLFFLTALAGTQAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
      10      20      30      40      50      60
      70      80      90     100     110     120
m525.pep  AEFVNSHPQWQKGRIGSKQAEPAAYLKHWKNGSRSYAPKAGELKQPVNTVSWXAANAYCA
g525      AEFVNSHPQWQKGRIGSKQAEPAAYLKHWKNGSRSYAPKAGELKQPVNTISWFAANAYCA
      70      80      90     100     110     120
      130     140     150     160     170     180
m525.pep  AQGKRLPTIDWEFAGLASATQKXRLKRTRLQPHYSRLVCRRRTERPARCRXKAARTTGA
g525      AQGKRLPTIDWEFAGLASATQKKRLKRTRLQPHYSRLVCRRRTERPARCRQSTARTTGV
      130     140     150     160     170     180

m525.pep  FMICTGX
g525      FMICTGX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1493>:

```

a525.seq
  1  ATGAAGTTTA CCCGGTTACT CTTTCTCTGT GCGGCACTCG CCGGCACTCA
 51  AGCGGCAGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
101  TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
151  GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTTG TCAACAGCCA
201  CCCCCAATGG CAAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251  ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301  GGCGATTTAA AACAACCGGT AACCAATGTT TCCTGGTTTC CCGCCAACGC
351  CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401  TTGCCGGACT TGCTTCCGCC ACGCAG.AAA AACGGCTCAA ACGAACCCGG
451  CTACAACCGC ACTATTCTCG ACTGGTATGC GGATGGCGAC CGGAAAGACC
501  TGCACGATGT CGGCAAAG.G TCGCCCGAAC TACTGGGGCG TTTATGATAT
551  GCACGGTCTG A

```

791

This corresponds to the amino acid sequence <SEQ ID 1494; ORF 525.a>:

```
a525.pep
  1  MKFTRLLEFLC AALAGTQAAA AEMVQIEGGS YRPLYLK KDT GLIKVKPFKL
 51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101  GDLKQPVTNV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQXKRLKRTR
151  LQPHYSRLVC GWRPERPARC RQXVARTTGA FMICTV*
```

m525/a525 90.8% identity in 185 aa overlap

```

              10      20      30      40      50      60
m525.pep      MKYVRLFXLGAALAXTQXAAAEMVQIEGGSYRPLYLK KDTGLIKVKPFKLDKYPVTNAEF
              ||::||: | |||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a525           MKFTRLLEFLCAALAGTQAAAEMVQIEGGSYRPLYLK KDTGLIKVKPFKLDKYPVTNAEF
              10      20      30      40      50      60

              70      80      90      100     110     120
m525.pep      AEFVNSHPQWQKGRIGSKQAEPAYLKHWKNGSRSYAPKAGELKQPVTNVSWXAANAYCA
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a525           AEFVNSHPQWQKGRIGSKQAEPAYLKHWKNGSRSYAPKAGDLKQPVTNVSWFAANAYCA
              70      80      90      100     110     120

              130     140     150     160     170     180
m525.pep      AQGKRLPTIDWEFAGLASATQXRLKRTRLQPHYSRLVCRRRTERPARCRXKAARTTGA
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a525           AQGKRLPTIDWEFAGLASATQXRLKRTRLQPHYSRLVCGWRPERPARCQXVARTTGA
              130     140     150     160     170     180

m525.pep      FMICTGX
              |||||
a525           FMICTVX
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1495>:

```
g525-1.seq
  1  ATGAAGTACG TCCGGTTATT TTTCCTCGGC ACGGCACTCG CCGGCACTCA
 51  AGCGGCGGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
101  TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
151  GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTG TCAACAGCCA
201  CCCCCAATGG CAAAAGGCA GGATCGGTTC CAAACAGGCA GAACCCGCTT
251  ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301  GGCGAATTGA AACAGCCGGT TACCAATATT TCCTGGTTTG CCGCCAACGC
351  CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATCGAC GAATGGGAAT
401  TTGCCGGACT TGCTTCCGCC ACGCAGAAAA ACGGCTCAAA CGAACC CGGC
451  TACAACCGCA CTATTCTCGA TTGGTATGCC GACGGCGGAC GGAAAGGCCT
501  GCACGATGTC GGCAAAGACC GCCCGAACTA CTGGGGTGTT TATGATATGC
551  ACGGGCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601  TCCGGCAATG CCAACGCGCA AATGTTTTGC AGCGGCGCAT CTGTCCGGGC
651  GAGCGACTCG TCCAACATAG CCGCCTTCCT CCGCTACGGC ATCCGCACCA
701  GCCTGCAATC CAAATACGTC CTGCACAAC TGGGCTTCCG CTGCGCAAGC
751  CGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1496; ORF 525-1.ng>:

```
g525-1.pep
  1  MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLK KDT GLIKVKPFKL
 51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101  GELKQPVTNI SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
151  YNRTILDWYA DGGRKGLHDV GKDRPNYWG VYDMHGLIEW TEDFNSSLLS
201  SGNANAQMFC SGASVGASDS SNYAAFLRYG IRTSLQSKYV LHNLGFRCAS
251  R*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1497>:

```
m525-1.seq
  1  ATGAAGTATG TCCGGTTATT TTTCCTCGGC GCGGCACTCG CCGGCACTCA
 51  AGCGGCGGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
101  TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
```

792

```

151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTG TCAACAGCCA
201 CCCCCAATGG CAAAAAGGCA GGATCGGTTC CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GGCGAATTAA AACAACCGGT AACCAATGTT TCCTGGTTTG CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCTTCCGCC ACGCAGAAAA ACGGCTCAAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA TTGGTATGCC GACGGCGGAC GGAAAGGCCT
501 GCACGATGTC GGCAAAGGCC GCCCGAACTA CTGGGGCGTT TATGATATGC
551 ACGGCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTTGC AGCGGCGCGT CTATCGGGTC
651 GAGCGACTCG TCCAACATG CCGCCTTCCT CCGCTACGGC ATCCGTACCA
701 GCCTGCAATC CAAATATGTC TTGCACAACT TGGGCTCCG TTGCACAAGC
751 CGATAA

```

This corresponds to the amino acid sequence <SEQ ID 1498; ORF 525-1>:

m525-1.pep

```

1 MKYVRLFFLG AALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHHMK NGSRSYAPKA
101 GELKQPVTNV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
151 YNRTILDWYA DGGKRLHDV GKGRPNYWGV YDMHGLIEWE TEDFNSSLSS
201 SGNANAQMFC SGASIGSSDS SNYAAFLRYG IRTSLQSKYV LHNLGFRCTS
251 R*

```

m525-1/g525-1 97.6% identity in 251 aa overlap

	10	20	30	40	50	60
m525-1.pep	MKYVRLFFLG	AALAGTQAAA	AEMVQIEGGS	YRPLYLKKDT	GLIKVKPFKL	DKYPVTNAEF
g525-1	MKYVRLFFLG	TALAGTQAAA	AEMVQIEGGS	YRPLYLKKDT	GLIKVKPFKL	DKYPVTNAEF
	10	20	30	40	50	60
m525-1.pep	AEFVNSHPQW	QKGRIGSKQA	EPAYLKHHMK	NGSRSYAPKA	GELKQPVTNV	SWFAANAYCA
g525-1	AEFVNSHPQW	QKGRIGSKQA	EPAYLKHHMK	NGSRSYAPKA	GELKQPVTNI	SWFAANAYCA
	70	80	90	100	110	120
m525-1.pep	AQGKRLPTID	EWEFAGLASA	TQKNGSNEPG	YNRTILDWYA	DGGKRLHDV	GKGRPNYWGV
g525-1	AQGKRLPTID	EWEFAGLASA	TQKNGSNEPG	YNRTILDWYA	DGGKRLHDV	GKDRPNYWGV
	130	140	150	160	170	180
m525-1.pep	YDMHGLIEWE	TEDFNSSLSS	SGNANAQMFC	SGASIGSSDS	SNYAAFLRYG	IRTSLSQSKYV
g525-1	YDMHGLIEWE	TEDFNSSLSS	SGNANAQMFC	SGASVGSADS	SNYAAFLRYG	IRTSLSQSKYV
	190	200	210	220	230	240
m525-1.pep	LHNLGFRCTS	RSX				
g525-1	LHNLGFRCA	SRX				
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1499>:

a525-1.seq

```

1 ATGAAGTTTA CCCGTTACT CTTTCTCTGT GCGGCACTCG CCGGCACTCA
51 AGCGGCAGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCCG
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTG TCAACAGCCA
201 CCCCCAATGG CAAAAAGGCA GGATCGGTTC CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GCGGATTTAA AACAACCGGT AACCAATGTT TCCTGGTTTC CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCTTCCGCC ACGCAGAAAA ACGGCTCAAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA CTGGTATGCG GATGGCGACC GGAAAGACCT
501 GCACGATGTC GGCAAAGGTC GCCCGAACTA CTGGGGCGTT TATGATATGC
551 ACGGTCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTTGC AGCGGCGCGT CTATCGGGTC
651 GAGCGACTCG TCCAACATG CCGCCTTCCT CCGCTACGGC ATCCGCACCA
701 GCCTGCAATC CAAATATGTC TTGCACAACT TGGGCTTCCG TTGCACAAGC
751 CGATAA

```


794

```

201 TAACckTGAT TTTATAGGGA AGGG.AATtk AgCkTCaGTy GrTwATaTCG
251 CsGATGTmTA TGGTTTTACT GTTTTTGACC TTCGAGCCGT TTACTTGAAC
301 CCTACCCAGT TCGATGTGCT TTTGCGCAAG GGAACGGGTC TTGAAAAAAC
351 GTGCCGCCCA AAGCCATTTG TCCAGCCGCA TGGCGGAAGA ATCGTGCTTG
401 TCTTTCATAC GATTTTGTTT GAAATAATTG AATTTGTTTC GAGTTTAGCA
451 TAA

```

This corresponds to the amino acid sequence <SEQ ID 1504; ORF 527>:

```

m527.pep
  1 MVLPVSFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCRXRVLF
 51 IQKPRXGCRA ALVVQTFNXD FIGKXNXASV XXIADVYGFT VFDLRAVYLN
101 PTQFDVLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
151 *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 527 shows 90.0% identity over a 150 aa overlap with a predicted ORF (ORF 527.ng) from *N. gonorrhoeae*:

```

m527/g527
      10      20      30      40      50      60
m527.pep MVLPVSFFQPVQLAAVALGRSAVGIGGSDAAELVELFALFPQCCRXRVLFIQKPRXGCRA
      |||||
g527      MVLPVSFFQPVQLAAVALGRSAVGMGGSDAAELVELFALFPQCCRFVFFIQKPRLGCRA
      |||||
      10      20      30      40      50      60
      70      80      90      100     110     120
m527.pep ALVVQTFNXDFIGKXNXASVXXIADVYGFTVFDLRAVYLNPTQFDVLLRKGTGLEKTCRP
      |||||
g527      ALVVQTFNLDFMGKGIERQVNDIADVYGFTVFDRAVYLNPTQFDMLLLRKGTGLEKTCRP
      |||||
      70      80      90      100     110     120
      130     140     150
m527.pep KPFVQPHGGRIVLVFHTILFEIIEFVSSLA
      |||||
g527      KPFVQPHGGRIVLVFHTILFEIIEFVSSLA
      |||||
      130     140     150

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1505>:

```

a527.seq
  1 ATGGTTTTAC CAGTCTCCTT TTTTCAGCCT GTCCAGTTGG CGGCGGTCGC
 51 GCTTGGTCGG TCTGCCGTCG GGATAGGCGG AAGTGATGCG GCTGAATTGG
101 TCGAGCTGTT TGCGCTCTTC CCTCAATGTT GCCGTTTTCG CGTCCTCTTC
151 ATACAGAAGC CGCGCCTCGG ATGCCGGGCG GCGTTGGTGG TTCAAACCTT
201 TAACCTTGAT TTTATAGGGA AGGGAATTGA GCGTCAGGTC GATAATATCG
251 CCGATGTCTA TGGTTTTACT GTTTTTGACC TTCGAGCCGT TTACTTGAAC
301 CCTACCCAGT TCGATGTGCT TTTGCGCAAG GGAACGGGTC TTGAAAAAAC
351 GTGCCGCCCA AAGCCATTTG TCCAGCCGCA TGGCGGAAGA ATCGTGCTTG
401 TCTTTCATAC GATTTTGTTT GAAATAATTG AATTTGTTTC GAGTTTAGCA
451 TAA

```

This corresponds to the amino acid sequence <SEQ ID 1506; ORF 527.a>:

```

a527.pep
  1 MVLPVSFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCRFRVLF
 51 IQKPRLGCRA ALVVQTFNLD FIGKGIERQV DNIADVYGFT VFDLRAVYLN
101 PTQFDVLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
151 *

```

m527/a527 93.3% identity in 150 aa overlap

```

      10      20      30      40      50      60
m527.pep MVLPVSFFQPVQLAAVALGRSAVGIGGSDAAELVELFALFPQCCRXRVLFIQKPRXGCRA
      |||||
a527      MVLPVSFFQPVQLAAVALGRSAVGIGGSDAAELVELFALFPQCCRFRVLFIQKPRLGCRA
      |||||
      10      20      30      40      50      60

```

795

	70	80	90	100	110	120
m527.pep	ALVVQTFNXXDFIGKXNXASVXXIADVYGFTVFDLRAVYLNPTQFDVLLRKGTGLEKTCRP					
	:					
a527	ALVVQTFNLDFIGKIERQVDNIADVYGFTVFDLRAVYLNPTQFDVLLRKGTGLEKTCRP					
	70	80	90	100	110	120
	130	140	150			
m527.pep	KPFVQPHGGRIVLVFHTILFEIIEFVSSLAX					
a527	KPFVQPHGGRIVLVFHTILFEIIEFVSSLAX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1507>:

```

g528.seq
1  atggaattc gggtaataaa atatacggca acggctgcgt tgtttgcatt
51  tacggttgca ggctgccggc tggcggggtg gtatgagtgt ttgtccttgt
101 cgggctggtg taagccgaga aaacctgccg ccatcgattt ttgggatatt
151 ggcgcgcgaga gtccgctgtc tttagaggac tacgagatac cgctttcaga
201 cggcaatcgt tccgtcaggg caaacgaata tgaatccgcg caaaaatctt
251 acttttatag gaaaataggg aagtttgaag cctgcggggt ggattggcgt
301 acgcgtgacg gcaaaccttt gggtgagagg ttcaaacagg aaggtttcga
351 ctgtttggaa aagcaggggt tgcggcgcaa cggcctgtcc gagcgcgtcc
401 gatggtaa

```

This corresponds to the amino acid sequence <SEQ ID 1508; ORF 528.ng>:

```

g528.pep
1  MEIRVIKYTA TAALFAFTVA GCRLAGWYEC LSLSGWCKPR KPAAIDFWDI
51  GGESPLSLED YEIPLSDGNS SVRANEYESA QKSYFYRKIG KFEACGLDWR
101 TRDGKPLVER FKQEGFDCLE KQGLRRNGLS ERVRW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1509>:

```

m528.seq (partial)
1  ATGGAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCAAT
51  TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTCA
101 CCGGCTGGTG TAAGCCGAGA AAACCGGCTG CCATCGATT TGGGATATT
151 GGCgcgcgaga GTCCGCCGTC TTTAGGGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATAGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG C.TGCGGGCT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG GAGGATTGTA
351 CTGCTTGGA AAG....

```

This corresponds to the amino acid sequence <SEQ ID 1510; ORF 528>:

```

m528.pep (partial)
1  MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLTGWCKPR KPAAIDFWDI
51  GGESPPSLGD YEIPLSDGNS SVRANEYESA QKSYFYRKIG KFEXCGLDWR
101 TRDGKPLIET FKQGGFDCLE K....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 528 shows 89.3% identity over a 121 aa overlap with a predicted ORF (ORF 528.ng) from *N. gonorrhoeae*:

m528/g528	10	20	30	40	50	60
m528.pep	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD					
	: :					
g528	MEIRVIKYTATAALFAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPLSLED					
	10	20	30	40	50	60
	70	80	90	100	110	120
m528.pep	YEIPLSDGNSSVRANEYESAQKSYFYRKIGKFEXCGLDWRTRDGKPLIETFKQGGFDCLE					
g528	YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEXCGLDWRTRDGKPLVERFKQEGFDCLE					
	70	80	90	100	110	120

796

```

m528.pep      K
               |
g528          KQGLRRNGLSERVRW

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1511>:

```

a528.seq
1   ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT
51  TACGGTTGCA GGCTGCCGGT TGGCAGGTTG GTATGAGTGT TCGTCCCTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATTT TTGGGATATT
151 GCGGCGGAGA GTCCTCCGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTGAAG CCTGCGGGTT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG AAGGTTTTGA
351 TTGTTTGAAA AAGCAGGGGT TCGGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1512; ORF 528.a>:

```

a528.pep
1   MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI
51  GGESPPSLED YEIPLSDGNR SVRANEYESA QQSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQEGFDCLK KQGLRRNGLS ERVRW*

```

m528/a528 95.0% identity in 121 aa overlap

```

              10      20      30      40      50      60
m528.pep      MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD
               |||||||
a528           MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPPSLED
              10      20      30      40      50      60

              70      80      90     100     110     120
m528.pep      YEIPLSDGNSSVRANEYESAQQSYFYRKIGKFEXCGLDWRTRDGKPLIETFKQGGFDCLE
               |||||||
a528           YEIPLSDGNRSVRANEYESAQQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQEGFDCLK
              70      80      90     100     110     120

```

```

m528.pep      K
               |
a528          KQGLRRNGLSERVRW
               130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1513>:

```

g528-1.seq
1   ATGGAAATTC GGGTAATAAA ATATACGGCA ACGGCTGCGT TGTTTGCATT
51  TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATTT TTGGGATATT
151 GCGGCGGAGA GTCCGCTGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCG CAAAAATCTT
251 ACTTTTATAG GAAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GTTGAGAGG TTCAAACAGG AAGGTTTCGA
351 CTGTTTGAAA AAGCAGGGGT TCGGCGCAA CGGCCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1514; ORF 528-1.ng>:

```

g528-1.pep
1   MEIRVIKYTA TAALFAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI
51  GGESPLSLED YEIPLSDGNR SVRANEYESA QKSYFYRKIG KFEACGLDWR
101 TRDGKPLVER FKQEGFDCLE KQGLRRNGLS ERVRW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1515>:

```

m528-1.seq
1   ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT

```

797

```

51  TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTCA
101 CCGGCTGGTG TAAGCCGAGA AAACCGGCTG CCATCGATTT TTGGGATATT
151 GGCGGCGAGA GTCCGCCGTC TTTAGGGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGCT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG GAGGATTTGA
351 CTGCTTGGA AAGCAGGGGT TCGGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1516; ORF 528-1>:

m528-1.pep..

```

1  MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLTGWCKPR KPAAIDFWDI
51  GGESPPSLGD YEIPLSDG NR SVRANEYESA QSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQGGFDCLE KQGLRRNGLS ERVRW*

```

g528-1/m528-1 92.6% identity in 135 aa overlap

```

              10      20      30      40      50      60
g528-1.pep  MEIRVIKYTATAALFAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPLSLED
              |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
m528-1      MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD
              10      20      30      40      50      60

              70      80      90     100     110     120
g528-1.pep  YEIPLSDGNRSVRANEYESAQSYFYRKIGKFEACGLDWRTRDGKPLVERFKQEGFDCLE
              |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
m528-1      YEIPLSDGNRSVRANEYESAQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCLE
              70      80      90     100     110     120

              130
g528-1.pep  KQGLRRNGLSERVRWX
              |||::|||::|||::|||::|||::|||::|||::|||::|||::|||
m528-1      KQGLRRNGLSERVRWX
              130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1517>:

a528-1.seq

```

1  ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT
51  TACGGTTGCA GGCTGCCGGT TGGCAGGTG GTATGAGTGT TCGTCCCTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATTT TTGGGATATT
151 GGCGGCGAGA GTCTCCGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG AAGGTTTTGA
351 TTGTTTAAA AAGCAGGGGT TCGGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1518; ORF 528-1.a>:

a528-1.pep

```

1  MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI
51  GGESPPSLED YEIPLSDG NR SVRANEYESA QSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQEGFDCLE KQGLRRNGLS ERVRW*

```

a528-1/m528-1 97.0% identity in 135 aa overlap

```

              10      20      30      40      50      60
a528-1.pep  MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPPSLED
              |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
m528-1      MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD
              10      20      30      40      50      60

              70      80      90     100     110     120
a528-1.pep  YEIPLSDGNRSVRANEYESAQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQEGFDCLE
              |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
m528-1      YEIPLSDGNRSVRANEYESAQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCLE
              70      80      90     100     110     120

              130
a528-1.pep  KQGLRRNGLSERVRWX
              |||::|||::|||::|||::|||::|||::|||::|||::|||::|||
m528-1      KQGLRRNGLSERVRWX
              130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1519>:

g529.seq (partial)

```

1 atgacccata tcaaaccctg cattgccgcg ctgcactca tcgggcttgc
51 cgctgctcc ggcagcaaaa ccgaacagcc caagctcgac taccaaagcc
101 ggctgcaccg cctgatcaaa ctgcaagtc cgctgattt gaacaacccc
151 gaccaaggca acctctaccg cctgcctgcc gggtcgggag ccgtccgcgc
201 cggggatttg gaaaaacgcc gcacaccgc cgtccaacag ccageggatg
251 ccggaagtat tgaaaagcgt caaaggcgtc cgcttcgagc ggcgacggca
301 gccaacgcct ggcttgctgt tgacggcaaa tccccgcgcg aaatctccgc
351 cgctttctg.

```

This corresponds to the amino acid sequence <SEQ ID 1520; ORF 529.ng>:

g529.pep (partial)

```

1 MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNNP
51 DQGNLYRLPA GSGAVRAGDL EKRRTPAVQQ PADAGSIEKR QRRPLRAATA
101 ANAWLVVDGK SPAEISAAF.

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1521>:

m529.seq

```

1 ATGACCCATA TCAAACCCGT CATTGCCGCG CTCGCACTCA TCGGGCTTGC
51 CGCCTGCTCC GGCAGCAAAA CCGAACAGCC CAAGCTCGAC TACCAAAGCC
101 GGTGCGCACC CTTGATCAAA CTTGAAGTCC CACCTGATTG GAACAACCCC
151 GACCAAGGCA ACCTCTACCG CCTGCCTGCC GGTTCGGGCG CCGTCCGCGC
201 CAGCGATTG GAAAAACGCC GCACACCCGC CGTCCAACAG CCTGCCGATG
251 CCGAAGTATT GAAAGCGTC AAAGTGTC GCCTCGAGCG CGACGGCAGC
301 CAACGCTGGC TCGTTGTGCA CGGCAAGTCT CCTGCCGAAA TCTGGCCGCT
351 CCTGAAAGCC TTTTGGCAGG AAAACGGCTT CGACATCAA TCCGAAGAAC
401 CCGCCATCGG ACAATGGAA ACCGAGTGGG CGGAAAACCG CGCCAAATC
451 CCCAAGACA GCTTGCGCCG CCTCTTCGAC AAAGTCGGCT TGGGCGGCAT
501 CTACTCCACC GGCAGCGCG ACAAATTCAT CGTCCGTATC GAACAGGGCA
551 AAAACGGCGT TTCCGACATC TTCTTCGCCC ACAAAGCCAT GAAAGAAGTG
601 TACGGCGGCA AAGACAAAGA CACGACCGTA TGGCAGCCCT CCCCGTCCGA
651 TCCCAACCTC GAAGCCGCTT TCCTGACGCG CTTTATGCAA TATTGGGCG
701 TTGACGGACA GCAGCGGAA AACGCATCGG CAAAAAACC TACCCTTCCC
751 GCCGCCAACG AAATGGCGCG TATCGAAGGC AAAAGCCTGA TTGTCTTTGG
801 CGACTACGGC AGAACTGGC GCGCACCCT GCTCGCCTC GACCGCATCG
851 GGCTGACCGT CGTCGGTCAA AACACCGAAC GCCACGCCTT CCTGGTTCAA
901 AAAGCCCCGA ACGAAAGCAA TGCAGTTACC GAACAAAAAC CCGGCCTGTT
951 CAAACGCCTG CTGGGCAAAG GCAAAGCGGA GAAACCTGCC GAACAGCCGG
1001 AACTGATTGT CTATGCAGAA CCTGTCGCCA ACGGCTCGCG CATCGTCCTG
1051 CTCAACAAAG ACGGCAGCGC ATATGCCGGC AAAGACGCAT CCGCATTATT
1101 GGGCAAATC CATTCCGAAC TGCCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1522; ORF 529>:

m529.pep

```

1 MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNNP
51 DQGNLYRLPA GSGAVRASDL EKRRTPAVQQ PDAEVLKSV KGVRLERDGS
101 QRWLVDGKS PAEIWPLLKA FWQENGFDIK SEEPAGQME TEWAENRAKI
151 PQDSLRLRFD KVGLGGIYST GERDKFIVRI EQGKNGVSDI FFAHKAMKEV
201 YGKDKDFTV WQSPSPDNL EAAFLTRFMQ YLGVGQQAE NASAKKPTLP
251 AANEMARIEG KSLIVFGDYG RNWRTVLAL DRIGLTVVGQ NTERHAFLVQ
301 KAPNESNAVT EQKPGLFKRL LGKGKAEKPA EQPELIVYAE PVANGSRIVL
351 LNKDGSAYAG KDSALLGKL HSELR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 529 shows 83.5% identity over a 115 aa overlap with a predicted ORF (ORF 529.ng) from *N. gonorrhoeae*:

g529/m529

```

              10      20      30      40      50      60
g529.pep      MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNNPDQGNLYRLPA

```

```

m529      |||||
           MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNPNPDQGNLYRLPA
           10      20      30      40      50      60

           70      80      90      100     110     120
g529.pep  GSGAVRAGDLEKRRTPAVQQPADAGSIEKQRRLPLRAATAANAWLVVDGKSPAEISAAFX
           |||||:|||||
m529      GSGAVRASDLEKRRTPAVQQPADAEVLKSVKGVRLER-DGSQRWLVDGKSPAEIWPLLK
           70      80      90      100     110

m529      AFWQENGFDIKSEEPaIGOMETEWAENRAKIPQDSLRLRLFDKVLGGIYSTGERDKFIVR
           120     130     140     150     160     170

```

```
a529.seq
1 ATGACCCTATA TCAAACCCCGT CATTGCCGCG CTCGCACTCA TCGGGCTTGC
51 CGCTTGCTCC GGCAGCAAAA CCGAACAGCC CAAGCTCGAC TACCAAAGCC
101 GGTCGCAACG CCTGATCAAA CTCGAAGTCC CACCTGATTT GAACAACCCC
151 GACCAAGGCA ACCTCTACCG CCTGCCTGCC GGTCGGGCG CCGTCCGCGC
201 CAGCGATTTG GAAAAACGCC GCACACCCGC CGTCCAACAG CCTCCCGATG
251 CCGAAGTATT GAAAGCGTC AAAGGTGCC GCCTCGAGCG GCAGCGCAGC
301 CAACGCTGGC TCGTTGTCSA CGGCAAGTCT CATGCGGAAA TCTGGCCGCT
351 CCTGAAAGCC TTTTGGCAGG AAAACGGCTT CGACATCAA TCCGAAGAAC
401 CCGCCATCGG ACAAAATGGA ACCGAGTGGG CGGAAAACCG TGCCAAAATC
451 CCCCAGACA GCTTGCCCGC CCTATTGAC ACAGTCGGTT TGGGCGGGAT
501 CTACTCCACC GGCGAGCGCG ACAAAATCAT CGTCCGTATC GAACAGGGCA
551 AAAACGGCGT TTCCGACATC TTCTTCGCCC ACAAGCCAT GAAAGAAGTG
601 TACGGCGGCA AAGACAAGA CACGACCGTA TGGCAGCCCT CCCCGTCCGA
651 TCCCAACCTC GAAGCCGCTT TCCTGACGCG CTTTATGCAA TATTTGGGCG
701 TTGACGGACA CGAGGCGGAA AACGCATCGG CAAAAAAACC TACCCCTCCC
751 GCCGCCAACG AAATGGCGCG TATCGAAGGC AAAAGCCTGA TTGTCTTTGG
801 CGACTACCGC AGAAACTGCG GGCGCACCCG GCTCGCCCTC GACCGCATCG
851 GGCTGACGGT CGTCGGTCAA AACACCGAAC GCCACGCTTT CCTGGTTCAA
901 AAAGCCCCGA ACGAAAGCAA TGCAGTTACC GAACAAAAAC CCGGCTGTTT
951 CAAACGCCTG CTGGGCAAAG GCAAAGCGGA GAAACCTGCC GAACAGCCGG
1001 AACTGATTGT CTATGCCGAG CCTGTCCGCA ACGGCTCGCG CATCGTCTTG
1051 CTCACAAGAG ACGGCAGCGC ATATGCCGCG AAAGACGCAT CCGCATTATT
1101 GGGCAAACTC CATTCCGAAC TGCGTTAA
```

a529.pep

1	<u>MTHIKPVIAA</u>	<u>LALIGLAACS</u>	GSKTEQPKLD	YQSRSHRLIK	LEVPPDLNNP
51	DQGNLYRLPA	GSQAVRASLD	EKRRTPAVQQ	PADAEVLKVS	KGVRLERDGS
101	QRWLVDVDGS	HAEIWPLLKA	FWQENGFDIK	SEEPATGOME	TWEAENRAKI
151	PQDSLRLRFL	TVGLGGIYST	GERDKFIVRI	EQGKNGVSDI	FFAHKAMKEV
201	YGGKDKDTTV	WQPSPSDPNL	EAAFLTRFMQ	YLGVDGQQAE	NASAKKPTLP
251	ANEMARIEG	KSLIVFGDYG	RNWRRTALAL	DRIGLTVVGQ	NTERHAFLVQ
301	KAPNESNAV	EQKPLGLFKRL	LKGKKAEPKA	EQPELIVYAE	PVANGSRIVL
351	LNKDGSAAYG	KDASALLGKL	HSELR*		

	10	20	30	40	50	60
m529.pep	MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNPNPDQGNLYRLPA					
a529	MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNPNPDQGNLYRLPA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m529.pep	GSGAVRASDLEKRRTPAVQQPADAIEVLKSVKGVRLERDGSQRWLVDGKSPAIEIWPLLKA					
a529	GSGAVRASDLEKRRTPAVQQPADAIEVLKSVKGVRLERDGSQRWLVDGKSHAEIWPLLKA					
	70	80	90	100	110	120
	130	140	150	160	170	180

800

```

m529.pep      FWQENGFDIKSEEPaIGQMETEWAENRAKIPQDSLRRLLFDKVLGGIYSTGERDKFIVRI
                |||
a529           FWQENGFDIKSEEPaIGQMETEWAENRAKIPQDSLRRLLFDTVLGGIYSTGERDKFIVRI
                130      140      150      160      170      180

                190      200      210      220      230      240
m529.pep      EQGKNGVSDIFFAHKAMKEVYGGKDKDTTVWQPSDPNLEAAFLTRFMQYLGVDGQQAE
                |||
a529           EQGKNGVSDIFFAHKAMKEVYGGKDKDTTVWQPSDPNLEAAFLTRFMQYLGVDGQQAE
                190      200      210      220      230      240

                250      260      270      280      290      300
m529.pep      NASAKKPTLPAANEMARIEGKSLIVFGDYGRNWRRTVLALDRIGLTVVGQNTERHAFIVQ
                |||
a529           NASAKKPTLPAANEMARIEGKSLIVFGDYGRNWRRTALALDRIGLTVVGQNTERHAFIVQ
                250      260      270      280      290      300

                310      320      330      340      350      360
m529.pep      KAPNESNAVTEQKPGFLFKRLLGKGAEKPAEQPELIVYAEPVANGSRIVLLNKDGSAYAG
                |||
a529           KAPNESNAVTEQKPGFLFKRLLGKGAEKPAEQPELIVYAEPVANGSRIVLLNKDGSAYAG
                310      320      330      340      350      360

                370
m529.pep      KDASALLGKLHSELRX
                |||
a529           KDASALLGKLHSELRX
                370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1525>:

```

g530.seq
1  atgagtgcga ggcgcggcaat gacgggtttg atatgggtca tctgtgtcatc
51 ctgtgtgatg gatattaaag tgtttgtcat gttatgccgt ccgaacgggtt
101 cagacggcat ggctataatt aaagtgtgcc tgaggcttcc agggcggcgc
151 ggacttttgc ctgtccgcct tccgtcagcg gaacgagcgg caggcgcacg
201 tgcggtccgc atccgccccaa ggcggatacc gccatttcg gtgcggcggg
251 actgggttcg cagaacatgg tgtcgtaa at cggaatcagc cggtcgttga

```

This corresponds to the amino acid sequence <SEQ ID 1526; ORF 530.ng>:

```

g530.pep
1  MSASAAMTGL IWVIVSSCVM DIKVFVMLCR PNGSDGMAIF KVVLRSLGRR
51  GLLPVRLPSA ERAAGARAVR IRPRRIPIIS VRRDWVRRTW CRKSESAGR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1527>:

```

m530.seq
1  wTGAGTGCGA GCGCGGCAAT GACGGGtYTG ATATGGGTCA TCGTGTcATC
51  sTGtGTGATG GATATTAAG TGTyTGTtGC GwTATGCCGT CCGAACGGTT
101 CGGACGGCAT GGmTATATTT AAAGTTGTCC TGAGGCTTTC AGGGCGGCGC
151 GGAckTTGC wTGTCGGTTT yCCGTcAGCG GAACGAGCGG CAGGCGGACG
201 TGCGGTTCG ATCTGCCCag GCGGATACC GCCATTTCG GTGCGGCGGG
251 GCTGGGTTCG CAGAACATGG TGTCGTAAAT CGGAATCAGT CGGTcGTtGA

```

This corresponds to the amino acid sequence <SEQ ID 1528; ORF 530>:

```

m530.pep
1  XSASAAMTGL IWVIVSSCVM DIKVXVAXCR PNGSDGMXIF KVVLRSLGRR
51  GLLXVRFPSA ERAAGGRAVR ICPGRIPPIIS VRRGWVRRTW CRKSESvGR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 530 shows 88.8% identity over a 98 aa overlap with a predicted ORF (ORF 530.ng) from *N. gonorrhoeae*:

m530/g530

```

m530.pep      XSASAAMTGLIWVIVSSCVM DIKVXVAXCRPNGSDGMXIFKVVLRSLGRRGLLXVRFPSA
                |||

```


g530	MSASAAMTGLIWIVSSCVMEDIKVFVMLCRPNGSDGMAIFKVVLRLSGRRGLLPVRLPSA	60
	10 20 30 40 50 60	
m530.pep	ERAAGGRAVIRICPGRIPPISVRRGWRRTWCRKSESVGR	99
	: :	
q530	ERAAGARAVRIRPRRIPPISVRRDWRRTWCRKSESAGR	99

```
a530.seq
1  ATGAGTGCGA GCGCGGCAAT GACGGGTTTG ATATGGGTCA TCGTGTCA TC
51  CTGTGTGATG GATATTAAAG TGTTTGTTGC GTTATGCCGT CCGAACGGTT
101 CGGACGGCAT GGCTATATTT AAAGTTGTCC TGAGGCTTTC AGGGCGGCGC
151 GGACTTTTGC CTGTCCGCC TCCGTACGCG GAACGAGCCG CAGGCGGACG
201 TGCGGTTCGC ATCTGCCCC GCGGATACC GCCCATCGG GTGCGGCGGG
251 GCTGGGTTCC CAGAACATGG TGTCGTAAT CCGAATCAGC CGTTCGTTGA
```

a530.pep
1 MSASAAMTGL IWVIVSSCVM DIKVFVALCR PNGSDGMAIF KVVLRLSGRR
51 GLLPVRLPSA ERAAGGRAVR ICPGRIPPIS VRRGWVRRTW CRKSESAGR*

```

      10      20      30      40      50      60
m530.pep  XSASAAMTGLIWVIVSSCVMDIKVXVAXCRPNGSDGMXIFKVVLRLSGRRGLLXVRFP
          |||||
a530      MSASAAMTGLIWVIVSSCVMDIKVFVACRPNGSDGMAIFKVVLRLSGRRGLLPVRLPS
          |||||

      70      80      90     100
m530.pep  ERAAGGRAVRI CPGRIPPISVRRGWVRRTWCRKSESVGRX
          |||||
a530      ERAAGGRAVRI CPGRIPPISVRRGWVRRTWCRKSESAGR
          |||||
      70      80      90     100

```

g531.seq	1	ATGACCGCCC	TACTCGTCAT	CCTCGCCCTC	GCCCTGATAG	CCGTCGGCAC
51	GGCAGGCAGT	GTCTATCCCG	CCCTGCCCGG	CTTGGCATTG	ATGTTTGCCG	
101	GAACATGGCT	GCTTGCCTAT	GCCGGCGGCT	ATCAAACTCA	CGGCGCAGGC	
151	ATCTTGTGGA	CGGTCGGACT	CATCAGCCTT	GGCGGCATAC	TGGCGGACTA	
201	TATGGCAGGC	ATGTTGGGGG	TAAATACAC	TGGGGCAGGC	AAACTCGCCG	
251	TCCGAGGTGC	ATTGGCCGGC	AGCATCATCG	GCATATTTT	CTCCCTTCCC	
301	GGACTAATAC	TCGGCCCCCT	TATCGGCGCG	GCGGCAGGCG	AACTGATCGA	
351	TCGGCGCAAT	ATGCTTCAGG	CAGGTAAGAG	GGGCTTGGGT	ACGCTGTTGG	
401	GGCTTGTCTT	CGGCACGGGC	TTCAAAATCG	GCTGCGCGGT	ATCCATCTTG	
451	TTTATCCTGT	TGGTGAAATA	CATCGCATAC	CTGTTTTAA		

g531.pap

1	<u>MTALLVILAL</u>	<u>ALIAVGTAGI</u>	<u>VYPALPGLAL</u>	<u>MFAGTWLLAY</u>	<u>AGGYQIYGAG</u>
51	<u>ILWTVGLISL</u>	<u>GGILADYMAg</u>	<u>MLGVKYTGAG</u>	<u>KLAVRGALAG</u>	<u>SIIGIFFSLP</u>
101	<u>GLILGPFIGA</u>	<u>AAGELIDRRN</u>	<u>MLQAGKAGLG</u>	<u>TLLGLVVGTA</u>	<u>FKIGCAVSIL</u>
151	<u>FLLVVKYIAY</u>	<u>LF</u>			

```
m531.seq
1  ATGACCGTAC TGACCGTCAT CCTCGCCCTC GCCCTGATAG CCGTCGGCAC
51  GCGGGGCATC GTTTaCCCG CCCTGCCCGG ATTGGCATTG ATGTTTGCCG
101 GAACATGGCT GCTTGCCCTAT GCCGGCGGCT ACCAAATCTA CGGCGCGGGC
151 GTTTGTGGA CGGTCCGACT CATCAGCCTT GCCGGCATA TGCGGAGTA
201 TGTGGCAGC ATATGGGGGA CAAATATAC CGGAGCGGGC AAGCTCGCG
251 TTCGCGCGC ATTGGCCGGC AGCATCATCG GCATATTTT CTCCCTTCCC
301 GGACTAATAC TCGGTCCCTT TATCGGCGCG CGCGGAGCGC AACTGATCGA
```

802

351 ACGGCGCAAT ATGCTTCAGG CAGGTAAAGC GGGCTTGGGT ACGCTGTTGG
 401 GGCTTGTCGT CGGCACGGCG TTCAAAATCG GCTGCGCnGT ATCCATCTTG
 451 TTTATCCTGT TGGTGAAATA CATCGCCTAC CTGTTTTAA

This corresponds to the amino acid sequence <SEQ ID 1534; ORF 531>:

m531.pep

1 MTVLTVILAL ALIAVGTAGI VYPALPGLAL MFAGTWLLAY AGGYQIYGAG
 51 VLWTVGLISL AGILADYVAG IWGKYTGAG KLAVRGALAG SIIGIFFSLP
 101 GLILGPFIGA AAGELIERN MLQAGKAGLG TLLGLVVGTA FKIGCAVSIL
 151 FILLVKYIAY LF*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 531 shows 94.4% identity over a 162 aa overlap with a predicted ORF (ORF 531.ng) from *N. gonorrhoeae*:

m531/g531

	10	20	30	40	50	60
m531.pep	MTVLTVILAL	ALIAVGTAGI	VYPALPGLAL	MFAGTWLLAY	AGGYQIYGAG	VLWTVGLISL
	:	:	:	:	:	:
g531	MTALLVILAL	ALIAVGTAGI	VYPALPGLAL	MFAGTWLLAY	AGGYQIYGAG	ILWTVGLISL
	10	20	30	40	50	60
	70	80	90	100	110	120
m531.pep	AGILADYVAG	IWGKYTGAG	KLAVRGALAG	SIIGIFFSLP	GLILGPFIGA	AAGELIERN
	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :
g531	GGILADYVAG	IWGKYTGAG	KLAVRGALAG	SIIGIFFSLP	GLILGPFIGA	AAGELIDRRN
	70	80	90	100	110	120
	130	140	150	160		
m531.pep	MLQAGKAGLG	TLLGLVVGTA	FKIGCAVSIL	FILLVKYIAY	LF	
	:	:	:	:	:	:
g531	MLQAGKAGLG	TLLGLVVGTA	FKIGCAVSIL	FILLVKYIAY	LF	
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1535>:

a531.seq

1 ATGACCGCCT TGCTCGTCAT CCTCGCCCTC GCCCTGATAG CCGCCGGTAC
 51 GCGGGGCATC GTTACCCCG CCTGCCCCG ATTGGCATTG ATGTTGCGG
 101 GAACCTGGCT GCTCGCCTAC TCCGGCGGCT ACCAAATCTA CGGCGCGGGC
 151 GTTTTGTGGA CGGTCGGACT CATCAGCCTT GCCGGCATA TGGCGGACTA
 201 TGTGGCAGGC ATATGGGGGA CAAAATATAC CGGAGCGGGC AAGCTCGCCG
 251 TTCGCGGCGC ATTGGCCGGC AGCATCATCG GCATATTTT CTCCCTTCCC
 301 GGAATAATAC TCGGTCCCTT TATCGGCGCG GCGGCAGGCG AACTGATCGA
 351 ACGGCGCAAT ATGCTTCAGG CAGGTAAAGC GGGCTTGGGT ACGCTGTTGG
 401 GGCTTATCGT CGGTACGGCG TTCAAAATCG GCTGCGCCGT ATCCATCTTG
 451 TTTATCCTGT TGGTGAAATA CATCGCCTAC CTGTTTTAA

This corresponds to the amino acid sequence <SEQ ID 1536; ORF 531.a>:

a531.pep

1 MTALLVILAL ALIAAGTAGI VYPALPGLAL MFAGTWLLAY SGGYQIYGAG
 51 VLWTVGLISL AGILADYVAG IWGKYTGAG KLAVRGALAG SIIGIFFSLP
 101 GLILGPFIGA AAGELIERN MLQAGKAGLG TLLGLIVGTA FKIGCAVSIL
 151 FILLVKYIAY LF*

m531/a531 96.9% identity in 162 aa overlap

	10	20	30	40	50	60
m531.pep	MTVLTVILAL	ALIAVGTAGI	VYPALPGLAL	MFAGTWLLAY	AGGYQIYGAG	VLWTVGLISL
	:	:	:	:	:	:
a531	MTALLVILAL	ALIAAGTAGI	VYPALPGLAL	MFAGTWLLAY	SGGYQIYGAG	VLWTVGLISL
	10	20	30	40	50	60
	70	80	90	100	110	120
m531.pep	AGILADYVAG	IWGKYTGAG	KLAVRGALAG	SIIGIFFSLP	GLILGPFIGA	AAGELIERN

803

```

          |||||||
a531      AGILADYVAGIWGTYTGTAGKLAVRGALAGSIIGIFFSLPGLILGPFFIGAAAGELIERN
          70      80      90      100      110      120

          130      140      150      160
m531.pep  MLQAGKAGLGTLLGLVVGTAFAKIGCAVSILFILLVKYIAYLFX
          |||||||:|||||
a531      MLQAGKAGLGTLLGLVVGTAFAKIGCAVSILFILLVKYIAYLFX
          130      140      150      160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1537>:

g532.seq (partial)

```

1  atggctgaaa caatgaaaaa acagggcgat tcgcctgatt tgggtgtacgg
51  tttggaagac aggccgccgt tcggtaaatgc gctcttgagc gcggttacct
101 atcttttggc gattttcgtg ccgatgatta cgcccgcgct gattgtgggc
151 ggcgcgctgg aattgccggt ggagatgacg gcgtatctgg tgcgatggc
201 gatggttgcg tcgggtgtcg gcacttattt gcaggccaac cgcttcgggt
251 cggtcggctc ggggatgctg tccatccagc gttaccgtca tgattgcgct
301 cggcgcgggg atgaaagagg gcggtttgag ...

```

This corresponds to the amino acid sequence <SEQ ID 1538; ORF 532.ng>:

g532.pep (partial)

```

1  MAETMKKQAD SPDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSMAMVA SGVGTYLQVN RFGSVGSGML SIQRYRHDC
101 RRGDERGRFE ...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1539>:

m532.seq

```

1  ATGAGCGGTC AGTTGGGCAA AGGTGCGGAT GCGCCTGATT TGGTGTACGG
51  TTTGGAAGAC AGGCCGCCGT TCGGTAATGC GCTCTTGAGC GCGGTTACCC
101 ATCTTTTGGC GATTTTGTG CCGATGATTA CGCCCGCGCT GATTGTGGGC
151 GGC CGCTGG AATTGCCG GTGAGATGAC GCGTATCTCG TGTCGATGGC
201 GATGGTTGCG TCGGGTGTG GCACTTATT GCAGGTCAAC CGCTTCGGGC
251 CGGTGCGTTC GGGGATGCTG TCCATCCAGT CGGTGAATTT TTCGTTCTGT
301 ACCGTGATGA TTGCGCTGGG CGCGGGGATG AAAGAGGGCG GTTTGACTAA
351 GGATGCGATG ATTTGACGCG TCTTGGGCGT ATCGTTTGTG GCGCGTTTTT
401 TGGTGTGTTT CTCGGCGTGG CTTCTGCCGT ATTTGAAAAA AGTGATTACG
451 CCGACGGTCA GCGGCGTGGT CGTGATGCTC ATTGGTTTGA GTTTGGTACA
501 CGTCGGCATT ACCGATTTCG GCGGCGGCTT CGGCGCGAAG GCGGACGGCA
551 CGTTGCGGCTC GATGGAAGAA TTGGGGCTGG CATCGCTGGT GTTGCTGATT
601 GTGTTGGTGT TCAACTGCAT GAAAAACCG CTGTTGCGCA TGAGCGGCAT
651 TGCGGTGCGG CTGATTGCCG GCTATATCGT CGCGCTGTTT TTGGGCAAGG
701 TGGATTTTTC CGCGCTGCAA AACCTGCCGC TGGTTACGCT GCCCGTACCG
751 TTAAATACG GTTTTGCTTT CACTGTCAC GCGTTTATTG TGGCGGGCGC
801 GATTTTCTTG TTGAGCGTGT TTGAGCGGCT CGGCGATTTA ACCGCGACGG
851 CAATGGTGTG CGACCAGCCG ATTGAAGGCG AGGAATACAC CAAACGCCTG
901 CGCGGCGGCG GTTGGCTGA CGGCTTGGTG TCGGTGATTG CGACGGCTTT
951 GGGTTCGCTG CCGCTGACGA CGTTTGC GCA AAACAACGCG GTGATTGAGA
1001 TGACCGGCGT GGCTTCGCGC CATGTGGGCA AATATATTGC CGTGATTTTG
1051 GTGCTGTTGG GTCTGTTCCC CGTTGTCGGT CGCGCGTTTA CGACGATTCC
1101 GAGTCCGGTG TTGGGCGGCG CGATGGTTT GATGTTTCGCG TTAATTGCGA
1151 TTGCGGGCGT GCGGATTTTG GTCAGTCACG GCATCCGCG GCGCGAAGCG
1201 GTGATTGCGG CAACGTCGGT CGGTTTGGGC TTGGGTGTCG CGTTTGAGCC
1251 GGAAGTGTG AAAAACCTGC CCGTCTTGT CCAAACCTCT ATTTCCGCCG
1301 GCGGCATTAC GGCAGTCTTG CTGAATTTG TCTTGCCCGA AGATAAAACC
1351 GAGGCGGCGG TCAAGTTTGA TACCGACCAC TTGGAACACT GA

```

This corresponds to the amino acid sequence <SEQ ID 1540; ORF 532>:

m532.pep

```

1  MSGQLGKGAD APDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSMAMVA SGVGTYLQVN RFGPVGSGML SIQSVNFSFV
101 TVMIALGAGM KEGGLTKDAM ISTLLGVSVF GAFLVCFSAW LLPYLKKVIT
151 PTVSGVVVML IGLSLVHVGI TDFGGGFGAK ADGTFGSMEN LGLASLVLLI

```

Homology with a predicted ORF from *N. gonorrhoeae*

g532/m532

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1541>:

This corresponds to the amino acid sequence <SEQ ID 1542; ORF 532.a>:

a532.pap

1	MSGQLGKGAD	APDLVYGLED	RPPFGNALLS	AVTHLLAIFV	PMITPALIVG
51	GALELPVEMT	AYLVSMAMVA	SGVGTYLQVN	RFGPVGSGML	SIQSVNFSFV

805

```

101 TVMIALGAGM KEGGLTKDAM ISTLLGVSFV GAFLVCFSAW LLPYLKKVIT
151 PTVSGVVVML IGLSLVHVGI TDFGGGFGAK ADGTFGSMEN LGLASLVLLI
201 VLVFNCMKNP LLRMSGIAVG LIAGYIVALF LGKVDFSALQ NLPLVTLPPV
251 FKYGFAFDWH AFIVAGAIFL LSVFEAVGDL TATAMVSDQP IEGEEYTKRL
301 RGGVLADGLV SVIATALGSL PLTTFAQNNG VIQMTGVASR HVGKYIAVIL
351 VLLGLFPVVG RAFTTIPSPV LGGAMVLMFG LIAIAGVRIL VSHGIRRREA
401 VIAATSVGLG LGVAFEPEVF KNLPVLFQNS ISAGGITAVL LNLVLPEDKT
451 EAAVKFDTDH LEH*

```

m532/a532 100.0% identity in 463 aa overlap

m532.pep	10	20	30	40	50	60
	MSGQLGKGADAPDLVYGLEDPRPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT					
a532	MSGQLGKGADAPDLVYGLEDPRPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT					
	10	20	30	40	50	60
m532.pep	70	80	90	100	110	120
	AYLVSMAMVASGVGTYLQVNRFGPVGSGMLSIQSVNFSFVTVMIALGAGMKEGGLTKDAM					
a532	AYLVSMAMVASGVGTYLQVNRFGPVGSGMLSIQSVNFSFVTVMIALGAGMKEGGLTKDAM					
	70	80	90	100	110	120
m532.pep	130	140	150	160	170	180
	ISTLLGVSFVGAFLVCFSAWLLPYLKKVITPTVSGVVVMLIGLSLVHVGITDFGGGFGAK					
a532	ISTLLGVSFVGAFLVCFSAWLLPYLKKVITPTVSGVVVMLIGLSLVHVGITDFGGGFGAK					
	130	140	150	160	170	180
m532.pep	190	200	210	220	230	240
	ADGTFGSMENLGLASLVLLIVLVFNCMKNPLLRRMSGIAVGLIAGYIVALFLGKVDFSALQ					
a532	ADGTFGSMENLGLASLVLLIVLVFNCMKNPLLRRMSGIAVGLIAGYIVALFLGKVDFSALQ					
	190	200	210	220	230	240
m532.pep	250	260	270	280	290	300
	NLPLVTLPPVPFKYGFAFDWHAFIVAGAIFLLSVFEAVGDLTATAMVSDQPIEGEEYTKRL					
a532	NLPLVTLPPVPFKYGFAFDWHAFIVAGAIFLLSVFEAVGDLTATAMVSDQPIEGEEYTKRL					
	250	260	270	280	290	300
m532.pep	310	320	330	340	350	360
	RGGVLADGLSVIATALGSLPLTTFAQNNGVIQMTGVASRHHVGKYIAVILVLLGLFPVVG					
a532	RGGVLADGLSVIATALGSLPLTTFAQNNGVIQMTGVASRHHVGKYIAVILVLLGLFPVVG					
	310	320	330	340	350	360
m532.pep	370	380	390	400	410	420
	RAFTTIPSPVLGGAMVLMFGLIAIAGVRILVSHGIRRREAVIAATSVGLGLGVAFEPEVF					
a532	RAFTTIPSPVLGGAMVLMFGLIAIAGVRILVSHGIRRREAVIAATSVGLGLGVAFEPEVF					
	370	380	390	400	410	420
m532.pep	430	440	450	460		
	KNLPVLFQNSISAGGITAVLLNLVLPEDKTEAAVKFDTDHLEHX					
a532	KNLPVLFQNSISAGGITAVLLNLVLPEDKTEAAVKFDTDHLEHX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1543>:

```

g535.seq
1  atgccctttc ccgttttcag acaantatth gcttngtcct tgctacgggt
51  ttttgccgta ggtcggattc tcgaatccga catttccaac agcgggtttt
101 cggaaacgat aaacgcgtca aatgtttttt ttgtcggata cgaatatccg
151 gcctgcattt caaatttaca tcgcttccaa ttctgcaaac ttggtatcca
201 gttctttcac gccctgtttg ccgaagttag ttggtcagtcg ggcggattcg
251 cctttgtctg cggcatcgat aatcacgccg gtgccgaatt tggcgtgacg
301 gacgttttgt ccgatgcgga agcctgcgta ggtttgcggc tgtttgaagt

```

806

```

351 catcgatgat tttgtcccg tgtacgggtg tttggcgcggt gttgccgtag
401 ctgtcgaagg cgggtttttt gacggacagg tagtgcaata cttctggcgg
451 gatttcttcg acgaagcggg atgcgatgcc gaattgggtt tgtccgtgca
501 gcatgcgctg ctgtgccatg gtgatgtaga ggcgtttgcg ggcgcgggtg
551 atggcgacgt acatgaggcg gcgttcttct tcgaggccgc cgcgctcggc
601 aaggctcatt tcgctgggga aacgccctc ttccataaccg gtgaggaaga
651 cggcgttgaa ttccaagcct ttggcgcggt ggacggtcat cagttggacg
701 gctttttcgc ctgccctgc ttggttttcg ccggattcga gggcgcggtt
751 gctcaagaag gcgaggatgg ggaaggcggg atcgtctga

```

This corresponds to the amino acid sequence <SEQ ID 1544; ORF 535.ng>:

g535.pep

```

1 MPFPVFRQXF AXSLLRFFAV GRILESDISN SGFSETINAS NVFFVGYEYP
51 ACISNLHRFQ FRKLGIQFFH ALFAEVDGQS GGFAFVCGID NHAGAEFGVT
101 DVLSDAEACV GLRLFVEIDD FVPLYGGLAR VAVAVEGGFF DGQVVQYFWR
151 DFFDEAGCDA ELGLSVQHAL LCHGDVEAFA GAGDGDVHEA AFFFEAAALG
201 KAHFAGETPL FHTGEEDGVE FQAFGGVDGH QLDGFFACPC LVFAGFEGGV
251 AQEGEDGEGG IV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1545>:

m535.seq

```

1 aTGCCCTTtC CCGTTTTCAG ACGGCCTTTT GCTTTGTCCT TACTtACGTT
51 TTTTGCCGTA AGTCAGATTC TTGTATCCGA CATTCCAAC AGCGGTGTTT
101 CGGAAACAAT AGACGCGTCA AATGTTTTTG TCGGATACGA ATATCCGACC
151 TACATTTCAA ATTTACATCT CTCCAATTT CGCAAATTTG GTGTCCAAC
201 CTTTCACGCC CTGTTTGCCG AAATTGATGG TCAGTCGGGC GGATTGCGCT
251 TTATCTGCGG CATCGATAAT CACGCCGGTG CCGAATTTGG CGTGGCGGAC
301 GTTTTGTCCG ATACGGAAAC CTGCGTAGGT TTGGGGCTGT TTGTAGTCGT
351 CGATGATTTT ATCTTTGGAT GCGGCGGTTT GGCGCGTGTT GCCGTAAC
401 TCGTAGGCAG GCTTTTTGAC GGACAGGTAG TGCAATACTT CGGGTGGGAT
451 CTCTTCGACG AAGCGGGAGA CGATGCCGAA TTGGGTTTGT CCGTGCAGCA
501 TGC GTTGTGTTG CGCCATGGTG ATGTAGAGGC GTTTCGGGC GCGGGTGATG
551 GCGACGTACA TGAGGCGGCG TTCTTCTTCG AGGCCGCCGC GTTCGGCAAG
601 GCTCATTTTC CTGGGAAGC GGCCTTCTTC CATGCCGGTG AGGAAGACGG
651 CGTTAAATTC CAAGCCTTTG GCGGCGTGGA CGGTCATGAG TTGGACGGCC
701 TTTTCGCCTG CGCCTGCCTG GTTTTCACCG GATTCGAGGG CGGCATTGCT
751 TAGGAAGGCG AGAATGGGGA AGGCGGGGTC GTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1546; ORF 535>:

m535.pep

```

1 MPFPVFRFRPF ALSLLTFFAV SQILVSDISN SGVSETIDAS NVFVGYEYPT
51 YISNLHLFQF RKLGVQLFHA LFAEIDGQSG GFAFICGIDN HAGAEGFVAD
101 VLSDTETCVG LGLFVVVDDF IFGCGGLARV AVTVVGRFLD GQVVQYFGWD
151 LFDEAGDDAE LGLSVQHALL RHGDVEAFAG AGDGDVHEAA FFFEAAAFGK
201 AHFAGEAAFF HAGEEDGVKF QAFGGVDGHE LDGLFACACL VFTGFEGGIA
251 XEGENGEGBV V*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 535 shows 80.9% identity over a 262 aa overlap with a predicted ORF (ORF 535.ng) from *N. gonorrhoeae*:

m535/g535

```

          10      20      30      40      50      59
m535.pep  MPFPVFRFRPFALSLLTFFAVSQILVSDISNSGVSETIDASNVF-VGYEYPTYISNLHLFQ
          |||||: || || ||||: || ||||| |||||: ||||| ||
g535      MPFPVFRQXFAXSLLRFFAVGRILESDISNSGFSETINASNVFFVGYEYPACISNLHRFQ
          10      20      30      40      50      60

          60      70      80      90      100     110     119
m535.pep  FRKLGVLQFHALFAEIDGQSGGFAFICGIDNHAGAEFGVADVLSDTETCVGLGLFVVVDD
          ||||: ||||| |||||: ||||| |||||: ||||| ||||| ||||| ||||| ||
g535      FRKLGIQFFHALFAEVDGQSGGFAFVCGIDNHAGAEFGVTDVLSDAEACVGLRLFVEIDD
          70      80      90      100     110     120

```

	120	130	140	150	160	170	179
m535.pep	FIFGCGGLARVAVTVVGRFLFDGQVVQYFGWDLFDEAGDDAELGLSVQHALLRHGDVEAFA						
	: : : :						
g535	FVPLYGGLARVAVAVEGGFFDGQVVQYFWRDFFDEAGCDAELGLSVQHALLCHGDVEAFA						
	130	140	150	160	170	180	
	180	190	200	210	220	230	239
m535.pep	GAGDGDVHEAAFFFEAAAFGKAHFAGEAAFFHAGEEDGVKFQAFGGVDGHELDGLFACAC						
	: : : : : :						
g535	GAGDGDVHEAAFFFEAAALGKAHFAGETPLFHTGEEDGVEFQAFGGVDGHQLDGGFFACPC						
	190	200	210	220	230	240	
	240	250	260				
m535.pep	LVFTGFEGGIIAXEGENGEGGVV						
	: : : :						
g535	LVFAGFEGGVAQEGEDGEGGIV						
	250	260					

```

a535.seq (partial)
1   TTCAGACGGC CTTTTGCCTT GTCTTGCTA CAGTTTTTTG CCATAGGTCG
51  GATTCTCGAA TCCGACATTT CCAACACGGC TTTTTCGGAA ACGTAAAGCG
101 CGTCAAATAT TTTTGTCCGA TACGAGTATC CAGCCTGCAT ACATAGATTTA
151 CATCGCTTCC AATTTCCGCA ACTTGGTGTC CAACTCTTTC ACGCCCTGTT
201 TGCCGAAATT GATGGTCAGT CGGGCGGATT CGCCTTTATC TGCGGCATCG
251 ATAATCACGC CGGTGCCCAA GTTGGCGTGG CGGACGTTTT GTCCGATACG
301 GAAACCTGCG TAGGTTTGGG GCTGTTTGTG TCGTCGATAG ATTTTGTCTT
351 TGGGCGCGGC GAGTTTGGCG GTGTTGCCAT AGCGGTCGTA GGGGGGTTTT
401 TTGACGGACA GGTAGTGCAA TACTTCGGGC GGGATTTCCT CGACGAAGCG
451 GGAGACGATG CCGAATTGGG TTTGTCCGTG CAGCATGCGT TGTTGCGCCA
501 TGGTGATGTA GAGGCGTTTG CGGGCGCGGG TGAATGGCGAC GTACATCAGG
551 CGGCGTTCTT CTTCCGAGCC CCGCGCTTCG GCAAGGCTCA TTTCTGCTGG
601 GAAGCGGCCT TCTTCCATGC CGGTGAGGAA TACGGCGTTA AATTCCAAGC
651 CTTTGGCGGC GTGCGAGCTC ATGAGTTGTA CGGCTTTTTT GCCCGCGCCT
701 GCTTGGTTTT GCCTGGATTC GAGAGCAGCA TTGCTTAGGA AAGCGAGGAT
751 GGGGAAGGCG GGGTCGTCG A

```

```
a535.pep      (partial)
  1  FRRPFALSLL QFFAIGRILE SDISNSGFSE TIDASNIFVG YEYPACISNL
  51  HRFQFRKLGV QLFHALFAEI DGQSGGFAFI CGIDNHAGAE FGVADVLSDT
101  ETCVGLGLFV VDDDFVFGRG GLARVAIAVV GGFDFGQVVQ YFGRDFFDEA
151  GDDAELGLSV QHALLRHGDV EAFAGAGDGD VHQAFFFEEA AAFGKAHFAG
201  EAAFFVHAGEE YGVKQFAFGG VHGHELYGFF ARACLVFAGF ESSIA*ESED
251  GEGGVV*
```

	10	20	30	40	50	60
m535.pep	MPFPVFRFPFALSLLTFFAVSQILVSDISNSGVSETIDASN VFVG YEYP TYISNLHLFQF					
	: : : : : : : : : : : : : : : :					
a535	FRRPFALSLLQFFAIGRILES DISNSGFSETIDASN IFVG YEYPACISNLHRFQF					
	10	20	30	40	50	
	70	80	90	100	110	120
m535.pep	RKLGVQLFHALFAEIDGQSGGF AFICGIDNHAGAEFGVADVLSDTETCVGLGLFVVVDDF					
	: : : : : : : : : : : : : : : :					
a535	RKLGVQLFHALFAEIDGQSGGF AFICGIDNHAGAEFGVADVLSDTETCVGLGLFVVVDDF					
	60	70	80	90	100	110
	130	140	150	160	170	180
m535.pep	IFGCGGLARVA VTVVGR LFDGQVVQYFGWDLFDEAGDDAELGLSVQHALLRHGDVEAFAG					
	: : : : : : : : : : : : : : : :					
a535	VFGRGGLARVA IAVVGGFFDGQVVQYFGRDFFDEAGDDAELGLSVQHALLRHGDVEAFAG					
	120	130	140	150	160	170

808

	190	200	210	220	230	240
m535.pep	AGDGDVHEAAFFFEAAAFGKAHFAGEAAFFHAGEEDGVKQAFGGVDGHELDGLFACACL					
a535	AGDGDVHQAAFFFEAAAFGKAHFAGEAAFFHAGEEYGVKQAFGGVHGHELYGFFARACL					
	180	190	200	210	220	230
	250	260				
m535.pep	VFTGFEGGIXEGENEGGVVX					
a535	VFAGFESSIAXESEDGEGGVVX					
	240	250				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1549>:

g537.seq

```

1  atgaaatccc tttttatttg gctgcttcta ttgggctcgg cggcaggcgt
51  tttctaccat acccaaaacc aatccctgcc cgcgggcgaa cttgtctatc
101 cgtccgcacc gcaaatcagg gacggcgggc atgcgctgca ctacctcaac
151 cgcacccgca cacaaatcgg ttgacgcgct ctggcacacg cgccggtttt
201 ggaaaattcc gcccgcaggc acgcacgcta tctcacgctc aatcccgaag
251 acggacacgg cgaacacccat cccgacaatc cgcactacac cgacacaaag
301 ctgaccgaac gcacacgcct tgccgggtat ctctacaacg gcgtgcatga
351 aaacatcagc acggaagagg aagccgccga atcgtccgac agcgacatcc
401 gcacgcagca acgccaagtg gacgctttga tgagcgcaat ctaccaccgc
451 ctttcgctgc ttgaccgcca taccgacgaa gcaggtgcgg catttgtgctg
501 cgaaaacggc aaaaccgtcc tcgtattcaa tcagggcaac ggcagcttcg
551 agcgcgcctg tgcaaaagga aggcggcagc cggaagcagg acggaatat
601 taccgcaacg cttgccacaa cgggtgcggc gtttatgctg acgaagccat
651 gcccgtaacg gaattgcttt ataccgccta tccggttggc ggcggcgctc
701 tgccttattt ttacggggaa cgtcccgacc cgtgcccga atatgaaatc
751 acaggcaatc ctgccagcat tgatttttcc gaggcggcag gcaaaattgc
801 gatgaaaagt ttcaagctgt atcagggtaa aaacgaaatc cgccccgtca
851 ggggtttaac cgccggcaac gaccctaacg gcaggctgac cgcgcaccaa
901 ttccgccttt tcccgtcaa acctttggaa tacggcacgc tttatacggc
951 ggtattcgac tatgtccgca acggacggca cgcgcaggcg aaatggcagt
1001 ttagaaccgg aaaaccgat tacccttatt ttgaggtaaa cggcggcgag
1051 acacttgctg ttagaaaagg cgaaaaatat ttcattccact ggcgcggacg
1101 ctggtgtctg gaagcgtgta cccgttatac ctaccggcgg cagttcggca
1151 acagcctgtc catactccgg caggaagcgg gcggcattgt cttcagcgctc
1201 agcgggaatg cggaagccg catcaggctt actccggaag acagcccgga
1251 acgcggtgta accctttatt tcaggattg a

```

This corresponds to the amino acid sequence <SEQ ID 1550; ORF 537.ng>:

g537.pep

```

1  MKSLFIWLLL LGSAGVFIYH TQNQSLPAGE LVYPSAPQIR DGGDALHYLN
51  RIRTQIGLHA LAHAPVLENS ARRHARYLTL NPEDGHGEHH PDNPHYTAQK
101 LTERTRLAGY LYNVHENIS TEEEAESSD SDIRTQQRQV DALMSAIYHR
151 LSLDDRHTDE AGAAFVRENG KTVLVFNQGN GSFERACAKG RROPEAGRKY
201 YRNACHNGAA VYADEAMPVT ELLYTAYPVG GGALPYFYGE RPDPVPEYEI
251 TGNPASIDFS EAAGKIAMKS FKLYQGKNEI RPVRVLTAGN DPNGRILTAHQ
301 FALFPLKPLE YGTLYTAVFD YVRNGRHAQA KWQFRTRKPD YPYFEVNGGE
351 TLAVRKGEKY FIHWRGRWCL EACTRYTYRR QFGNSLSILR HEAGGIVFSV
401 SGMAGSRIRL TPEDSPERGV TLYLQD *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1551>:

m537.seq (partial)

```

1  ATGAAATCCC TTTTATTTCG GCTGCTCCTG TTGGGTTCGG CGGCAGGCGT
51  TTTCTACCAT ACCCAAACC AATCCCTGCC CGCGGGCGAA CTTGTCTATC
101 CGTCCGCACC GCAAATCAGG GACGGCGGCG ATGCGCTGCA CTACCTCAAC
151 CGCATCCGAG CCCAAATCGG TTTGCACAAG CTGGCACACG CGCCGTTTTT
201 GGAAACTCC GCCCGCAGGC ACGCAAGCTA CCTCAGCTC AATCCCGAAG
251 ACGGACACGG CGAACACCAT CCCGACAATC CGCACTACAC CGCACAAAAG

```


809

301 CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA
 351 AAACATCAGC ACGGAAGAAG AAGCCGCCGA ATCGTCCGAC AGCGACATCC
 401 GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC
 451 CTTTCCTAC TTGACCGCCA TACGGATGAG TCAGGAGCGG CATT...

This corresponds to the amino acid sequence <SEQ ID 1552; ORF 537>:

m537.pep (partial)
 1 MKSLFIRLLL LGSAAGVFYH TQXQSLPAGE LVYPSAPQIR DGGDALHYLN
 51 RIRAQIGLHK LAHAPVLENS ARRHASYLTL NPEDGHGEHH PDNPHYTAQK
 101 LTERTRLAGY LYNGVHENIS TEEEAESSD SDIRTQQRQV DGLMSAIYHR
 151 LSLDRHTDE SGAA...

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 537 shows 95.7% identity over a 164 aa overlap with a predicted ORF (ORF 537.ng) from *N. gonorrhoeae*:

m537/g537

m537.pep	10	20	30	40	50	60
	MKSLFIRLLL LGSAAGVFYHTQXQSLPAGELVYPSAPQIRDGGDALHYLN RIRAQIGLHK					
g537	MKSLFIWLLL LGSAAGVFYHTQXQSLPAGELVYPSAPQIRDGGDALHYLN RIRITQIGLHA					
	10	20	30	40	50	60
m537.pep	70	80	90	100	110	120
	LAHAPVLENSARRHASYLTLNPEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNGVHENIS					
g537	LAHAPVLENSARRHARYLTLNPEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNGVHENIS					
	70	80	90	100	110	120
m537.pep	130	140	150	160		
	TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLDRHTDESGAA					
g537	TEEEAESSDSDIRTQQRQVDALMSAIYHRLSLDRHTDEAGAAVRENGKTVLVFNQGN					
	130	140	150	160	170	180
g537	GSFERACAKGRRQPEAGRKYRNACHNGAAVYADEAMPVTELLYTAYPVGGGALPYFYGE					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1553>:

a537.seq
 1 ATGAAATCCC TTTTATTTCG GCTGCTCCTG TTGGGTTCGG CGGCCGGCGT
 51 TTTCTATCAT ACCCAAAC AATCCCTGCC CGCGGGCGAA CTTGTCTATC
 101 CGTCCGCACC GCAAATCAGG GACGGCGGCG ATGCGCTGCA CTACCTCAAC
 151 CGCATCCGCG CCCAAATCGG TTTGCACAAG CTGGCACACG CGCCGGTTTT
 201 GGAAAATTCC GCCCGCAGGC ACGCACGCTA TCTCACGCTC AATCCCGAAG
 251 ACGGACACGG CGAACACCAT CCCGACAATC CGCACTACAC CGCACAAAAG
 301 CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA
 351 AAACATCAGC ACGGAAGAGG AAGCCGCCGA ATCGTCCGAC AGCGACATCC
 401 GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC
 451 CTTTCCTAC TTGACCGCCA TACGGATGAG GCAGGAGCGG CATTGTGCG
 501 CGAAAACGGT AAAACCGTTC TCGTATTCAA TCAGGCAAC GGCAGGTTTG
 551 AGCGGCATTG CGCCCAAGGC AGAAATCAGC CGGAAGCAGG ACGGAAATAT
 601 TACCGCAACG CCTGCCATAA CGGTGCGGTC GTGTACACG ACGAAGCCAT
 651 GCCCGCACAG GAGCTGCTCT ATACAGCCTA TCCCGTCGGC AACGGCGCAC
 701 TGCCCTATTT CCACGGCGAG CGTCCAGACC CCGTGCCGGA ATATGAAATC
 751 ACGGGCAATC CTGCCAGCAT TGATTTTCC GAGGCGCGAG GCAAATATAC
 801 GATGAAAAGT TTCAAGCTGT ATCAGGGTAA AAACGAAATC CGCCCCGTCA
 851 GGGTTTAAAC CGCCGGCAAC GACCCCAACG GCAGGCTGAC CGGTACCAA
 901 TTCGCGCTTT TCCCGCTCAA GCCTTTGGAA TACGGTACGC TTTATACGGC
 951 GGTATTCGAC TATGTCCGCA ACGGACGGCG CGCGCAGGCG AAATGGCAGT
 1001 TTAGAACCGG AAAACCGGAT TACCTTATT TTGAGGTAAA CGGCGCGCAG
 1051 ACACTTGCGG TTAGAAAAGG CGAAAAATAT TTCATCCACT GGC GCGGACG
 1101 CTGGTGTTTG GAAGCGTGT CCCGTATAC CTACCGGCAG CGACCCGGCA

810

1151 GCCGCCTGTC CATAGGAAGG CACAAGGCGG GCGGCATCGT CTTACAGCGTT
 1201 GACGGAATGG CGGGCAGCCG CATCACGCTT GCACCGGAAG GAGAAACGGA
 1251 ACGAGGCGTA ACCCTTTATT TACAGGATTG A

This corresponds to the amino acid sequence <SEQ ID 1554; ORF 537.a>:

a537.pep
 1 MKSLFIRLLLL LGSAAGVFYH TQNQSLPAGE LVYPSAPQIR DGGDALHYLN
 51 RIRAQIGLHK LAHAPVLENS ARRHARYLTL NPEDGHGEHH PDNPHYTAQK
 101 LTERTRLAGY LYNGVHENIS TEEEAESSD SDIRTQQRQV DGLMSAIYHR
 151 LSLDDRHTDE AGAAFVRENG KTVLVFNQGN GRFERHCAQG RNQPEAGRKY
 201 YRNACHNGAV VYTDEAMPAQ ELLYTAYPVG NGALPYFHGE RPDVPEYEI
 251 TGNPASIDFS EAAGKITMKS FKLYQGKNEI RFPVRVLTAGN DPNGRLTAYQ
 301 FALFPLKPLE YGTLYTAVFD YVRNGRRAQA KWQFRTRKPD YPYFEVNGGE
 351 TLAVRKGEKY FIHWRGRWCL EACTRYTYRQ RPSRLSISGR HKAGGIVFSV
 401 DGMAGSRITL APEGETERGV TLYLQD*

m537/a537 98.2% identity in 164 aa overlap

	10	20	30	40	50	60
m537.pep	MKSLFIRLLLLGSAAGVFYHTQXQSLPAGELVYPSAPQIRDGGDALHYLN					
a537	MKSLFIRLLLLGSAAGVFYHTQXQSLPAGELVYPSAPQIRDGGDALHYLN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m537.pep	LAHAPVLENSARRHASLYTLNPEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNGVHENIS					
a537	LAHAPVLENSARRHARYLTLNPEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNGVHENIS					
	70	80	90	100	110	120
	130	140	150	160		
m537.pep	TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLDDRHTDESGAA					
a537	TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLDDRHTDEAGAAFVRENGKTVLVFNQGN					
	130	140	150	160	170	180
	190	200	210	220	230	240
a537	GRFERHCAQGRNQPEAGRKYRNACHNGAVVYTDEAMPAQELLYTAYPVGNGALPYFHGE					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1555>:

g538.seq
 1 atgtcaggta gaacaggacg gaacagtgcc actcaggcgc aaccggaacg
 51 cgtcatgctg gtgggcgtaa tgttgataa agatgatac ggcagcaatg
 101 ccgccgtct gaacggtttt cagacggcat tggcggagc cgtcagagctg
 151 gtcaaagcgg cgggcggcga ttccgtacgc gtggagactg ccaaacgcga
 201 ccgccgcac actgcgctgt ttgtcggcac gggcaaggcg gcggagctgt
 251 cggaagcagt tgccgcagac ggcattgatt tggctgtatt caaccacgaa
 301 cttactcca cgcaggaacg caatttgaa aaaatcctcc aatgccgcgt
 351 attggacaga gtggggctga ttctggcgat ttctgccgc cgcgccgca
 401 cgcaggaagg caggctgcaa gtcgagttgg cgcaattgag ccatttgcg
 451 ggacgcttga tacgcggtta cggacatttg caaagccagc gcggcggtat
 501 cggcatgaaa gggccgggag aaaccaaact ggaaaccgac cgccgattaa
 551 ccgccatcg gatcaacgcc ttgaaaaaac agcttgccaa cctcaaaaaa
 601 cagcgcgccc tgcgcgcaa gtcccgagag tcgggcagaa tcaaaacggt
 651 tgcgctggtc ggctatacca atgtcggcaa atccagcctg ttcaaccggc
 701 tgaccaagtc gggcatatat gcgaaagacc agcttttcgc cactctcgac
 751 acgacggcgc ggcggctgta catcagtcgc gcatgcagca ttatcctgac
 801 cgataccgct ggattcgtca gcatctgcc gcacaaactg atttccgcct
 851 tttccggcac cttggaagaa accgtgcaag ccgatgtgct gctgcacgct
 901 gtcgatgctg ccgccgggaa cagcgggag cagattgaag acgtggaaaa
 951 cgtactgcaa gaaatccatg cccacgatat tccgtgcatc aagggtgtaca
 1001 acaaaaccga cctgctgccg tctgaagaac aaaacacggg catatggcgc
 1051 gacgctgcgg gaaaaattgc cgccgtccgc atttccgttg ctgaaaatac

g538.pep

1	<u>MSGRTGRNSA</u>	<u>TQAQPERVML</u>	<u>VGVMLDKDDT</u>	<u>GSNAARLNGF</u>	<u>QTALAEAVEL</u>
51	VKAAGGDSVR	VETAKRDRPH	TALFVGTKA	AELSEAaad	GIDLvVFNHE
101	LTPTQERNLE	<u>KILQCRVLDL</u>	<u>VGLILAIFAR</u>	RARTQEGRLQ	VELAQLSHLA
151	GRLIRGYGHL	<u>QSQRGGIGMK</u>	<u>GPGETKLETD</u>	RRLTAHRINA	LKKQLANLKK
201	QRALRRKSRE	SGRIKTFALV	GYTNVGKSSL	FNRLTKSGIY	AKDQLFATLD
251	TTARRLYISP	ACSIILTDTV	GFVSDLPHLK	ISAFSATLEE	TVQADVLLHV
301	VDAAARNSGQ	QIEDVENVLQ	EIHADIPCI	KVYNKTDLLP	SEeqNTGIWR
351	DAAGKIAAVR	ISVAENTGID	ALREAIAYEC	AAAPNTDETE	MP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1557>:

```
m538.seq
1 ATGACAGGCA GAACAGGCGG CAACGGCAGT ACCCAAGCGC AACC CGAACG
51 CGTCATGCTG GTGGGCGTAA TGTTGGACAA AGATGGTACG GG CAGTAGTG
101 CCGCCCGTCT GAACGGT TTT CAGACGGCAT TGGCGGAAGC TGTCGAGCTG
151 GTCAAAGCGG CGGGCGGCGA TTCCTGCGCG GTGGAGACTG CCAAACGCGA
201 CCGTCCGCAC ACCGCGCTGT TTGT CGGCAC GGGCAAGGCG GCGGAGCTGT
251 CAGAAGCAGT TGCCGCAGAC GGCATCGATT TGGTCGTATT CAACCACGAA
301 CTCACGCCCA CGCAGGAACG CAACCTTGAA AAAGAACTsa AATGCCGCGT
351 ATTGGACAGG GTAGGGCTGA TTCTGGCGAT TTTCTGCTCGC CGCGCCCGCA
401 CGCAGGAAGG CAGGCTGCAA GTCGAGTTTG CGCAATTGAG CCATTTGGCG
451 GGACGCTTGA TACGCGTTA GCGCCATTCG CAGAGCTGAG CGCGCGGTAT
501 CGGCATGAAA GCGCCCGCGG AAACCAAAC TGGAAACCGAC CGCCGATTGA
551 TCGCCCATCG GATCAATGCC TTGATAAAAC AGCTTGCCAA CCTCAAAAAA
601 CAGCGCGCCC TCGCGCGCAA GTChCGCGAA TCGGGCACAA TCAAACGTT
651 TGCGCTGGTC GGCTATACAA ATGTCGGA AA ATCCAGCCTG TCAACCGGC
701 TGACAAAGTC GGGCATATAT GCAAAGGACA AGCTTAGTCC CGAATGCAGC
751 ATTATCTGA CCGATACCGT CGGATTCTG Tn AGCGATCTGC CGCAcAAACT
801 GATTTCGCC TTTTCgCC . A CGCTGGAAGA AACCGCGCAA GCGGATGTGC
851 TGCTGCACGT CGTCGATGCC GCCGCTCCGA ACAGCGGACA GCAGATTGAA
901 GACGTGGAAA ACGTACTGCA AGAAATCCAT GCCGGCGATA TTCCGTGCAT
951 cAAGGTGTAC AACAAAACCG ACCTGCTGCC GTCTGAAGAA CAAAACACGG
1001 GCATATAGCG CGACGCTGCG GGAAAAATTG CCGCGCTGCC CATTTCCGTT
1051 GCTGAAAATA CCGGTATAGA CGCAATGCGC GAAGCcATTG CCGAGTCTTG
1101 TGCCGCGCGCA CCAAACACAG ACAGAAACCGA AATGCCATGA
```

This corresponds to the amino acid sequence <SEQ ID 1558; ORF 538>:

```
m538.pap
1  MTGRTGGNGS  TQAQPERVML  VGVMLDKDGT  GSSAARLNGF  QTALAEAVEL
51  VKAAGGDSVR  VETAKRDRPH  TALFVGTGKA  AELSEAVAAD  GIDLVVFNHE
101 LTPTOERNLE  KELKCRVLDR  VGLILAIFAR  RARTQEGRLQ  VELAQLSHLA
151 GRLIRGYGHL  QSQRGGIGMK  GPGETKLETD  RRLIAHRINA  LIKQLANLKK
201 QRALRRKSRE  SGTIKTFALV  GYTNVGKSSL  FNRLTKSGIY  AKDKLSPECS
251 IILTDTVGfV  SDLPHKLISA  FSXTLEETAQ  ADVLLHVUDA  AAPNSGQOIE
301 DVENVLQEIH  AGDIPCIKVY  NKTDLLPSEE  QNTGIWRDAA  GKIAAVRISV
351 AENTGIDALR  EAIAESCAAA  PNTDETEMP*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 538 shows 92.1% identity over a 392 aa overlap with a predicted ORF (ORF 538.ng) from *N. gonorrhoeae*:

m538/g538

	10	20	30	40	50	60
m538.pep	MTGRTGGNGSTQAQPERVMLVGVMLDKDGTGSSAARLNGFOTALAEAVELVKAAGDSVR					
	:	:	:	:	:	:
g538	MSGRTGRNSATQAQPERVMLVGVMLDKDDTGSNAARLNGFOTALAEAVELVKAAGDSVR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m538.pep	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDLNVFNHFLTPTQERNLEKELKCRVLDR					
g538	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDLNVFNHFLTPTQERNLEKILQCRVLDR					

812

	70	80	90	100	110	120
	130	140	150	160	170	180
m538.pep	VGLILAI FARRARTQEGRLQVELAQLSHLAGRLIRGYGHLQSQRGGIGMKGPGETKLETD					
g538	VGLILAI FARRARTQEGRLQVELAQLSHLAGRLIRGYGHLQSQRGGIGMKGPGETKLETD					
	190	200	210	220	230	240
m538.pep	RRLIAHRINALIKQLANLKKQALRRKSRESGRIKTFALVGYNVGVKSSLFNRLTKSGIY					
g538	RRLTAHRINALKKQLANLKKQALRRKSRESGRIKTFALVGYNVGVKSSLFNRLTKSGIY					
	190	200	210	220	230	240
	250	260	270	280		
m538.pep	AKDKL-----SPECSIILTDTVGVFVSDLPKHLISAFSXTLEETAQADVLLHV					
	:					
g538	AKDQLFATLDTTARRLYISPACSIILTDTVGVFVSDLPKHLISAFSATLEETVQADVLLHV					
	:					
	250	260	270	280	290	300
	290	300	310	320	330	340
m538.pep	VDAAAPNSGQOIEDVENVLQEIHAHDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
g538	VDAAARNSGQOIEDVENVLQEIHAHDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
	310	320	330	340	350	360
	350	360	370	380		
m538.pep	ISVAENTGIDALREAIAESCAAPNTDETEMPX					
g538	ISVAENTGIDALREAIAEYCAAPNTDETEMPX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1559>:

```

a538.seq
1   ATGACAGGCA GAACAGGCCG CAACGGCAGT ACCCAAGCGC AACCCGAACG
51  CGTCATGCTG GTGGGCGTAA TGTGGACAA AGATGGTACG GGCAGCAGTG
101 CCACCCGCTC GAACGGTTT CAGACGGCAT TGGCGGAAGC TGTCGAGCTG
151 GTCAAAGCGG CGGGCGGCCA TTCCGTGCGC GTGGAGACTG CCAAACGCGA
201 CCGTCCGCAC ACCGCGCTGT TTGTCGGCAC GGGCAAGGCG GCGGAGCTGT
251 CGGAAGCAGT TGCCGCAGAC GGCATCGATT TGGTCGTATT CAACCACGAA
301 CTTACGCCCA CGCAGGAACG CAATTTGGAA AAAATCCTCC AATGCCGCGT
351 ATTGGACAGA GTGGGGCTGA TTCTGGCGAT TTTCCGCCGC CGCGCCCGCA
401 CGCAGGAAGG CAGGCTGCAA GTCGAGTTGG CACAATTGAG CCATTTGGCG
451 GGACGCTTGA TACGCGGTTA CGGCCATCTG CAGAGCCAGC GCGGCGGTAT
501 CGGCATGAAA GGCCCCGGCG AAACCAAACT GGAAACCGAC CGCCGATTGA
551 TCGCCCATCG GATCAATGCC TTGAAAAAAC AGCTTGCCAA CCTCAAAAAA
601 CAGCGCGCCC TGCGCCGCAA GTCCCGCGAA TCGGGCACAA TCAAACGTT
651 TGCGCTGGTC GGCTATACCA ATGTCGGCAA ATCCAGTCTG TTCAACCGGC
701 TGACCAAGTC GGCATATAT GCGAAAGACC AGCTTTTCGC CACACTCGAC
751 ACGACGGCGC GCGGCTGTA CATCAGTCCC GAATGCAGCA TTATCCTGAC
801 CGATACCGTC GGATTCTCA GCGATCTGCC GCACAACTG ATTTCCGCCT
851 TTTCCGCCAC GCTGGAAGAA ACCGCGCAAG CCGATGTGCT GCTGCACGTC
901 GTCGATGCCG CCGCTCCGAA CAGCGGACAG CAGATTGAAG ACGTGGAAAA
951 CGTACTGCAA GAAATCCATG CCGGCGATAT TCCGTGCATC AAGGTGTACA
1001 ACAAACCGA CCTGCTGCCG TCTGAAGAAC AAAACACGGG CATATGGCGC
1051 GACGCTGCGG GAAAAATTGC CGCCGTCCGC ATTTCCGTG CTGAAAATAC
1101 CGGTATAGAC GCACTGCGCG AAGCCATTGC CGAGTATTGT GCCGCCGCAC
1151 CAAACACAGA CGAAACCGAA ATGCCATGA

```

This corresponds to the amino acid sequence <SEQ ID 1560; ORF 538.a>:

```

a538.pep
1   MTGRTGRNGS TQAQPERVML VGVMLDKDGT GSSATRLNGF QTALAEAVEL
51  VKAAGDSVR VETAKRDRPH TALFVGTKGA AELSEAVALD GIDLVFVNHE
101 LTPTQERNLE KILQCRVLDL VGLILAI FAR RTQEGRLQ VELAQLSHA
151 GRLIRGYGHL QSQRGGIGMK GPGETKLETD RRLIAHRINA LKKQLANLKK

```

813

201 QRALRRKSRE SGTIKTFALV GYTNVGKSSL FNRLTKSGIY AKDQLFATLD
 251 TTARRLYISP ECSIILTDTV GFVSDLPKHL ISAFSATLEE TAQADVLLHV
 301 VDAAAPNSGQ QIEDVENVLQ EIHAGDIPCI KVYNKTDLLP SEEQNTGIWR
 351 DAAGKIAAVR ISVAENTGID ALREAIAEYC AAPNTDETE MP*

m538/a538 94.6% identity in 392 aa overlap

m538.pep	10	20	30	40	50	60
	MTGRTGGNGSTQAQPERV	MLGVMLDKDGTGSSA	ARLNGFQTALAEAVEL	VKAAGGDSVR		
a538	10	20	30	40	50	60
	MTGRTGRNGSTQAQPERV	MLGVMLDKDGTGSSA	TRLNGFQTALAEAVEL	VKAAGGDSVR		
m538.pep	70	80	90	100	110	120
	VETAKRDRPHTALFVGTG	KAAELSEAVAADGIDL	VVFNHETPTQERNLEKE	LKCRVLDR		
a538	70	80	90	100	110	120
	VETAKRDRPHTALFVGTG	KAAELSEAVAADGIDL	VVFNHETPTQERNLEKI	LQCRVLDR		
m538.pep	130	140	150	160	170	180
	VGLILAI FARRARTQEG	RQLQVELAQLSHLAGRL	IRGYGHLQSQRGGIGMK	GPGETKLETD		
a538	130	140	150	160	170	180
	VGLILAI FARRARTQEG	RQLQVELAQLSHLAGRL	IRGYGHLQSQRGGIGMK	GPGETKLETD		
m538.pep	190	200	210	220	230	240
	RRLIAHRINALIKQLANL	KKQRALRRKSRESGTIK	T FALVGYTNVGKSSLF	NR LTKSGIY		
a538	190	200	210	220	230	240
	RRLIAHRINALKKQLANL	KKQRALRRKSRESGTIK	T FALVGYTNVGKSSLF	NR LTKSGIY		
m538.pep	250	260	270	280		
	AKDKL-----SPECSI	IILTDTVGFVSDLPKHL	ISAFSXTLEETAQADVLL	HV		
a538	250	260	270	280	290	300
	AKDQLFATLDTTARRLYI	SPECSIILTDTVGFVSDLP	KHLISAFSATLEETAQADV	LLHV		
m538.pep	290	300	310	320	330	340
	VDAAAPNSGQQIEDVENVL	QEIHAGDIPCIKVYNKTD	LLPSEEQNTGIWRDAAGK	IAAVR		
a538	290	300	310	320	330	340
	VDAAAPNSGQQIEDVENVL	QEIHAGDIPCIKVYNKTD	LLPSEEQNTGIWRDAAGK	IAAVR		
m538.pep	350	360	370	380		
	ISVAENTGIDALREAIAES	CAAPNTDETEMPX				
a538	350	360	370	380	390	
	ISVAENTGIDALREAIAEY	CAAPNTDETEMPX				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1561>:

g539.seq

1	atggaggatc	tgcaggaaat	cgggttcgat	gtcgccgccg	taaaggtagg
51	tcggcagcgc	gaacatcatc	gtctgcatca	taccagttcc	ggcaacggca
101	aggcggacga	tgtattgttt	gcgttctttt	tggttggcgg	cttcgatttt
151	ttgcgcgtca	taggggtcgg	cgggtgtagc	tgtctgccgg	attttcaaca
201	gaatgtcggg	gaggcggatt	ttgccgtcgt	cccagacgac	gcggcagcgg
251	tgcgtgctgt	aattgaggtc	gatgcggacg	atgccgtctg	tgcgcaaaag
301	ctgctgttcg	atcagccaga	cgcaggcggc	gcaggtaatg	ccgctgagca
351	tcagcactgc	ttcgtgcgtg	ccattatggg	ttccacaaa	gtcggattgg
401	acttcgggca	ggctgtacag	gcggatttgg	tcgaggattt	cttggggcgg
451	cagttcgggt	tttttcgcgt	cggcgggtgc	tcgtttgtaa	taactgccca
501	agccggaatc	gatgatgctt	tgtgcgactg	cctgacagcc	gacgcagcag
551	gtttcgcggg	cttcgccttc	gtagcggacg	gtcagatgca	ggttttcggg
601	aacgtccagc	ccgcagtggg	aacaggtttt	tttcatggca	tttcggtttc

```

651 gtctgtgttt ggtgcggcgg cacaatactc ggcaatggct tcgcgcagtg
701 cgtctatacc ggtattttca gcaacggaaa tgcggacggc ggcaattttt
751 cccgcagcgt cgcgccatat gcccggtgtt tgttcttcag acggcagcag
801 gtcgggtttg ttgtacacct tgatgcacgg aatatcgtgg gcatggattt
851 cttgcagtac gttttccacg tcttcaatct gctgcccgtt gttccgggcg
901 gcagcatcga cgacgtgcag cagcacatcg gcttgcacgg tttcttccaa
951 ggtggcgga aaggcgga tcaagttgtg cggcagatcg ctgacgaatc
1001 cgacggatc ggtcaggata atgctgcatg cgggactgat gtacagccgc
1051 cgcgccgtcg tgcgagagt ggcgaaaagc tggctcttcg catatatgcc
1101 cgacttggtc agccggttga acaggtgga tttgccgaca ttggtatag

```

This corresponds to the amino acid sequence <SEQ ID 1562; ORF 539.ng>:

```

g539.pep
1 MEDLQEIGFD VAAVKVGRQR EHHRLHHTQS GNGKADDVLF AFFLVGGFDF
51 LRVIGCGGVA CLPDFQONVG EADFAVVPDD AAARAVIEV DADDAVCAQK
101 LLFDQPDAGG AGNAAEHQHC FVRAIMGPHK VGLDFGQVVQ ADLVEDFLGR
151 QGFFFRVGGG SFVITAQAGI DDALCDCLTA DAAGFAVFVF VADGQMVFVG
201 NVQPAVETGF FHGISVSSVF GAAAQYSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHMPVF CSSDGSRSVL LYTLMHGISW AWISCSTFST SSICPLFRA
301 AASTTCSSTS ACTVSSKVAE KAEISLCGRS LTNPVSVRI MLHAGLMYSR
351 RAVVSRVAKS WSFAYPDLV SRLNRLDLPT LV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1563>:

```

m539.seq (partial)
1 ATGGAGGATT TGCAGGAAAT CGGGTTCGAT GTCGCCGCCG TAAAGGTAGG
51 TCGGCAGCGC GAACATCATC GTCTGCATCA TCCCCAGCCC GGCAACGGCG
101 AGGCGGACGA TGTATTGTTT GCGTTCTTTT TGGTTGGCGG CTTCGATTTT
151 TTGCGCGTCA TAGGGTGCAG CGGTGTAGCC TATCTGCCTG ATTTTCAACA
201 GAATGTCGGA AAGGCGGATT TTGCCGTCGT CCCAGACGAC GCGGCAGCgG
251 TCGGTGCTGT AATTGAGGTC GATGCGGACG ATGCCGTCTG TACGCAAAAG
301 CTGCTGTTTC ATCAGCCAGA CGCAGGCGGC GCAGGTGATG CCGCCGAGCA
351 TTAACACCGC CTCGCGCGTG CCGCCGTGGG TTTCCACAAA GTCGGGACTGG
401 ACTTCGGGCA GGTCTGACAG CGCGATTGGG TCGAGGATTT CTGCGGGCGG
451 CAGCTCGGTT TTTTGCAGCT CGGCGGTGCG TTGTTTGTA TAACTGCCCA
501 AGCCCGCGTC AATAATGCTT TGTGCGACCG CCTGACAGCC GGCGCaCAGG
551 GTTTCGCGGT CTTCGTTTTT GTAACGGACA GTCAGGTGGA GGTGTTCCGG
601 AACATCCAGA CCGCAGTGGA AACAGGTTTT TTTCATGGCA TTTCCGTTTC
651 GTCTGTGTTT GGTGCGGCGG CACAAGACTC GGCAATgGCT TCGCGCAGTG
701 CGTCTATACC GGTATTTTCA GCAACGGAAA TCGCGACGGC GGCAATTTTT
751 CCGCAGCGT CGCGCCATAT GCGCGTGTTC TGTCTTCAG ACGGCAGCAG
801 GTCGGTTTTG TTGTACACCT TgATGCACGG AATATCGCCG GCATGGATTT
851 CTTGCAGTAC GTTTTCCACG TCTTCAATCT GCTGTCCGCT GTTCGGAGCG
901 GCGGCATCGA CGACGTGCAG CAGCACATCG GCTTGCGCGG TTTCTTCCAG
951 CGTGGcG.AA AAGGCGGAAA TCAGTTTgTG CGGCAGATCG CTnACGAATC
1001 CGACGGTATC GGTCAGGATA ATGCTGCATT CGGGAC...

```

This corresponds to the amino acid sequence <SEQ ID 1564; ORF 539>:

```

m539.pep (partial)
1 MEDLQEIGFD VAAVKVGRQR EHHRLHHPQP GNGEADDVLF AFFLVGGFDF
51 LRVIGCGGVA YLPDFQONVG KADFAVVPDD AAARAVIEV DADDAVCTQK
101 LLFDQPDAGG AGDAAEH*NR LARAAGVFHK VGLDFGQVVQ ADLVEDFLGR
151 QLGLFRVGGG LfVITAQARV NNALCDRLTA GAQGFVVFVF VTDSQVEVFG
201 NIQTAVETGF FHGISVSSVF GAAAQDSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHMPVF CSSDGSRSVL LYTLMHGISP AWISCSTFST SSICPLFLGA
301 AASTTCSSTS ACAVSSSVAX KAEISLCGRS LTNPVSVRI MLHSG....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 539 shows 89% identity over a 345 aa overlap with a predicted ORF (ORF 539.ng) from *N. gonorrhoeae*:

```

m539/g539
          10      20      30      40      50      60
m539.pep MEDLQEIGFDVAAVKVGRQREHHRLHHPQPNGEADDVLF AFFLVGGFDFLRVIGCGGVA
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g539      MEDLQEIGFDVAAVKVGRQREHHRLHHTQSGNGKADDVLF AFFLVGGFDFLRVIGCGGVA

```

815

	10	20	30	40	50	60
	70	80	90	100	110	120
m539.pep	YLPDFQQNVGKADFAVVPDDAAAVRAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR					
g539	CLPDFQQNVGEADFAVVPDDAAAVRAVIEVDADDAVCAQKLLFDQPDAGGAGNAAEHQHC					
	70	80	90	100	110	120
	130	140	150	160	170	180
m539.pep	LARAAVGfHKVGLDFGQVQADLVEDFLGRQLGFLRVGGALFVITAQARVNNALCDRLTA					
g539	FVRAIMGfHKVGLDFGQVQADLVEDFLGRQFGFFRVGGASFVITAQAGIDDALCDCLTA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m539.pep	GAQGFAVFVFTDSQVEVFGNIQTAVETGFFHGISVSSVFGAAAQDSAMASRSASIPVFS					
g539	DAAGFAVFVADGQMVFVFGNVQPAVETGFFHGISVSSVFGAAQYSAMASRSASIPVFS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m539.pep	ATEMRTAAIFPAASRHMpVFCSSDGSRSVLLYTLMHGISPAWISCSTFTSSICCPLEGA					
g539	ATEMRTAAIFPAASRHMpVFCSSDGSRSVLLYTLMHGISWAWISCSTFTSSICCPLEGA					
	250	260	270	280	290	300
	310	320	330	340		
m539.pep	AASTCSSTSACAVSSSVAXKAEISLCGRSLTNPTVSVRIMLHSG					
g539	AASTCSSTSACTVSSKVAEKAEISLCGRSLTNPTVSVRIMLHAGLMYSRRRAVVSRAKS					
	310	320	330	340	350	360
g539	WSFAYMPDLVSRLNRLDLPTLV					
	370	380				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1565>:

```

a539.seq
1  ATGGAGGATT TGCAGGAAAT CGGTTTCGAT GTCGCCGCCG TAAAGGTAGG
51  TCGGCAGCGC GAACATCATC GTCTGCATCA TCCCAGCCCC GGCAACGGCG
101 AGGCGGACGA TGTATTGTTT GCGTTCCTTT TGGTTGCGCG CTTCGATTTT
151 TTGCGCGTCA TAGGGTGCGG CCGTGTAGCC TATCTGCCTG ATTTTCAACA
201 GAATGTCGGA AAGGCGGATT TTGCCGTCGT CCCAGACGAC GCGGCAGCGG
251 TGCCTGCTGT AATTGAGGTC GATGCGGACG ATGCCGTCGT TACGCAAAAG
301 CTGCTGTTCT ATCAGCCAGA CGCAGGCGGC GCAGGTGATG CCGCCGAGCA
351 TTAAAACCGC CTCGCGCGTG CCGCCGTGGG TTTCCACAAA GTCGGACTGG
401 ACTTCGGGCA GGTCGTACAG GCGGATTGG TCGAGGATTT CTGGGGCGG
451 CAGCTCGGTT TTTTGCGCGT CGGCGGTGCG TTGTTGTAA TAAGTCCCA
501 AGCCCGCGTC AATAATGCTT TGTGCGACTG CCTGACAACC GGCGCAGCAG
551 GTTTCGCGGT CTTCTGTTTC GTAACGGACG GTCAGATGCA GGTTTTCGGG
601 AACGTCCAGC CCGCAGTGGA AACAGGTTT TTTCATGGCA TTTCGGTTTC
651 GTCTGTGTTT GGTGCGGCGG CACAATACTC GGCAATGGCT TCGCGCAGTG
701 CGTCTATACC GGTATTTTCA GCAACGGAAA TGCGGACGGC GGCAATTTT
751 CCCGCAGCGT CGCGCCATAT GCCCGTGTG TTGTTCTTCA ACGGCAGCAG
801 GTCGGTTTGT TTGTACACCT TGATGCACGG AATATCGCG GCATGGATTT
851 CTTGCAGTAC GTTTTCCACG TCTTCAATCT GCTGTCCGCT GTTCGGAGCG
901 GCGGCATCGA CGACGTGACG CAGCACATCG GCTTGCAGCG TTTCTTCCAG
951 CGTGGCGGAA AAGGCGGAAA TCAGTTTGTG CCGCAGATCG CTGACGAATC
1001 CGACGGTATC GGTCAGGATA ATGCTGCATT CGGGACTGAT GTACAGCCGC
1051 CGCGCCGTCG TGTCGAGTGT GGCGAAAAGC TGGTCTTTCG CATATATGCC
1101 CGACTTGCTC AGCCGGTTGA ACAGACTGGA TTTGCCGACA TTGGTATAG

```

This corresponds to the amino acid sequence <SEQ ID 1566; ORF 539.a>:

```

a539.pep
1  MEDLQEIGFD VAAVKVGRQR EHHRLHHPQP GNGEADDVLF AFFLVGGGDF

```

816

```

51  LRVIGCGGVA YLPDFQQNVG KADFAVVPDD AAARAVIEV DADDAVCTQK
101 LLFDQPDAGG AGDAAEH*NR LARAAGVGHK VGLDFGQVVQ ADLVEDFLGR
151 QLGFLRVGGA LRVITAQARV NNALCDCLTT GAAGFAVEVE VTDGQMVFVG
201 NVQPAVETGF FHGISVSSVF GAAAQYSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHMPVF CSSDGSRSVL LYTLMHGISP AWISCSTFST SSICCPLFGA
301 AASTTCSSTS ACAVSSSSVAE KAEISLCGRS LTNPVSVRI MLHSGLMYSR
351 RAVVSSVAKS WSFAYMPDLV SRLNRLDLPT LV*

```

m539/a539 97.1% identity in 345 aa overlap

	10	20	30	40	50	60
m539.pep	MEDLQEIGFDVAAVKVGRQREHRLHHPQPGNGEADDVLFAFFLVGGFDFLRVIGCGGVA					
a539	MEDLQEIGFDVAAVKVGRQREHRLHHPQPGNGEADDVLFAFFLVGGFDFLRVIGCGGVA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m539.pep	YLPDFQQNVGKADFAVVPDDAAARAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR					
a539	YLPDFQQNVGKADFAVVPDDAAARAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m539.pep	LARAAGVGHKVGLDFGQVVQADLVEDFLGRQLGLFLRVGGALFVITAQARVNNALCDRLTA					
a539	LARAAGVGHKVGLDFGQVVQADLVEDFLGRQLGLFLRVGGALFVITAQARVNNALCDCLTT					
	130	140	150	160	170	180
	190	200	210	220	230	240
m539.pep	GAQGFAVFVFTDSQVEVFGNIQTAVETGFFHGISVSSVFGAAAQDSAMASRSASIPVFS					
	: : : :					
a539	GAAGFAVFVFTDGQMVFQVPAVETGFFHGISVSSVFGAAAQYSAMASRSASIPVFS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m539.pep	ATEMRTAAIFPAASRHMPVFCSSDGSRSVLLYTLMHGISP AWISCSTFSTSSICCPLFGA					
a539	ATEMRTAAIFPAASRHMPVFCSSDGSRSVLLYTLMHGISP AWISCSTFSTSSICCPLFGA					
	250	260	270	280	290	300
	310	320	330	340		
m539.pep	AASTTCSSTSACAVSSSVAXKAEISLCGRSLTNPTVSVRIMLHSG					
a539	AASTTCSSTSACAVSSSVAEKAEISLCGRSLTNPTVSVRIMLHSGLMYSRRRAVVSSVAKS					
	310	320	330	340	350	360
a539	WSFAYMPDLVSRLNRLDLPTLVX					
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1567>:

g540.seq

```

1  atgccgccct cccgacgcgg caacggggtg ttttatcaaa acggcaaact
51  tgccaatgcg gtttccgctt gccgattgcc aaaccggcaa acctttcccg
101  tgccgggtgc gaacccgatg ccgtctgaac cttcagacgg catcgggtgt
151  ttatttgtcc actcggacgg gtgcagggtc gtattgtgtc gattcgtcgc
201  cgtaatacag cagccgagt ttgacgggga tgcgtccctg cgatttgagg
251  tggcggttgg aatcgcgcaa ggaatacggc cagccgagt attcctgctg
301  gtagaagttt tcgcgtttgc tgatttcaat catacgcgcg ccgccgcgcg
351  ctttgcgcca gttgaagtcc caataggcca catcatcgta aggcgcggcg
401  gcacgggtgc cgcagtcgtt gatttgcgcc atatttttcc agcgtga

```

This corresponds to the amino acid sequence <SEQ ID 1568; ORF 540.ng>:

g540.pep

```

1  MPPSRRNGNV FYQNGKLANA VSACRLPNRQ TFPVPVPNPM PSEPSDGIGC

```



```
m540.seq (partial)
1    ..CCGAACCCGA TGCCGTCTGA ACCTTCAGAC GGCATCGGGT GTTTATTTGT
51   CCACCCGGAT GGGGGCAGGT TCGTATTGTG TCGATTCTGC GCCGTAATAC
101  AGCACGCCGA GTTTGATGGG GATTCTGCCC TGTGATTTCG GGTGGGCATT
151  GGAATCCCTC AGGGAATAGG CACAACCGCA ATATTCCTGC TGGTAGAAGT
201  TTTCACGTTT GCTGATTTC AATCATCGCG CGCTGCCCGC GCCTTTGCGC
251  CAGTTGAATT CCCAATACAC CATCATCTCG TAAGGCGCGG CGGCGCGGTG
301  TCCGCAAGTC TTGATTTCG CCATATTTT CCAGCGTGA
```

m540.pep (partial)

1 ..PNMPSEPSD GIGCLFVHPD GGRFVLCRFV AVIQHAEDFG DSAL*FAVGI

51 GIPOGIGTTA IFLLVEVFTE ADFNHARAAA AFAPVEIPIH HIIVRRGGAV

101 SAVVDLRHIF PA*

```

m540/g540
                                10      20      30
m540.pep                      PNPMPSEPSDGIGCLFVHPDGGFRVLCRFV
                                |||||
g540                          GNGVIFYQNGKLANAVSACRLPNRQTFVPVFPNPMPSEPSDGIGCLFVHSDGCRFVLCRFV
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m540.pep                      AVIQHAEFDGDSALXFAVGIGIPQGIGTTAIFLLVEVFTFADFNHARAAAFAFAPVEIPIH
                                |||||:| |||:| |||::| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
g540                          AVIQHAEFDGDASLRFAVGVGIAQGIRAAAVFLLVEVFADFNHTRAAAFAFAPVEVPIG
                                70      80      90      100     110     120

                                100     110
m540.pep                      HIIVRRGGAVSAVVDLRHIFPAX
                                |||||:| |||||
g540                          HIIVRRGGTVSAVVDLRHIFPAX
                                130     140

```

a540.seq

1	ATGCCGTCCT	CCCACGCGG	CAACGGGGTG	TTTTATCAA	ACGGCAAAC
51	TGCCAATGCG	GTTTCCGATT	GCAGATTGCC	AAACCGGCAA	ACCTTTCCCG
101	TGCCGATGCC	GAACCCGATG	CCGCTGTAAC	CTTCAGGCGG	CATCGGGTGT
151	TTATTTGTCC	ACCGGATGG	GTGCAGGTTT	GTATTGTGTC	GATTCCTCGC
201	CGTAATACAG	CACGCCGAGT	TTGATGGGGA	TTCTGCCCTG	TGATTTGCGG
251	TGGGCGTTGG	AATCCCTCAG	GGAATAGGCA	CAACCGCAAT	ATTCTCTGCT
301	GTAGAAGTTT	TCACGTTTGC	TGATTTCAAT	CATACGCGCG	CTGCCGCCGC
351	CTTTGGGCCA	GTTGAAATCC	CAATAACACA	CATCATCGTA	AGGCGCGGCG
401	GCGCGGCGGC	GCGACGTCGT	AATCTGGTTC	ATGTTTTTCC	A

```
a540.pep (partial)
1  MPSRRRNGV FYQNGLANA VSDCLRPNRQ TFPVPMPNPM PSEPSDGIGC
51  LFVHPDGCRF VLCRFVAVIQ HAEFDGDSAL *FAVGVGIPQ GIGTTAIFLL
101 VETTFADFN HTAAAAFAP VEIPIHHIIV RRGGAAAADV NLVHVFP
```

818

m540/a540 92.8% identity in 111 aa overlap

```

                                10      20      30
m540.pep                      PNPMPSEPSDGIGCLFVHPDGGRFVLCRFV
                                |||||
a540      GNGVFYQNGKLANAVSDCRLPNRQTFVPMPNPNMPSEPSDGIGCLFVHPDGCRCFVLCRFV
              10      20      30      40      50      60

                                40      50      60      70      80      90
m540.pep      AVIQHAEFDGDSALXFAVGIGIPQIGIGTTAIFLLVEVFTFADFNHARAAAAFAPVEIPIH
              |||||:|||||:|||||:|||||:|||||:|||||
a540      AVIQHAEFDGDSALXFAVGIGIPQIGIGTTAIFLLVEVFTFADFNHTRAAAAFAPVEIPIH
              70      80      90      100     110     120

                                100     110
m540.pep      HIIVRRGGAVSAVVDLRHIFPAX
              |||||:|:|:|
a540      HIIVRRGGAAAAVNLVHVFP
              130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1573>:

```

g542.seq
1  atgccgaat ggtcgcgcat acggcggttc agcgctcctt cgctgatggt
51 cagcgcggt gtcagccggt tgacttggtg tgcgcccgcg tcgaacgcgg
101 cattcagggt gcggctgaag tcttcagacg gcatagcgtc tgcttcgcc
151 gtttgccccg ccgcccgcgc gatgccgtct gaaaccgtgt cccacaaatc
201 cgacagcagc cgcaacacgt ccgcctcgcg gcgcaatggt tcgcccacaa
251 gccctttgg gacggttgc aggcaggatg ccgccaagcc gcgcagggtt
301 gggggcaaat cccatatcct gaccggttcg cggtaa

```

This corresponds to the amino acid sequence <SEQ ID 1574; ORF 542.ng>:

```

g542.pep
1  MPKWSRIRRC SVLSLMFSAA VSRLTWCAPP SNAAFRVRLK SSDGIASASA
51  VCPAAGSMPS ETVSHKSDSS RNTSASRRNV SPKCPFGTVC RQDAAKPRRF
101 GGKSHILTGS R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1575>:

```

m542.seq
1  ATGCCGAAAT GGTGCGCAT ACGGCGTTGC AGCGTCCTTT CACTGATGTT
51  CAGCGGTCT GTCAGCCGGT TGAATTGGTG TGCGCCGTCG GCAAACGCGG
101 CATTTAGGGT GCGGCTGAAG TCTTCAGACG GCATAGCGTC TGCTTCCGCC
151 GTTTGCCCGG CCGCCGGCCC GATGCCGTCT GAAACCGTGT CCCACAAGTC
201 CGACAGCAGC CGCAACACGT CCGCCTCGCG .CGCAATGTT TCGCCCAAAT
251 GCCCCTTTGG GACGGCTTTC AGGCAGGATG CCGCCAAGCC GCGCAGGTTT
301 GGGGGCAAAT CCCATATCCT GACCGGTTTC CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1576; ORF 542>:

```

m542.pep
1  MPKWSRIRRC SVLSLMFSAS VSRLTWCAPS ANAAFRVRLK SSDGIASASA
51  VCPAAGFMPS ETVSHKSDSS RNTSASRAMF RPNAPLGRNV SPKCPFGTAF
101 RQDAAKPRRF GGKSHILTGS R*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 542 shows 93.7% identity over a 111 aa overlap with a predicted ORF (ORF 542.ng) from *N. gonorrhoeae*:

```

m542/g542

                                10      20      30      40      50      60
m542.pep      MPKWSRIRRC SVLSLMFSAS VSRLTWCAPS ANAAFRVRLK SSDGIASASAVCPAAGPMPS
              |||||:|||||:|||||:|||||:|||||:|||||
g542      MPKWSRIRRC SVLSLMFSAAVSRLTWCAPP SNAAFRVRLK SSDGIASASAVCPAAGSMPS
              10      20      30      40      50      60

                                70      80      90      100     110
m542.pep      ETVSHKSDSSRNTSASRRNVSPKCPFGTAFRQDAAKPRRF GGKSHILTGSRX

```

819

```

|||||
g542      ETVSHKSDSSRNTSASRRNVSPKCPFGTVCRQDAAKPRRFGGKSHILTGSRX
              70          80          90          100         110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1577>:

```

a542.seq
1   ATGCCGAAAT GGTGCGGCAT ACGGCGTTGC AGCGTCCTTT CGCTGATGTT
51  CAGCGTGTCT GCCAGCCGGT TGACTTGATG TGCGCCGCCG GCAAACGCGG
101 CATTGAGGAT GCGGCTGAAG TCTTCAGACG GCATAGCGTC TGCTTCCGCC
151 GTTTGCCCCG CCGCCGGCCC GATGCCGTCT GAAACCGTGT CCCACAAGTC
201 CGACAGCAGC CGCAACACGT CCGCCTCGCG GCGCAATGTT TCGCCCAAAT
251 GCCCCTTTGG GACGGCTTTC AGGCAGGATG CCGCCAAGCC GCGCAGGTTC
301 GGGGGCAAAT CCCATATCCT GACCGTTTCG CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1578; ORF 542.a>:

```

a542.pep
1   MPKWSRIRRC SVLSLMFSVS ASRLT*CAPP ANAAFRMLK SSDGIASASA
51  VCPAAGPMPS ETVSHKSDSS RNTSASRRNV SPKCPFGTAF RQDAAKPRRF
101 GGKSHILTGS R*

```

m542/a542 94.6% identity in 111 aa overlap

```

              10          20          30          40          50          60
m542.pep      MPKWSRIRRC SVLSLMFSVSASRLTWCAPSANAAFRVRLKSSDGIASASAVCPAAGPMPS
              |||||
a542           MPKWSRIRRC SVLSLMFSVSASRLTXCAPPANAAFRMLKSSDGIASASAVCPAAGPMPS
              10          20          30          40          50          60

              70          80          90          100         110
m542.pep      ETVSHKSDSSRNTSASRRNVSPKCPFGTAFRQDAAKPRRFGGKSHILTGSRX
              |||||
a542           ETVSHKSDSSRNTSASRRNVSPKCPFGTAFRQDAAKPRRFGGKSHILTGSRX
              70          80          90          100         110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1579>:

```

g543.seq
1   atggtttgtc gggtatttgc cgccgttttt ggctttcaac tcggcaatca
51  gcccgctgat gcctttggct ttgatgattt cgccgaattg gttgcggtac
101 acggttaacca ggctcgtgcc ttcgatggcg acgtgtagg tacggtattt
151 gccgccgctt tggtaggttg taaagtccat attgacgggc ttctgaccgg
201 ggatgccgac ttcggcacgg acgacgattt ccttgccgcc cttattgacg
251 atgggattgt ctttgacgtt gacggtcgcg tttttgaatt tcagcatcgt
301 gccggaatag gtgcggatca gcagggtttg aaattccttg gccaacgctt
351 gtttttgcgc gtcggacgcg gtacgccaag ggttgccgac cgccaatgcg
401 gtcatacgtt ggaaatcgaa atagggaacc gcataggctt cggcttttgg
451 gcgtgcagaa gccgcgtcgc cgcttttgag gatggtcaaa acctgtgtgg
501 cgttttggcg gatttgtccc actgcgtcgg ccggggaggc aaatgccatg
551 ccgatgctca aaataccgat gcccaatgcg ctgatgaagg aggatttttt
601 cacgatgtct ttcctgaaaa tggatgtgta tgtttattct gcggcttttt
651 ccgcattgcc gccctcagcg tttttctcgg cgaagctggt catgaattta
701 ccgatcaggt tttccagaac cattgcagaa ctggttacgg agatggtgtc
751 gccgagcaga aggttttccg tatcgccgcc ctgctgcagc ccgatgtact
801 gttcgcccaa aagtcgccga gtcaggattt gcgcggaaac gtactgctg
851 aactgatact tgccgtccaa atcaaggcgc accctcgcct gataggattt
901 cgggtcaagc ccgatagcgc cgacgcgccc gaccaatacg cctgcggatt
951 tgacgggggc attgaccttc aaaccgccga tgtcgccgaa atcggcataa
1001 acggcgtaag ttttgtccga accgccgaac gccgcgccgc ccgccacgcg
1051 gaaagcgaga aaggcaaccg ccgcccgcgc gatcaagacg aacagtccga
1101 cccaaaattc caatatgttc tttttcatta a

```

This corresponds to the amino acid sequence <SEQ ID 1580; ORF 543.ng>:

```

g543.pep
1   MVCRLFAAVF GFQLGNQPVDF AFGFDDFAEL VAVHGNQARA FDGDVVGTVF

```

820

```

51  AAALVGGKVH IDGLLTGDAD FGTDDDFLAA LIDDGIVFDV DGRVFEFQHR
101 AGIGADQOGL KFFGQRLFLR VGRGTPRVAD RQCGHTLEIE IGNRIGFGFW
151 ACRSRVAAFE DGQNLGCVLA DLSHCVGRGG KCHADAQNTD AQCADEGGFF
201 HDVFPENGCV CLFCGFFRIA ALSVFLGEAG HEFTDQVFQN HCRTGYGDGV
251 AGSKVFRIAA LLQPDVLFQA KSRSDQLRGN VTAEILAVQ IKAHPRLIGF
301 RVKPDSDADAP DQYACGFDGG IDLQADVAE IGINGVSFVR TAERRAARHA
351 ESEKGNRRRA DQDEQSDPKF QYVLFH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1581>:

```

m543.seq
1  ATGGTTTGTC GGTATTATTC CGCCGTTTTT GGCTTTCAAC TCGGCAATCA
51  GTCCGTCCAC GCCTTTCGCT TTGATAATTT CGCCGAATTG GTTGCGGTAC
101 ACGGTAACCA GGCTCGCGCC TTCGATGGCG ACGTTGTAGG TACGGTATTT
151 ACCGCCGCTT TGGTAGGTGG TGAAGTCCAT GTTGACGGGT TTTTGCCCGG
201 GTACGCCGAC TTCGGCGCGG ACGATGATTT CTTTGCCGCC TTTATTGACG
251 ATGGGATTGT CTTTGACGTT GACGTGGCG TTTTAAATTC TCAGCATCGT
301 GCCGAATAG GTGCGGATCA GCAGGGTTTG AAATTCCTTG GCCAACGCTT
351 GTTTTGCGC GTGCGACGCG GTGCGCCAAG GGTGCGGAC CGCCAATCGG
401 GTCATACGTT GAAATCGAA ATAGGGAATC GCATAGGCTT CGGCTTTTTG
451 GCGAGCGGTG TTGCGATCGC CGTTTTTTAA GATGCTCAAT ACTTGAGTGG
501 CGTTTTGACG GATTTGGCTT ACCGCGTCGG CAGGGGCGGC AAATGCCATG
551 CCGATGCTCA AAATACCGAT GCCCAATGCG CTGATGAGGG AGGATTTTTT
601 CATGATTAAG TGTCTAGTT TGAATATGAT GGCATACGTT TATTCGCGCG
651 CTTTTCCGC ATTGCGCGCG TCGGCATTTT TCTCGGCAAA ACTCGTCATG
701 AATTTGCCGA TAAGGTTTTT CAGAACCATT GCAGAACTGG TTACGGAGAT
751 GGTGTCGCCG GCAGCAAGGT TTTCCGTGTC GCCGCCCTGC TGCAGCCCGA
801 TGTACTGCTC GCCCAAAGT CCCGAAGTCA GGATTGCGC GGAAACGTCT
851 CTGCTGAAC TACTTTGCC GTCCAAATCG AGGCGCACCC TCGCTGATA
901 GGATTCGGG TCAAGTCCGA TAGCGCCGAC GCGCCCGACC AATACGCCTG
951 CGGATTTGAC GGGGGCATTG ACCTTCAAAC CGCCGATGTC GCCGAAATCG
1001 GCATAAACGG CGTAAGTTTT GTCCGAACCG CCGAACGCCG CACCGCCGGC
1051 CACGCGGAAA GCGAGAAAGG CAACCGCCGC CGCGCCAATC AGGACGAACA
1101 GTCCGACCCA AAATCCAAT ATGTTCTTCT TCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1582; ORF 543>:

```

m543.pep
1  MVCRLFAAVF GFQLGNQSVH AFRFDNFAEL VAVHGNQARA FDGDVVGTVF
51  TAALVGGEVH VDGFPLGYAD FGADDDFFAA FIDDGIVFDV DVGVFVFXQHR
101 AGIGADQOGL KFFGQRLFLR VGRGAPRVAD RQCGHTLEIE IGNRIGFGFL
151 ASGVGIAXFX DAQYLSGVLT DLAYRVGRGG KCHADAQNTD AQCADEGGFF
201 HDXVSXFEYD GIRLFGGFFR IAAVGIFLKG TRHEFADKVF QNHCRGTGYD
251 GVAGSKVFRV AALLQPDVLL AQKRSQDLR GNVAELILA VQIEAHPRLI
301 GFRVKSDSAD APDQYACGFD GGIDLQADV AEINGVVSF VRTAERRTAG
351 HAESEKGNRR RANQDEQSDP KFQYVLLH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 543 shows 84.2% identity over a 379 aa overlap with a predicted ORF (ORF 543.ng) from *N. gonorrhoeae*:

```

m543/g543
10      20      30      40      50      60
m543.pep MVCRLFAAVFGFQLGNQSVHAFRFDNFAELVAVHGNQARAFDGDVVGTVFTAALVGGEVH
|||||
g543      MVCRLFAAVFGFQLGNQPVDAFGFDDFAELVAVHGNQARAFDGDVVGTVFAALVGGKVH
10      20      30      40      50      60

70      80      90      100     110     120
m543.pep VDGFPLGYADFGADDDFFAAFIDDGIVFDVDVGVFVFXQHRAGIGADQOGLKFFGQRLFLR
:|:|:|
g543      IDGLLTGDADFGTDDDFLAALIDDGIVFDVDGRVFEFQHRAGIGADQOGLKFFGQRLFLR
70      80      90      100     110     120

130     140     150     160     170     180

```

821

```

m543.pep      VGRGAPRVADRQCGHTLEIEIGNRIGFGFLASGVGIAVFXDAQYLSGVLTDLAYRVGRGG
               |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g543          VGRGTPRVADRQCGHTLEIEIGNRIGFGFWACRSRVAAFEDGQNLGCVLADLSHCVGRGG
               130      140      150      160      170      180

               190      200      210      220      230      239
m543.pep      KCHADAQNTDAQCADEGGFFHDXVSXFEYDG-IRLFGGFFRIAAGVIFLGKTRHEFADKV
               |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g543          KCHADAQNTDAQCADEGGFFHDXV---FPENGCVCLFCGFFRIAALSVFLGEAGHEFTDQV
               190      200      210      220      230

               240      250      260      270      280      290      299
m543.pep      FQNHCRITGYGDGVAGSKVFRVAALLQPDVLLAQKRSQDLRGNVAAELILAVQIEAHPRL
               |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g543          FQNHCRITGYGDGVAGSKVFRVAALLQPDVLLFAQKRSQDLRGNVTAELILAVQIKAHPRLL
               240      250      260      270      280      290

               300      310      320      330      340      350      359
m543.pep      IGFRVKSDSADAPDQYACGFDGGIDLQTDVAEIGINGVSFVRTAERRTAGHAESEKGNR
               |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g543          IGFRVKPDSADAPDQYACGFDGGIDLQTDVAEIGINGVSFVRTAERRAARHAESEKGNR
               300      310      320      330      340      350

               360      370      379
m543.pep      RRANQDEQSDPKFQYVLLHX
               |||:|||||:|||||:|||||:
g543          RRADQDEQSDPKFQYVLFHX
               360      370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1583>:

```

a543.seq
1  ATGGCTTATG GATTACTTGC TGCCGTTTNT AGCCTTCAAC TCGNCAATCA
51  GTCCGTCCAC GCCTTTTCGCT TTGATAATTT CGCCGAATTG GTTGC GGTTAC
101 ACGGTAACCA GGCTCGCGCC TTCGATGGCG ACGTTGTAGG TACGGTATTT
151 ACCGCCGCTT TGGTAGGTGG TGAAGTCCAT GTTGACGGGT TTTGCCCGG
201 NNACGCCGAC TTCGGCGCGG ACGATGATTT CTTTGCCGCC TTTATTGACG
251 ATNGGATTGT CTTTGACGTT GACGTTGGCG TTTTTTAATT TCAGCATCGT
301 GCCGGAATAG GTGCGGATCA GCAGGGTTTG AAATTCTTTG GCCAACGCTT
351 GTTTTTCGCG GTCGGACGCG GTGCGCCAAG GGTGCGGAC CGCCAATGCG
401 GTCATACGTT GGAAATCGAA ATAGGGAATC GCATAGGCTT CGGCTTTTGT
451 GCGGGCGGTG TTGGCATCAC CGCTTTTAA GATGCTCAAT ACTTGAGTGG
501 CGTTTTCGAC GATTTGGTTT ACCGCGTCGG CAGGGGCGGC AAATGCCATG
551 CCGATGCTCA AAATACCGAT GCCCAATGCG CTGATGAAGG AGGATTTTTT
601 CATGATTAAG TGTCTAGTT TGAATATGAT GGCATACGTT TATTCGGCGG
651 CTTTTTCCGC ATTGCCGCGC TCGGCATTTT TCTCGGCAAA ACTCGTCATG
701 AATTTGCCGA TAAGGTTTTT CAGAACCATT GCAGAACTGG TTACGGAGAT
751 GGTGTCGCCG GCAGCAAGGT TTTCCGTGTC GCCGCCCTGC TGCAGCCCGA
801 TGTACTGCTC GCCCAAAGT CCCGAAGTCA GGATTTGCGC GGAAACGTCG
851 CTGCTGAAC TACTTTGCC GTCCAAATCG AGGCGCACCC TCGCCTGATA
901 GGATTTCCGG TCAAGTCCGA TAGCGCCGAC GCGCCCGACC AATACGCCCTG
951 CGGATTTGAC GGGGGCATTG ACCTTCAAAC CGCCGATGTC GCCGAAATCG
1001 GCATAAACGG CGTAAGTTT GTCCGAACCG CCGAACGCCG CACCGCCGGC
1051 CACGCGGAAA GCGAGAAAGG CAACCGCCGC CGCGCCAATC AGGACGAACA
1101 GTCCGACCCA AAATTCCAAT ATGTTCTTTT TCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1584; ORF 543.a>:

```

a543.pep
1  MAYGLLAHVX SLQLXNQSVH AFRFDNFAEL VAVHGNQARA FDGDVVGVTF
51  TAALVGGEVH VDGFLPGXAD FGADDDFFAA FIDDXIVFDV DVGVF*FQHR
101 AGIGADQOGL KFFGQRLFLR VGRGAPRVAD RQCGHTLEIE IGNRIGFGFL
151 AGGVGITAF* DAQYLSGVLT DLVYRVGRGG KCHADAQNTD AQCADEGGFF
201 HD*VS*FEYD GIRLFGGFFR IAAVGIFLGK TRHEFADKVF QNHCRITGYGD
251 GVAGSKVFRV AALLQPDVLL AQKRSQDLR GNVAELILA VQIEAHPRLI
301 GFRVKSDSAD APDQYACGFD GGIDLQTDV AEIGINGVSF VRTAERRTAG

```

822

351 HAESEKGNRR RANQDEQSDP KFQYVLFH*

m543/a543 96.0% identity in 378 aa overlap

	10	20	30	40	50	60
m543.pep	MVCRLFAAVFGFQ	LGNSVHAFRDNFAELVAVHGNQARAFDGDVVGTVFTAALVGGEVH				
a543	MAYGLLAAVXSLQLXNQSVHAFRDNFAELVAVHGNQARAFDGDVVGTVFTAALVGGEVH					
	70	80	90	100	110	120
m543.pep	VDGFLPGYADFGADDDFFAAFI	DDGIVFDVDVGVEFXFQHRAGIGADQQGLKFFGQRLFLR				
a543	VDGFLPGXADFGADDDFFAAFI	DDXIVFDVDVGVEFXFQHRAGIGADQQGLKFFGQRLFLR				
	130	140	150	160	170	180
m543.pep	VGRGAPRVADRQCGHTLEIEIGNRIGFGFLASGVGIAVFXDAQYLSGVLTDLAYRVGRGG					
a543	VGRGAPRVADRQCGHTLEIEIGNRIGFGFLAGGVGITAFXDAQYLSGVLTDLVYRVGRGG					
	190	200	210	220	230	240
m543.pep	KCHADAQNTDAQCADEGGFFHDXVSXFEYDGIRLFGGFFRIA	AVGIFLGKTRHEFADKVF				
a543	KCHADAQNTDAQCADEGGFFHDXVSXFEYDGIRLFGGFFRIA	AVGIFLGKTRHEFADKVF				
	250	260	270	280	290	300
m543.pep	QNHCR	TGYGDGVAGSKVFRVAALLQPDVLLAQKSR	SQDLRGNVAAELILAVQIEAHPRLI			
a543	QNHCR	TGYGDGVAGSKVFRVAALLQPDVLLAQKSR	SQDLRGNVAAELILAVQIEAHPRLI			
	310	320	330	340	350	360
m543.pep	GFRVKSDSADAPDQYACGFDGGIDLQ	TADVAEIGINGVSFVRTAERRTAGHAESEKGNRR				
a543	GFRVKSDSADAPDQYACGFDGGIDLQ	TADVAEIGINGVSFVRTAERRTAGHAESEKGNRR				
	370	379				
m543.pep	RANQDEQSDPKFQYVLLHX					
a543	RANQDEQSDPKFQYVLFHX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1585>:

g544.seq

```

1  atgaaaaaaa tactcaccgc cgccgccgctc gcactgatcg gcattcctcct
51  cgccaccgctc ctcatccccg acagtaaaac cgcgccccgcc ttctccctgc
101 ccgacctgca cggaaaaaac gtttccaacg ccgacctgca aggcaaagtc
151 accctgatta attttggtt tccctcctgt ccgggttggtg tgagcgaaat
201 gcccaaaagtc accaaaacgg caaacgacta caaaaataaa gatttccaag
251 tcctcgccgt tgcccagccc atcgatccga tagaaagcgt ccgccaatac
301 gtcaaagact acggactgcc gtttaccgctc atttatgatg cggacaaagc
351 cgtcggacag gcattcggca cacagggtta tccgacttcc gtccttatcg
401 gcaaaaaagg cgaaatctc aaaacttatg tcggcgaaac cgatttcggc
451 aaactctacc aagaaatcga taccgcgctg gcgcaatag

```

This corresponds to the amino acid sequence <SEQ ID 1586; ORF 544.ng>:

g544.pep

```

1  MKKILTAAAV ALIGILLATV LIPDSKTAPA FSLPDLHGKT VSNADLQGV
51  TLINFWFPSC PGCVSEMPKV TKTANDYKNK DFQVLAVAQP IDPIESVRQY
101 VKDYGLPFTV IYDADKAVGQ AFGTQVYPTS VLIKKGEIL KTYVGEPDFG

```

m544.seq

1	TTAGAAAAAA	TACTCACCGC	CGCCGTCGTC	GCACTGATCG	GCATCCTCCT
51	TGCCATCGTC	CTCmTCCCG	ACAGCAAAC	CGCGCCCGCC	TTCTCCmTGC
101	CCGACCTGCA	CGGAAAAACC	GTTTCCAACG	CCGACCTGCA	AGGCAAAGTA
151	ACCCTGATTA	ATTTTTGGTT	TCCCTCCTGT	CCGGTGTGTG	TGAGCGAwAT
201	GCCCCAAATC	ATTA AACCG	CAATGACTA	TAAAaWCAAA	AACTTCCAAG
251	TACTTGCCGT	CGCCCAGCCC	ATCGATCCGA	TAGAAAGCGT	CCGCCAATAT
301	GTCAAAGACT	ACGGTTTGCC	GTTTACCGTC	ATGTATGATG	CGGACAAAGC
351	TGTCGGACAG	CGCTTCGGCA	CACAGGTTTA	TCCGACTTCC	GTCTTTATCG
401	GCAAAATAAGG	CGAAATCTTC	AAAACCTACG	TCGGCGAACC	CGATTTCGGC
451	AAACTCTACC	AAGAAATCGA	TACGCGCGTG	GCgCAATAG	

m544 . pep

1 MXKILTA~~AA~~AVV ALIGILLAIV LXPDSKTAPA FSXPD~~L~~HGKT VSNADLQ~~G~~KV
51 TLINFWF~~P~~SC PGCVSXMPKI IKTANDYK~~X~~K NFQVLAVAQP IDPIESVRQY
101 VKDYGLPFTV MYDADKAVGQ AFGTQVYPTS V~~L~~IGK*GEIF KTYVGE~~P~~DFG
151 KLYOEIDTRV AQ*

ORF 544 shows 90.7% identity over a 162 aa overlap with a predicted ORF (ORF 544.ng) from *N. gonorrhoeae*:

m544/g544

	10	20	30	40	50	60			
m544 . pep	MXKILTA	AAVVALIGILL	AIVLXPDSKT	APAFSXPDL	HGKTVSNADL	QGKVTLINFWFPSC			
g544	MKKILTA	AAVVALIGILL	ATVLI	PD	SKTAPAFSL	PD	LHGKTVSNADL	QGKVTLINFWFPSC	
	10	20	30	40	50	60			
	70	80	90	100	110	120			
m544 . pep	PGCVSX	MPKIIKT	ANDYKX	KNFQVL	AVAQPID	PIESVR	QYVKDYGL	PFTVMYDADKAVGQ	
g544	PGCVSE	MPKVTK	TANDYK	KNKDFQ	VL	AVAQPID	PIESVR	QYVKDYGL	PFTVIYDADKAVGQ
	70	80	90	100	110	120			
	130	140	150	160					
m544 . pep	AFGTQV	YPTSVL	IGKXGE	IFKTYV	GEPDFG	KLYQE	IDTR	VAQX	
g544	AFGTQV	YPTSVL	IGKXGE	ILKTYV	GEPDFG	KLYQE	IDT	LAQX	
	130	140	150	160					

a544.seq

1	ATGAAAAAAA	TACTCACCGC	CGCGTCGTC	GCACTGATCG	GCATCCTCCT
51	TGCCATCGTC	CTCATCCCG	ACAGCAAAC	CGCGCCCGCT	TTCTCCCTGT
101	CCGANCTGCA	CGGAAAAANC	GTTTNCAACG	CCGACCTGCA	AGGCNAAGTT
151	ANCTTGATTA	ANTTTTGGTT	TCCCTCTGT	CCGGTTGT	TGAGCGAAAT
201	GNCCANAATC	ATTAACACGG	CAACTGACTA	TAAAAACAAA	AAGTCCAAG
251	TCCTTGCCGT	CGCCCAGCCC	ATCGATCCGA	TAGAAAGCGT	CCGCCAATAT
301	GTCAAAGACT	ACGGTTTGCC	GTTTACCGTC	ATGTATGATG	CGGACAAAGC
351	TGTCGGACAG	CGCTTCGGCA	CACAGGTTTA	TCCGACTTCC	GTCCTTATCG
401	GCAAAAAAGG	CGAAATCCTC	AAAATTATG	TCGGCGTAAC	CGATTTCGGC
451	AAACTCTACC	AAGAAATCGA	TACCGCGCTG	GCACAATAG	

a544.pwp

1 MKKILTAADV ALIGILLAIV LIPDSKTAPA FSLSLHGKX VVNADLQGXV
51 XLIXFWFPC PGCVSEMXXI IKTANDYKNK NFQVLAVAQP IDPIESVRQY
101 VKDYGLPFTV MYDADKAVGO AFGTOVYPTS VLIGKKGEIL KTYVGEPEFG

824

151 KLYQEIDTAL AQ*

m544/a544 88.9% identity in 162 aa overlap

	10	20	30	40	50	60
m544 . pep	MXKILTA	AVVALIG	ILLAIVL	XPDSKT	APAFSXP	DLHGKT
a544	MKKILTA	AVVALIG	ILLAIVL	IPDSKT	APAFSL	SXLHGK
	10	20	30	40	50	60
	70	80	90	100	110	120
m544 . pep	PGCVSX	MPKIIK	TANDYK	XKNFQV	LAVAQPI	DSVRQY
a544	PGCVSEM	XXIIK	TANDYK	XKNFQV	LAVAQPI	DSVRQY
	70	80	90	100	110	120
	130	140	150	160		
m544 . pep	AFGTQV	YPTSVL	IGKXGE	IFKTYV	GEPDFG	KLYQEID
a544	AFGTQV	YPTSVL	IGKKGE	ILKTYV	GEPDFG	KLYQEID
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1591>:

g547 . seq

```

1  atgttcgtag ataacggatt taataaaacg gtagcagatt ttgcccaaat
51  cgtcgaaact ttcgacgtat tcttcttttag gaacgattgc gcctttttta
101 cgcagatgaa acagcgggtgc ggttgggtct gctcgttggt atatctcggt
151 gatataattta caagatgctgc cttcgagatt ccgaaccgct cctttaaaga
201 gcttgggctt ttgatacaga taagtctgtc ggaacgtttt aggactaatg
251 ccgaagtcga gatggatgcc cattacttcc ccttactcag aaaatattta
301 aaatttataa tgttacatat agttacaaat attagagttt tttgtgtgtg
351 cgtcaaggaa ttgttgacaa ttttagttaa aaatttgtct ccaaacggaa
401 aaaagcgggt tgttttttgt tgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1592; ORF 547.ng>:

g547 . pep

```

1  MFVDNGFNKT VASFAQIVET FDVFFFRNDC AFFTQMKQRC GWVCSLVYLV
51  DIFTRCGFEI PNRSFKELGL LIQISLSERF RTNAEVEMDA HYFPLLRKYL
101 KFIMLHIVTN IRVFCVCVKE LLTILVKNLSPNGKKRFVFC C*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1593>:

m547 . seq

```

1  ATGTTTCGTAG ATAACGGATT TAATAAAACG GTAGCAGATT TTGCCCAAAT
51  CGTCGAAACT TTCGACGTAT TCTTCTTTAG GAACGATTGC GCCTTTTSTA
101 CGCAGATGAA ACAGCGGTGC GGTGCGGTCT GCTCGTTGGT ATATCTCGTT
151 GATATCTTTC CAAGATGCGG ATTCGAGATT CCGAACCCTC CCTTTAAAGA
201 GCTTGGGCTT TTGATACAGA TAAGTCTGTC GGAACGTTTT AGGACTAATG
251 CCGAAGTCGA GATGGATGCT CATTACTTCC CCTTACTCAG AAAATATTTA
301 AAATTTATAA TGTTACATAT ATTTACAAAT ATTAAAGTTT TTTWTGTGT
351 GTGCGTCAAG GAATTGTTGA CAATTTTAGT TAAAAATTG TCTCCAAACG
401 GAAAAAAGCG GTTTGTTTTT TGTGTGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1594; ORF 547>:

m547 . pep

```

1  MFVDNGFNKT VASFAQIVET FDVFFFRNDC AFFTQMKQRC GWVCSLVYLV
51  DIFPRCGFEI PNRSFKELGL LIQISLSERF RTNAEVEMDA HYFPLLRKYL
101 KFIMLHIFTN IKVFXCVCK ELLTILVKNLSPNGKKRFVF CC*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 547 shows 97.2% identity over a 142 aa overlap with a predicted ORF (ORF 547.ng) from *N. gonorrhoeae*:

m547/g547

825

	10	20	30	40	50	60
m547.pep	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
g547	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFTRCGFEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m547.pep	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYPLLRKYLKFIMLHIFTNIKVFXCVCVK					
g547	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYPLLRKYLKFIMLHIVTNIRVF-CVCVK					
	70	80	90	100	110	
	130	140				
m547.pep	ELLTILVKNLSPNGKKRFVFCCX					
g547	ELLTILVKNLSPNGKKRFVFCCX					
	120	130	140			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1595>:

```

a547.seq
  1  ATGTCGTAG ATAACGGATT TAATAAACG GTAGCGAGTT TTGCCCAAAT
 51  CGTCGAAACT TTCGACGTAT TCTTCTTTAG GAACAATTGC ACCTTTTSTA
101  CGCAGATGAA ACAGCGGTGC GGTGGGTCT GCTCGTTGGT ATATCTCGTT
151  GATATCTTTC CAAGATGCGG CTTCGAGATT CCGAACCGCT CCTTTAAAGA
201  GCTTGGGCTT TTGATACAGA TAAGTCTGTC GGAACGTTT AGGACTAATG
251  CCGAAGTCGA GATAGATGCT CATTACTTCC CCTTACTCAG AAAATATTTA
301  AAATTTATAA TGTTACATAT ATTTACAAAT ATTAAAGTTT TTTT.TGTGT
351  GTGCGTCAAG GAATTGTTGA CAATTTTAGT T

```

This corresponds to the amino acid sequence <SEQ ID 1596; ORF 547.a>:

```

a547.pep
  1  MFVDNGFNKT VASFAQIVET FDVFFFRNNC TFFTQMKQRC GWVCSLVYLV
 51  DIFPRCGFEI PNRSFKELGL LIQISLSERF RTNAEVEIDA HYFPLLRKYL
101  KFIMLHIFTN IKVFXCVCVK ELLTILV

```

m547/a547 97.6% identity in 127 aa overlap

	10	20	30	40	50	60
m547.pep	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
a547	MFVDNGFNKTVASFAQIVETFDVFFFRNNTFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m547.pep	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYPLLRKYLKFIMLHIFTNIKVFXCVCVK					
a547	PNRSFKELGLLIQISLSERFRTNAEVEIDAHYPLLRKYLKFIMLHIFTNIKVFXCVCVK					
	70	80	90	100	110	120
	130	140				
m547.pep	ELLTILVKNLSPNGKKRFVFCCX					
a547	ELLTILV					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1597>:

```

g548.seq
  1  atgttttccg taccgcgttc ctttttgccg ggcgttttcg tacttgccgc
 51  gcttgccgcc tgcaaacctc aagacaacag tgcggcgcaa gccgcttctt
101  caagtgcacg cgcgcgggct gcggaatatg cggcaaaagg gcaaacgcgc
151  ggtacggata tgcgtaagga agacatcggc ggcgatttca cactgaccga
201  cggcgaaggc aagcctttca gcctgagcga tttgaaaggc aaggtcgtga
251  ttctgtcttt cggcttttac cactgtcccg atgtctgccc gacagggctt

```

826

```

301 ttgacgtaca gcgacacttt gaagcagttg ggcgggcagg ctaaggacgt
351 gaaagtgggtg ttcgtcagca tcgatccgga acgcgacacg cctgaaatca
401 tcggcaagta tgccaaacag ttcaatccgg actttatcgg tctgacggca
451 acgggcggcc aaaacctgcc ggtcatcaag cagcaatacc gcgtggtttc
501 tgccaaaatc aatcaaaaag acgacagcga aaactatttg gtcgaccact
551 cttccggtgc gtatcttatc gataaaaacg gtgaggttgc cattttctcg
601 cttacggaa gcgagccgga aacgattgct gccgatgtaa ggaccctgct
651 ctga

```

This corresponds to the amino acid sequence <SEQ ID 1598; ORF 548.ng>:

g548.pep

```

1 MFSVPRSFLP GVFLAALAA CKPQDNSAAQ AASSASAPA AENAAKPQTR
51 GTDMRKEDIG GDFLTLDGEG KPFSLSDLKG KVVILSFGFT HCPDVCPTGL
101 LTYSDTLKQL GGQAKDVKVV FVSIDPERDT PEIIGKYAKQ FNPDFIGLTA
151 TGGQNLPIVK QQYRVVSAKI NQKDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1599>:

m548.seq

```

1 ATGTTTTCCG TACCGCGTTC CTTTTTGCCG GCGTTTTTCG TACTTGCCGC
51 GCTTGCCGCC TGCAAACCTC AAGACAACAG TGCGGCGCAA GTCGCTTCTT
101 CAAGTGCATC CGCGTCGGCT GCGGAAATG CGGCAAAGCA AnACACGCGC
151 GGTACGGATA TGCGTAAGGA AGACATCGGC GGCGATTTCA CGCTGACCGA
201 CGGCGAAGGC AAGCCTTTCA ACCTGAGCGA TTTGAAAGGC AAGGTCGTGA
251 TTCTGTCTTT CGGCTTTACG CACTGTCCCG ATGTCTGCCC GACAGAGCTT
301 TTGACGTACA GCGACACGTT GAAGCAGTTG GGCGGCGAGG CTAAGGACGT
351 GAAAGTGGTG TTCGTCAGCA TCGATCCGGA ACGCGACACG CCTGAAATCA
401 TCGGCAAGTA TGCAAACAG TTCAATCCGG ACTTTATCGs TCTGACGGCA
451 ACGGGCGGCC AAAACCTGCC GGTCATCAAG CAGCAATACc GCGTGGTTTC
501 TGCCAAAGTC AATCAAAAmG ACGACAGCGA AAACATTTTG GTCGACCACT
551 CTTCCGGTGC GTATCTCATC GACAAAAACG GTGAGGTTGC CATTTTCTCG
601 CCTTACGGAA GCGAGCCGGA AACGATTGCT GCCGATGTAA GGACCCTGCT
651 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1600; ORF 548>:

m548.pep

```

1 MFSVPRSFLP GVFLAALAA CKPQDNSAAQ VASSASASA AENAAKQXTR
51 GTDMRKEDIG GDFLTLDGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTGL
101 LTYSDTLKQL GGQAKDVKVV FVSIDPERDT PEIIGKYAKQ FNPDFIXLTA
151 TGGQNLPIVK QQYRVVSAKV NQXDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTLL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 548 shows 95.9% identity over a 217 aa overlap with a predicted ORF (ORF 548.ng) from *N. gonorrhoeae*:

m548/g548

	10	20	30	40	50	60
m548.pep	MFSVPRSFLPGVFLAALAAACKPQDNSAAQVASSASASAAENAAKQXTRGTDMRKEDIG					
g548	MFSVPRSFLPGVFLAALAAACKPQDNSAAQAASSASAPAAENAAKPQTRGTDMRKEDIG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m548.pep	GDFLTLDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTELLTYSDTLKQLGGQAKDVKVV					
g548	GDFLTLDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTGLLTYSIDLKQLGGQAKDVKVV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m548.pep	FVSIDPERDTPEIIGKYAKQFNPDFIXLTATGGQNLPIVKQQYRVVSAKVNQXDDSENYL					
g548	FVSIDPERDTPEIIGKYAKQFNPDFIGLTATGGQNLPIVKQQYRVVSAKINQKDDSENYL					
	130	140	150	160	170	180

827

	190	200	210
m548.pep	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX		
g548	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX		
	190	200	210

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1601>:

```
a548.seq
1  ATGTTTTCCTG TACCGCGTTC CTTTTTGCCG GCGGTTTTTCG TACTTGCCGC
51  GCTTGCCGCC TGCAAACCTC AAGACAACAG TCGGGCGCAA GTCGCTTCTT
101 CAAGTGCATC CGCGTCGGCT GCGGAAAATG CGGCAAAGCC GCAAACGCGC
151 GGTACGGATA TGCCTAAGGA AGACATCGGC GCGGATTTC ACGTGACCGA
201 CGGCGAAGGC AAGCCTTCA ACCTGAGCGA TTTGAAAGGC AAGGTCGTGA
251 TTCTGTCTTT CGGCTTTACG CACTGTCCCG ATGTCTGCCC GACAGAGCTT
301 TTGACGTACA GCGACACGTT GAAGCAGTTG GCGGGGAGG CTAAGGACGT
351 GAAAGTGGTG TTCGTACGCA TCGATCCGGA ACGCGACACG CCTGAAATCA
401 TCGGCAAGTA TGCCAAACAG TTCAATCCGG ACTTTATCGG TCTGACGGCA
451 ACGGGCGACC AAAACCTGCC GGTCAATCAAG CAGCAATACC GCGTGGTTTC
501 TGCCAAAGTC AATCAAAAAG ACGACAGCGA AAACATTTTG GTCGACCACT
551 CTTCCGGTGC GTATCTCATC GACAAAAACG GTGAGGTTGC CATTTTCTCG
601 CCTTACGGAA GCGAGCCGGA AACGATTGCT GCCGATGTAA GGACCCTGCT
651 CTGA
```

This corresponds to the amino acid sequence <SEQ ID 1602; ORF 548.a>:

```
a548.pep
1  MFSVPRSFLP GVFVLAALAA CKPQDNSAAQ VASSSASASA AENAAKPQTR
51  GTDMRKEDIG GDFLTLDGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTL
101 LTYSDTLKQL GGQAKDVKV VFSIDPERDT PEIIGKYAKQ FNPDFIGLTA
151 TGDQNLPIVK QQYRVVSAKV NQKDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTLTX*
```

m548/a548 97.7% identity in 217 aa overlap

	10	20	30	40	50	60
m548.pep	MFSVPRSFLPGVFVLAALAAACKPQDNSAAQVASSSASASAENAAKQXTRGTDMRKEDIG					
a548	MFSVPRSFLPGVFVLAALAAACKPQDNSAAQVASSSASASAENAAKQXTRGTDMRKEDIG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m548.pep	GDFLTLDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTLTYSDTLKQLGGQAKDVKV					
a548	GDFLTLDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTLTYSDTLKQLGGQAKDVKV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m548.pep	FVSIDPERDTP EIIGKYAKQFNPDFIXLTATGGQNLPIVKQQYRVVSAKVNQXDDSENYL					
a548	FVSIDPERDTP EIIGKYAKQFNPDFIGLTATGDQNLPIVKQQYRVVSAKVNQXDDSENYL					
	130	140	150	160	170	180
	190	200	210			
m548.pep	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX					
a548	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1603>:

```
g550.seq
1  atgataacgg acaggtttca tctctttcat ttccagtat ctttcattta
51  tcaatctgac aacaaaatgc cgcctgaaaa cagttcagac ggcatthtaa
101 ccacaaacgg cttacagctt ccattcgccc aacttggcag cgtaagcttc
```

828

```

151 caaatctgca atcggacggg ttgccacgcc gctttccatc gctgcttttg
201 cggcagccgt agcgacgcga ggcagcaggc ggaatcgaa cggagtagga
251 atcaggtatt ccgcgccgaa ttcgaatttc ttaccgtaag cggcaaccac
301 ttcttcgggt acttcttcca tcgccaaatc tgccaaagca tacacgcagg
351 cgcgtttcat ttcttcggtt atggtgggtt cgccgacatc caacgcgccc
401 cggaagatga acgggaagca caatacgtt ttcacttggg tcgggaagtc
451 ggagcggccg gtaccgataa ccacgtcccg acgggtttct ttcgccagcg
501 gcggcaggat ttccggattc gggttggcca tggcgaacac gatggggttt
551 tcgttcacgt tgttcaacat ttcaggcgtc agcagggttg cgccggagag
601 gcccaagaag atgtctttgc cttaaccgc atcggaagt acgcgccggc
651 cggttcttcc aacggcgtag aatttttttg attcgtccat gcggtctttg
701 tcttcgcggg tttggtaaat cagcctttg gagttgcaa cggttacgtt
751 ttcacgtttc aagcccaaat ccagcagttg gttcaggcag gcaatcgcg
801 cggcacctgc gccggagcac accaaagtcg cttcttcgat ttacggccg
851 gtataacgca gggcggtcaa tacggcgggc gcggtaatga tggccgtgcc
901 gtgctggtca tcatgaaata cggggatttt gcagcgtttg cgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1604; ORF 550.ng>:

```

g550.pep
  1 MITDRFHLFH FVPSFIYQSD NKMPPENSSD GILTTNGLQL PFAQLGSVSF
 51 QICNRTGCHA AFHRCFGGSR SDARQQAGIE RSRNQVFRAE FEFLTVSGNH
101 FFGYFFHRQI CQSIHAGAFH FFVDGGCADI QRAPEDEREA QYVVLHVREV
151 GAAGTDNHVR TGFFRQRQD FRIRVGHGEH DGFFVHRVQH FRRQQVCAGE
201 AQEDVFAFNR IGKYAPAVVF NGVEFFGFVH AVFVFAGLVN HAFGVANGYV
251 FTFQAQIQQL VQAGNRGGTC AGAHQSRFFD FTAGITQGVQ YGGGGNDGRA
301 VLVIMKYGDF AAFA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1605>:

```

m550.seq (partial)
  1 ..GACGGCATCG GCAAGCACGC GCTGGCCGTT GTCTTCAATG GCGTAGAACT
 51 GTTTGGACTC GTCCATACGG TCTTTGTCTT CGCGGGTTTG GTAAATCACG
101 CCTTTGGAGT CGCAAACGGT CACGTTTTCG CGTTTCAAGC CCAAATCCAG
151 CAATTGGwTC AAGCAGGCAA TCGCGGCCGC ACCTGCGCCG GAACACACCA
201 AAGTCGCTTC TTCGATTTTA CGGCCGGTAA AACCGAkgGC GTTCAATACG
251 GCGGCGGCCG TAATGATGGC CGTGCCGTGC TGGTCGTCGT GGAATACGGG
301 GATTTTGCAG CGTTTGCCTA A

```

This corresponds to the amino acid sequence <SEQ ID 1606; ORF 550>:

```

m550.pep (partial)
  1 ..DGIGKHALAV VFNGVELFGL VHTVVFVAGL VNHAFGVANG HVFAFQAQIQ
 51 QLXQAGNRGR TCAGTHQSRF FDFTAGKTXG VQYGGGGNDG RAVLVVVEYG
101 DFAAFA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 550 shows ___% identity over a ___ aa overlap with a predicted ORF (ORF 550.ng) from *N. gonorrhoeae*:

```

m550/g550

m550.pep
                                     10      20      30
                                     DGIGKHALAVVFNGVELFGLVHTVVFVAGLVN
                                     |||:| ||||| |||:| |||:| |||:|
g550      DGFFVHRVQHFRROQVCAGEAQEDVFAFNRIGKYAPAVVFNGVEFFGFVHAVFVFAGLVN
           190      200      210      220      230      240

           40      50      60      70      80      90
m550.pep      HAFGVANGHVFAFQAQIQQLXQAGNRGRTCAGTHQSRFFDFTAGKTXGVQYGGGGNDGRA
           |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
g550      HAFGVANGYVFTFQAQIQQLVQAGNRGGTCAGAHQSRFFDFTAGITQGVQYGGGGNDGRA
           250      260      270      280      290      300

           100
m550.pep      VLVVVEYGDFAAFAX
           |||:| |||:| |||:| |||:|
g550      VLVIMKYGDFAAFAX

```

310

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1607>:

```
a550.seq
1   CTATATCAAT CTGACAGCAA AATGCCGCCT GAAAACAGTT CAGACGGCAT
51  TTTAACCGCA AACGGCTTAC AGCTTCCATT CGCTCAGCTT GGCAGCGTAA
101 GCTTCCAAAT CTGCAATCGG ACGGGTTGCC ACGCCGCTTT CCATCGCTGC
151 TTTGGCGGCA GCCGTAGCAA CGCGCGGCAG CAGGCGGGAA TCGAACGGAG
201 TCGGAATCAG GTATTCCGCG CCGAATTCAA ATTTCTTACC GTAAGCGGCA
251 ACCACTTCTT CGGTTACCTC TTCCATCGCC AAATCCGCCA AAGCATACAC
301 GCAGGCGCGT TTCATTTCTT CGTTGATGGT CGTCGCGCCG ACATCCAACG
351 CACCGCGGAA GATGAACGGG AAGCACAATA CATTGTTTAC TTGGTTCGGG
401 AAGTCGGAGC GGCCGGTACC GATAACCACG TCCGGACGGG TTTCTTTTCG
451 CAGCGGCGGC AGGATTTCGG GATTGCGGTT GCCCATAGCG AACACGATGG
501 GTTTTTCGTT CATGGTGTTT AGTATTTTCA GCGTCAGCAG GTTCGCGCCG
551 GAGAGGCCCA AGAAGATGTC TTTGCCTTTG ACGGCATCGG CAAGCACGCG
601 CTGGCCGTTG TCTTCAATGG CGTAGAACTG TTTGGACTCG TCCATACGGT
651 CTTTGTCTTC GCGGGTTTGG TAAATCACGC CTTTGGAGTC GCAAACGGTC
701 ACGTTTTTCG GTTTCAAGCC CAAATCCAGC AATTGGTTCA AGCAGGCAAT
751 CGCGGCCGCA CCTGCGCCGG AACACACCAA AGTCGCTTCT TCGATTTTAC
801 GGCCGGTAAA ACGCAGGGCG TTCAATACGG CAGCGGCGGT AATGATGGCC
851 GTGCCGTGCT GGTGCTCGTG GAATACGGGG ATTTTGCAGC GTTTGCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1608; ORF 550.a>:

```
a550.pep
1   LYQSDSKMPP ENSSDGILTA NGLQLPFAQL GSVSFQICNR TGCHAAFHRC
51  FGGSRSNARQ QAGIERSRNQ VFRAEFKFLT VSGNHFFGYL FHRQIRQSIH
101 AGAFHFVVDG RRADIQRTAE DEREAYIVH LVREVGAAAT DNHVRTGFFR
151 QRRQDFRIRV GHSEHDGFFV HGVQYFRRQQ VRAGEAQEDV FAFDGIGKHA
201 LAVVFNGVEL FGLVHTVFVF AGLVNHAFGV ANGHVFAFQA QIQQLVQAGN
251 RGRTCAGTHQ SRFFDFTAGK TQGVQYGS GG NDGRAVLVVV EYGDFAAFA*
```

m550/a550 97.2% identity in 106 aa overlap

				10	20	30
m550.pep				DGIGKHALAVVFNGVELFGLVHTVFVFAGL		
a550	EHDGFFVHGVQYFRRQQVRAGEAQEDVFAFDGIGKHALAVVFNGVELFGLVHTVFVFAGL					
	170	180	190	200	210	220
		40	50	60	70	80
m550.pep		VNHAFGVANGHVFAFQAQIQQLXQAGNRGRTCAGTHQSRFFDFTAGKTXGVQYGGGGNDG				
a550		VNHAFGVANGHVFAFQAQIQQLVQAGNRGRTCAGTHQSRFFDFTAGKTQGVQYGS GGNDG				
		230	240	250	260	270
						280
		100				
m550.pep		RAVLVVVEYGDFAAFAX				
a550		RAVLVVVEYGDFAAFAX				
		290	300			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1609>:

```
g552.seq
1   atgaagctga aaaccttggt attgcccttc gccgcactgg cattgtgtgc
51  caacgcattt gccgccccgc ccggcgacgc gtcgttggca cgttggctgg
101 atacgcagaa tttcgaccgg gatatagaaa aaaatatgat tgaaggcttt
151 aatgccggat ttaaaccgta tgcggacaaa gcccttgccg aaatgccgga
201 agcgaaaaaa gatcaggcgg cagaagcctt taatcgttat cgtgagaatg
251 ttttgaaaga tttgattacg cccgaagtga aacaggctgt ccgcaatacc
301 ttattgaaga atgcccggtg aatatacacg caagaagaaa ttgacggcat
351 gattgccttt tacggttcgc ctgtcgggtc gtccgtcggt gccaaaaatc
401 cgcgcctaat caagaaatcg atgagtgaat tagcggatc ttggactgca
```

830

451 ttgtcagggg aaatcgcgcg acatcatctg cccgagttta cggaagagtt
 501 acggcgcatc atctgcggcg gtatagtggg ttaa

This corresponds to the amino acid sequence <SEQ ID 1610; ORF552.ng>:

g552.pep

1 MKLKTLLLPF AALALCANAF AAPPGDASLA RWLDTQNFDR DIEKNMIEGF
 51 NAGFKPYADK ALAEMPEAKK DQAAEAFNRY RENVLKDLIT PEVKQAVRNT
 101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
 151 LSGKIARHHL PEFTEELRRI ICGGIVD*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1611>:

m552.seq (partial)

1 ..ATTAACTGA AAACCTTGTT ATTGCCCTTC GCCACGCTGG CATTGTGCAC
 51 CAATGCTTTT GCCGCCCCGC CCAGCGACGC GTCGTTGGCG CGTTGGCTGG
 101 ATACGCAGAA TTTTGACCGG GATATAGAAA AAAATATGAT TGAGGGCTTT
 151 AATGCCGGAT TTAAACCGTA TGCGGACAAA GCCCTTGCCG AAATGCCGGA
 201 AGCGAAAAAA GATCAGGCGG CAGAAGCCTT TAACCGTTAT CGTGAGAATG
 251 TTTTGAAAGA TTTGATTACG CCCGAAGTGA AACAGGCTGT CCGCAATACT
 301 TTATTGAAGA ATGCCCGTGA GATATACACG CAAGAAGAAA TTGACGGCAT
 351 GATTGCCTTT TACGGTTCGC CTGTCGGTCA GTCCGTCGTT GCCAAAAATC
 401 CGCGCTTAAT CAAGAAATCG ATGAGTGAAG TAGCGGTATC TTGGACTGCA
 451 TTGTCAGGGA AAATCGCGCA ACATCATCTG CCCGAGTTTA CGGAAGAGTT
 501 GCGGCGCATC ATCTGCGGCG GTAAAAATCC CGATGCGGGC TGTAACAACG
 551 CCGGACAGGT TGGGAAAAGG CATCAGAAAT AA

This corresponds to the amino acid sequence <SEQ ID 1612; ORF 552>:

m552.pep (partial)

1 ..IKLKTLLLPF ATLALCTNAF AAPPSDASLA RWLDTQNFDR DIEKNMIEGF
 51 NAGFKPYADK ALAEMPEAKK DQAAEAFNRY RENVLKDLIT PEVKQAVRNT
 101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
 151 LSGKIAQHHL PEFTEELRRI ICGKPNPDAG CKQAGQVGKR HQK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 552 shows 97.1% identity over a 174 aa overlap with a predicted ORF (ORF 552.ng) from *N. gonorrhoeae*:

m552/g552

	10	20	30	40	50	60
m552.pep	IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYADK					
g552	MKLKTLLLPFAALALCANAFAPPGDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYADK					
	10	20	30	40	50	60
m552.pep	ALAEMPEAKKDQAAEAFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
g552	ALAEMPEAKKDQAAEAFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
	70	80	90	100	110	120
m552.pep	YGSPVGQSVVAKNPRLIKKS MSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKPNPDAG					
g552	YGSPVGQSVVAKNPRLIKKS MSEIAVSWTALSGKIARHHLPEFTEELRRIICGGIVDX					
	130	140	150	160	170	
m552.pep	CKQAGQVGKRHQKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1613>:

a552.seq

1 ATTAACTGA AAACCTTGTT ATTGCCCTTC GCCACGCTGG CATTGTGCAC
 51 CAATGCTTTT GCCGCCCCGC CCAGCGACGC GTCGTTGGCG CGTTGGCTGG
 101 ATACGCAGAA TTTTGACCGG GATATAGAAA AAAATATGAT TGAGGGCTTT
 151 AATGCCGGAT TTAAACCGTA TGCGGACAAA GCCCTTGCCG AAATGCCGGA

831

```

201 AGCGAAAAAA GATCAGGCGG CAGAAGCCTT TAACCGTTAT CGTGAGAATG
251 TTTTGAAGA TTTGATTACG CCCGAAGTGA AACAGGCTGT CCGCAATACT
301 TTATTGAAGA ATGCCCGTGA GATATACACG CAAGAAGAAA TTGACGGCAT
351 GATTGCCTTT TACGGTTTCG CTGTCTCGTCA GTCCGTCGTT GCCAAAAATC
401 CGCGCTTAAT CAAGAAATCG ATGAGTGAAA TAGCGGTATC TTGGACTGCA
451 TTGTCAGGGA AAATCGCGCA ACATCATCTG CCCGAGTTTA CGGAAGAGTT
501 GCGGCGCATC ATCTGCGGCG GTAAAAATCC CGATGCGGGC TGTAACAACG
551 CCGGACAGGT TGGGAAAAGG CATCAGAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1614; ORF 552.a>:

```

a552.pep
  1 IKLKTLLLPF ATLALCTNAF AAPPSDASLA RWLDTQNFDR DIEKNMIEGF
 51 NAGFKPYADK ALAEMPEAKK DQAAEAFNRY RENVLKDLIT PEVKQAVRNT
101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRIKKS MSEIAVSWT
151 LSGKIAQHHL PEFTEELRRI ICGKKNPDAG CKQAGQVGKR HQK*

```

m552/a552 100.0% identity in 193 aa overlap

	10	20	30	40	50	60
m552.pep	IKLKTLLLPFATLALCTNAFAAPPSDASLARWLD	TQNFDRDIEKNMIEGFNAGFKPYADK				
a552	IKLKTLLLPFATLALCTNAFAAPPSDASLARWLD	TQNFDRDIEKNMIEGFNAGFKPYADK				
	10	20	30	40	50	60
	70	80	90	100	110	120
m552.pep	ALAEMPEAKKDQAAEAFNRYRENV	LKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF				
a552	ALAEMPEAKKDQAAEAFNRYRENV	LKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF				
	70	80	90	100	110	120
	130	140	150	160	170	180
m552.pep	YGSPVGQSVVAKNPRIKKS	MSEIAVSWTALSGKIAQHHLPEFTEELRRI	ICGKKNPDAG			
a552	YGSPVGQSVVAKNPRIKKS	MSEIAVSWTALSGKIAQHHLPEFTEELRRI	ICGKKNPDAG			
	130	140	150	160	170	180
	190					
m552.pep	CKQAGQVGKR	HQKX				
a552	CKQAGQVGKR	HQKX				
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1615>:

```

m552-1.seq
  1 TTGAATATTA AACTGAAAC CTTGTTATTG CCCTTCGCCA CGCTGGCATT
 51 GTGCACCAAT GCTTTTGCCG CCCCGCCAG CGACGCGTCG TTGGCGCGTT
101 GGCTGGATAC GCAGATTTT GACCGGGATA TAGAAAAAAA TATGATTGAG
151 GGCTTTAATG CCGGATTTAA ACCGTATGCG GACAAAGCCC TTGCCGAAAT
201 GCCGGAAGCG AAAAAAGATC AGCGGCAGAG AGCCTTTAAC CGTTATCGTG
251 AGAATGTTTT GAAAGATTG ATTACGCCG AAGTGAAACA GGCTGTCCGC
301 AATACTTTAT TGAAGAATGC CCGTGAGATA TACACGCAAG AAGAAATTGA
351 CGGCATGATT GCCTTTTACG GTTCGCCTGT CGGTCAGTCC GTCGTTGCCA
401 AAAATCCGCG CTTAATCAAG AAATCGATGA GTGAAATAGC GGTATCTTGG
451 ACTGCATTGT CAGGGAAAAT CGCGCAACAT CATCTGCCCG AGTTTACGGA
501 AGAGTTGCGG CGCATCATCT GCGGCGGTAA AAATCCCGAT GCGGGCTGTA
551 AACAGCCCG ACAGGTTGGG AAAAGGCATC AGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1616; ORF 552-1>:

```

m552-1.pep
  1 LNIKLTLLL PFATLALCTN AFAAPPSDAS LARWLDQNF DRDIEKNMIE
 51 GFNAGFKPYA DKALAEMPEA KKDQAAEAFN RYRENVKDL ITPEVKQAVR
101 NTLLKNAREI YTQEEIDGMI AFYGSVPVQS VVAKNPRIK KSMSEIAVSW
151 TALSGKIAQH HLPEFTEELR RIICGKKNPD AGCKQAGQVG KRHQK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1617>:

a552-1.seq

832

```

1  TTGAATATTA AACTGAAAAC CTTGTTATTG CCCTTCGCCA CGCTGGCATT
51  GTGCACCAAT GCTTTTGCCG CCCC GCCCAG CGACGCGTCG TTGGCGCGTT
101 GGCTGGATAC GCAGAATTTT GACCGGGATA TAGAAAAAAA TATGATTGAG
151 GGCTTTAATG CCGGATTTAA ACCGTATGCG GACAAAGCCC TTGCCGAAAT
201 GCCGGAAGCG AAAAAAGATC AGGCGGCAGA AGCCTTTAAC CGTTATCGTG
251 AGAATGTTTT GAAAGATTG ATTACGCCCG AAGTGAAACA GGCTGTCCGC
301 AATACTTTAT TGAAGAATGC CCGTGAGATA TACACGCAAG AAGAAATTGA
351 CGGCATGATT GCCTTTTACG GTTCGCCTGT CGGTCAGTCC GTCGTTGCCA
401 AAAATCCGCG CTTAATCAAG AAATCGATGA GTGAAATAGC GGTATCTTGG
451 ACTGCATTGT CAGGGAAAAT CGCGCAACAT CATCTGCCCG AGTTTACGGA
501 AGAGTTGCGG CGCATCATCT GCGGCGGTAA AAATCCCGAT GCGGGCTGTA
551 AACAAGCCGG ACAGGTTGGG AAAAGGCATC AGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1618; ORF 552-1.a>:

a552-1.pep

```

1  LNIKLKTL LL PFATLALCTN AFAAPPSDAS LARWLDTQNF DRDIEKNMIE
51  GFNAGFKPYA DKALAEMPEA KKDQAAEAFN RYRENVLKDL ITPEVKQAVR
101 NTLLKNAREI YTQEEIDGMI AFYGSPVQGS VVAKNPRLIK KSMSEIAVSW
151 TALSGKIAQH HLPEFTEELR RIICGGKNPD AGCKQAGQVG KRHQK*

```

a552-1/m552-1 100.0% identity in 195 aa overlap

	10	20	30	40	50	60
a552-1.pep	LNIKLKTL LL PFATLALCTN AFAAPPSDAS LARWLDTQNF DRDIEKNMIE GFNAGFKPYA					
m552-1	LNIKLKTL LL PFATLALCTN AFAAPPSDAS LARWLDTQNF DRDIEKNMIE GFNAGFKPYA					
	10	20	30	40	50	60
a552-1.pep	DKALAEMPEAK KDQAAEAFN RYRENVLKDL ITPEVKQAVR NTLLKNAREI YTQEEIDGMI					
m552-1	DKALAEMPEAK KDQAAEAFN RYRENVLKDL ITPEVKQAVR NTLLKNAREI YTQEEIDGMI					
	70	80	90	100	110	120
a552-1.pep	DKALAEMPEAK KDQAAEAFN RYRENVLKDL ITPEVKQAVR NTLLKNAREI YTQEEIDGMI					
m552-1	DKALAEMPEAK KDQAAEAFN RYRENVLKDL ITPEVKQAVR NTLLKNAREI YTQEEIDGMI					
	70	80	90	100	110	120
a552-1.pep	AFYGSPVQGS VVAKNPRLIK KSMSEIAVSW TALSGKIAQH HLPEFTEELR RIICGGKNPD					
m552-1	AFYGSPVQGS VVAKNPRLIK KSMSEIAVSW TALSGKIAQH HLPEFTEELR RIICGGKNPD					
	130	140	150	160	170	180
a552-1.pep	AFYGSPVQGS VVAKNPRLIK KSMSEIAVSW TALSGKIAQH HLPEFTEELR RIICGGKNPD					
m552-1	AFYGSPVQGS VVAKNPRLIK KSMSEIAVSW TALSGKIAQH HLPEFTEELR RIICGGKNPD					
	130	140	150	160	170	180
a552-1.pep	AGCKQAGQVG KKRHQKX					
m552-1	AGCKQAGQVG KKRHQKX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1619>:

g553.seq

```

1  atggattatc tgcaaaacct gtctttgggc ttgacaaaaa agctgcccgt
51  tatactgcaa acagaagtag cggagtgtgg ctggcatgtg ctagcggctg
101 tggccggatt ttatggtttc tatacggatt tgcgcgcact gcgttcaaaa
151 tactgtctgt cacttaaggg tgagaatttg gcagatattg ttcgttttgc
201 tgatgatatg gggctgacgg gacgggctgt gaggtggat ttagacgaat
251 tgggcagttt gcgcctgccc tgtattctac attgggattt gaatcatttt
301 gtggtgctgg aatcggatc ttcggacggg gctgccgtca tggatccggc
351 ttcgggacga cgaaagtca agacggagga aatatcgcg aagtttacgg
401 gaattgtctt ggaactgtgg ccaaacacgc gtctcgaggc aggggaagaa
451 aagcaggaat tccgcatact acccatgttg cgcgggattt ctgggctggg
501 gcggacattg tttcagcttt tggctttggc agcagcaatg gaagtgtttg
551 cttttttaca aaacgtcagc ttcaagatcg gacgtggtga atcgcttgcg
601 ttaatcggac gatcgggctg cggtaaactg acacttttgg atattttaag
651 cggcaatcta cctcccgaat caggcaaatg catgataaat gggcacgaca
701 ttacagctt accgccacct ttattccgc aatttgagtg cgatggtcaa
751 ggcaggacga tgttttatag tggattaaat ttaaacgggt ag

```

This corresponds to the amino acid sequence <SEQ ID 1620; ORF 553.ng>:

g553.pep

833

```

1 MDYLQNLSLG LTKKLPVILQ TEVAECGLAC LAAVAGFYGF YTDLRALRSK
51 YCLSLKGENL ADIVRFADDM GLTGRALRLD LDELGSLRLP CILHWDNLNHF
101 VVLESVSSDG AAVMDPASGR RKVKTEEISR KFTGIALELW PNTRFEAGEE
151 KQEIRILPML RGISGLGRTL FQLLALAAAM EVFAFLQNVS FKIGRGESLA
201 LIGRSGCGKS TLLDILSGNL PPESGKVMIN GHDIYSLPPP FIPQFECDGQ
251 GRTMFYSLN LNR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1621>:

```

m553.seq (partial)
1 ATGGATTATT TATCAAGACT GTCCTTTGGA TTTAACAAAA AGCTACCTGT
51 CATTCTGCAA ACAGAAGTTG CTGAATGTGG TTTAGCATGC CTGACATCCA
101 TCTTGTCCTA TTATGGCTTT CACACTGATT TAAGAACGTT ACGCCAAAAA
151 TACACCCTGT CATTAAAGGG CGCAAATCTT GCAGACATCA TGAGATTGG
201 CAATGAAATG AATTTAACGC CACGAGCTTT GCGTTTAGAG TTAGATGAGC
251 TGTCAAATTT ACAACTACCC TGCATTCTCC ATTGGAACTT AAACCATTTT
301 GTTGTACTTT GTTCCATTTC CAAAGACAGT ATCGTCATTA TGGACCCTGC
351 TGTCGGTATG CGAAAAATCA AAATGGACGA AGTTTCACAA AAATTACAG
401 GGATTGCCCT AGAATTATTC CCAATACCC ATTTTGAAGA GAAAAAGAA
451 ACAAAGAAAA TCAAATATT ATCTCTATTA AGGGGGGG.T CAGGCTTAAA
501 ACGCTCTTTA ATCAAATGC TTATATTAGC TATTTCTTTG GAAGTCTTTG
551 CATTG...

```

This corresponds to the amino acid sequence <SEQ ID 1622; ORF 553>:

```

m553.pep (partial)
1 MDYLSRLSFG FNKKLPVILQ TEVAECGLAC LTSILSYYG FHTDLRTLQK
51 YTLSLKGANL ADIMRFGNEM NLTPRALRLE LDELNLQLP CILHWNLNHF
101 VVLSISKDS IVIMDPAVGM RKIKMDEV SQKFTGIALELF PNTHFEKKKE
151 TKKIKILSL RGSXGLKRSL IQMLILAISL EVFAL...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 553 shows 65.5% identity over a 185 aa overlap with a predicted ORF (ORF 553.ng) from *N. gonorrhoeae*:

m553/g553

	10	20	30	40	50	60
g553.pep	MDYLQNLSLGLTKKLPVILQTEVAECGLACLA	AAVAGFYGFYTDLRALRSKYCLSLKGENL				
m553	MDYLSRLSFGFNKKLPVILQTEVAECGLACL	LTSILSYYG FHTDLRTLQK YTLSLKGANL				
	10	20	30	40	50	60
g553.pep	ADIVRFADDMGLTGRALRLDLDELGSLRLP	CILHWDNLNHFVVLESVSSDGAAVMDPASGR				
m553	ADIMRFGNEMNLTPRALRLELDELNLQLP	CILHWNLNHFVVVLSISKDSIVIMDPAVGM				
	70	80	90	100	110	120
g553.pep	RKVKTEEISRKFTGIALELWPNTRFEAGEEK	QEIRILPMLRGISGLGRTLFQLLALAAAM				
m553	RKIKMDEV SQKFTGIALELF PNTHFEKKET	KKIKILSLLRGSXGLKRSLIQMLILAISL				
	130	140	150	160	170	180
g553.pep	EVFAFLQNVSFKIGRGESLALIGRSGCGKST	LDDILSGNLPPESGKVMINGHDIYSLPPP				
m553	EVFAL					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1623>:

```

a553.seq
1 ATGCCCCATC TGCAAAACCT GTCTTTGGGC TTAAAGAAAA AGCTGCCTGT
51 TATCCTGCAA ACAGAAATAT CAGAATGCGG CTTGGCATGT CTGGCGGCTG
101 TGGCGGGATT TCATGGTTTC CATACGAATT TACGCGCACT GCGTTCAAAA
151 TAC

```

This corresponds to the amino acid sequence <SEQ ID 1624; ORF 553.a>:

```
a553.pep
      1  MPHQLQNLSLG LKKKLPVILQ TEISECGLAC LAAVAGFHGF HTNLRALRSK
     51  Y
```

m553/a553 62.7% identity in 51 aa overlap

	10	20	30	40	50	60
m553.pep	MDYLSRSL	SFGFNKKLPVILQTEVAECGLAC	TSILSYGFHTDLRTL	RQKYTL	SLKGANL	
	: : : ::	::	::	::	::	::
a553	MPHQLQNLSLG	LKKKLPVILQTEISECGLAC	LAAVAGFHGFHTNLRALRSKY			
	10	20	30	40	50	
	70	80	90	100	110	120
m553.pep	ADIMRFGNEMNLT	PRALRLELDEL	SNLQLPCILHWN	LNHFVVLCSISKDS	SIVIMDPAVGM	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1625>:

```
g554.seq..
      1  atgacagcac ataaaatcct gcccgtcctt cttcccatca tcttaggcgt
     51  ttctcacgca acggctgcat cgcccgcgcc caacagaccg acggtacacg
    101  ccgccccac gctccaaaca cccgaaaccc tcacggcggc acacatcggt
    151  atcgaccttc aaagcaggca gactttatcc gccaaaaaca ccaatacccc
    201  tgtcgaaccg gcggcactaa cccaactgat gaccgcata tgggttttca
    251  aaaacatgaa atcgggaaat atccaatctg aagaaaactt aaaaataccc
    301  gaatccgcat gggcttcaga aggaagcaga atgtttgtac gtcccggcga
    351  tacggtcagc accgacaaac tcttaaaagg catgattgcc ctatgcgcaa
    401  acgatgccgc cctaaccctt gccgaccggc tgggcaacgg ctcgattgaa
    451  aattttgtgc aacaaatgaa caaagaagcc cgacgcttgg gcatgaagaa
    501  caccgtattc aaaaaccgca caggcttggg tagagaagga cagggtttcca
    551  ccgccaaga cctctccctg ctgtctgaag cattgatgcg cgactttccg
    601  gaattattac cgctgttttc catcaaactg ttcaagtgtt aaaaacataga
    651  acaaaacaac cgcaatatcc ttttatatag ggacaacaat gtaaacggcc
    701  tgaaagccgg gcacacagaa agcggcggtt acaaccttgc cgtgtcatac
    751  tccggcaacg gcaggcacat ccttgtcatc acactaggtt cggaatcggc
    801  ggaaaccgca gcacacagaa acagcaagct gctgaaccgg gcattgcagg
    851  ccttcgatac gcccaaaata tatccgaaag gcaaaaccgt tgcccaaatc
    901  caaatttccg gaggcagcaa aaaaaccgtc cgcgagggtt tcctcaaaga
    951  agcctacatc actctgccac ataaagaagc gaaaatggca gaacagattt
   1001  tggaaccat acagccgatt cccgccccgg taaaaaaagg gcagatttta
   1051  ggaaaaatca aaatcaggca aaacggacat accattgccg aaaaagaaat
   1101  cgtcgcactg gaaaacgtag aaaaaagaag ccggtggcaa aggccttggg
   1151  cgctctgac agggcagtaa
```

This corresponds to the amino acid sequence <SEQ ID 1626; ORF 554.ng>:

```
g554.pep..
      1  MTAHKILPVL LPIILGVSHA TAASPAPNRP TVHAAPTLLQ PETLTAAHIV
     51  IDLQSRQTL AKNTNTPVEP AALTQLMTAY LVFKNMKSGN IQSEENLKIP
    101  ESAWASEGSR MFVRPGDTVS TDKLLKGMIA LCANDAALTL ADRLGNGSIE
    151  NFVQQMNKEA RRLGMKNTVF KNPTGLGREG QVSTAKDLSL LSEALMRDFP
    201  EYYPLFSIKS FKFNIEQNN RNILLYRDNN VNGLKAGHTE SGGYNLAVSY
    251  SGNRHLVI TLGSESAETR ASDNSKLLNR ALQAFDTPKI YPKGKTVAQI
    301  QISGGSKKTV RAGFLKEAYI TLPHEAKMA EQILETIQPI PAPVKKGQIL
    351  GKIKIRQNGH TIAEKEIVAL ENVEKRSRWQ RLWTRLTGQ*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1627>:

```
m554.seq..
      1  ATGACAGCAC ATAAAATCCT GCCCGTCCTG CTTTCCATCA TCTTAGGCGT
     51  TTCTCAGGCA ACGGCTGCAT CGCCCGCGCC CAACAGACCG ACGGTACACG
    101  CCGCCCCAC GTTCCAAACA CCGGAAACCC TCACAGCGGC ACACATCGTT
    151  ATCGACCTTC AAAGCAAACA GATTTTATCC GCCAAAAACA TCAATACCCC
    201  TGTGTAACCG GCGGCACTAA CCCAACTGAT GACCGCATAT CTGGTTTTC
    251  AAAACATGAA ATCGGGCAAT ATCCAATCTG AAGAAAACCT AAAAATACCC
```

835

```

301 GAATCCGCAT GGGCTTCAGA AGGAAGCAGA ATGTTTGTAC GTCCCGGCGA
351 TACGGTCAGC ACCGACAAAC TCTTAAAAGG CATGATTGCA CTATCCGCAA
401 ACGATGCCGC CCTAACCCCTT GCCGGCCGCG TGGGCAACGG CTCGATTGAA
451 AATTTTGTGC AACAAATGAA CAAAGAAGCC CGACGCTTGG GCATGAAGAA
501 CACTGTATTC AAAAACCCGA CAGGCTTGAG TAGAGAAGGA CAGGTTTCCA
551 CCGCCAAAGA CCTCGCCCTG CTGTCTGAAG CATTGATGCG CGACTTTCCG
601 GAATATTACC CGCTGTTTTT CATCAAATCT TTCAAATTCA AAAATATAGA
651 ACAAAACAAC CGCAATATCC TTTTATATAG GGACAACAAT GTAAACGGTC
701 TGAAAGCCGG ACACACAGAA AGCGGCGGCT ACAACCTTGC CGTGTCATAC
751 TCCGGCAACG GCAGGCACAT CCTTGTCATC ACATTGGGTT CGGAATCGGC
801 GGAAACACGC GCATCAGACA ACAGCAAGCT GCTGAACTGG GCATTGCAGG
851 CCTTCGATAC GCCCAAATA TATCCGAAAG GCAAAACCGT TGCCCAAATC
901 CAAATTTCCG GAGGCAGCAA AAAAACCGTC CGCGCAGGCT TCCTCAAAGA
951 AGCCTACATC ACTCTGCCAC ATAAGGAAGC GAAAATGGCA GAACAAATTC
1001 TAGAAACCAT ACAGCCGATT CCCGCCCCAG TAAAAAAGG GCAAATTTTA
1051 GGAAAAATCA AAATCAGACA AAACGGATAC ACCATTGCCG AAAAAGAAAT
1101 CGTCGCACTG GAAAATGTAA AAAAAAGAAG CCGGTGGCAA AGGCTTTGGG
1151 CGTGTCTGAC AGGGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1628; ORF 554>:

m554.pep..

```

1  MTAHKILPVL LSIILGVSHA TAASPAPNRP TVHAAPTFTQ PETLTAAHIV
51  IDLQSKQILS AKNINTPVEP AALTQLMTAY LVFKNMKSGN IQSEENLKIP
101 ESAWASEGSR MFVRPGDTV TDKLLKGMIA LSANDAALTL AGR LGNSIE
151 NFVQOMNKEA RRLGMKNTVF KNPTGLSREG QVSTAKDLAL LSEALMRDFP
201 EYYPLFSIKS FKFKNIEQNN RNILLYRDNN VNGLKAGHTE SGGYNLAVSY
251 SGNRHLILVI TLGSESAETR ASDNSKLLNW ALQAFDTPKI YPKGKTVAQI
301 QISGGSKKT V RAGFLKEAYI TLPHEAKMA EQILETIQPI PAPVKKGQIL
351 GKIKIRQNGY TIAEKEIVAL ENVKRSRWQ RLWACLTGQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 554 shows 96.1% identity over a 389 aa overlap with a predicted ORF (ORF 554.ng) from *N. gonorrhoeae*:

m554/g554

```

          10      20      30      40      50      60
m554.pep  MTAHKILPVLLSIILGVSHATAASPAPNRP TVHAAPTFTQ PETLTAAHIVIDLQSKQILS
          |||||
g554      MTAHKILPVLLPIILGVSHATAASPAPNRP TVHAAPTFTQ PETLTAAHIVIDLQSRQTL
          10      20      30      40      50      60

          70      80      90      100     110     120
m554.pep  AKNINTPVEPAALTQLMTAYLVFKNMKSGNIQSEENLKIPESAWASEGSRMFVRPGDTV
          |||
g554      AKNTNTPVEPAALTQLMTAYLVFKNMKSGNIQSEENLKIPESAWASEGSRMFVRPGDTV
          70      80      90      100     110     120

          130     140     150     160     170     180
m554.pep  TDKLLKGMIALSANDAALTL AGR LGNSIENFVQOMNKEARRLGMKNTVFNPTGLSREG
          |||||
g554      TDKLLKGMIALCANDAALTLADRLGNSIENFVQOMNKEARRLGMKNTVFNPTGLGREG
          130     140     150     160     170     180

          190     200     210     220     230     240
m554.pep  QVSTAKDLALLSEALMRDFPEYYPLFSIKSFKFNIEQNRRNILLYRDNNVNGLKAGHTE
          |||||
g554      QVSTAKDLSLLSEALMRDFPEYYPLFSIKSFKFNIEQNRRNILLYRDNNVNGLKAGHTE
          190     200     210     220     230     240

          250     260     270     280     290     300
m554.pep  SGGYNLAVSYSGNRHLILVITLGSESAETRASDNSKLLNWALQAFDTPKIYPKGKTVAQI
          |||||

```

836

```

g554      SGGYNLAVSYSGNGRHILVITLGSESAETRASDNSKLLNRLQAFDTPKIYPKGKTVAQI
           250      260      270      280      290      300
           310      320      330      340      350      360
m554 . pep QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIAPVKKGQILGKIKIRQNGY
           |||||
g554      QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIAPVKKGQILGKIKIRQNGH
           310      320      330      340      350      360
           370      380      390
m554 . pep TIAEKEIVALENVKKRSRWQRLWACL TGQX
           |||||
g554      TIAEKEIVALENVEKRSRWQRLWTRLTGQX
           370      380      390

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1629>:

```

a554 . seq
1   ATGACAGCAC ATAAAATCCT GCCCGTCCTG CTTTCCATCA TCTTAGGCGT
51  TTCTCACGCA ACGGCTGCAT CGCCCCGCGC CAACAGACCG ACGGCACACG
101 CCGCCCCCAC GTTCCAAACA CCCGAAACCC TCACAGCGGC ACACATCGTT
151 ATCGACCTTC AAAGCAAACA GATTTTATCC GCCAAAACA TCAATACCCC
201 TGTGGAACCG GCGGCACTAA CCCAACTGAT GACCGCATAT CTGGTTTTC A
251 AAAACATGAA ATCGGGAAAT ATCCGATCTG AAGAAAACCT AAAAATACCC
301 GAATCCGCAT GGGCTTCAGA AGGAAGCAGA ATGTTGTGAC GTCCCGCGCA
351 TACGGTCAGC ACCGACAAAC TCTTAAAGG CATGATTGCA CTATCCGCAA
401 ACGATGCCGC CCTAACCCTT GCCGGCCGGC TGGGCAACGG CTCGATTGAA
451 AATTTTGTGC AACAAATGAA CAAAGAAGCC CGACGCTTGG GCATGAAGAA
501 CACTGTATTC AAAAATCCGA CAGGCTTGAG TAGAGAAGGA CAGGTTTCCA
551 CCGCCAAAGA CCTCGCCCAG CTGTCTGAAG CATTGATGCG CGACTTTCGG
601 GAATATTACC CGCTGTTTTT CATCAAATCT TTCAAATTCA AAAATATAGA
651 GCAAAACAAC CGCAATATCC TTTTATATAG GGACAACAAT GTAAACGGTC
701 TGAAAGCCGG ACACACAGAA AGCGGCGGCT ACAACCTTGC CGTGTCTATC
751 TCCGGCAACG GCAGGCACAT CCTTGTCTATC ACATTGGGTT CGGAATCGGC
801 GGAAACACGC GCATCAGACA ACAGCAAGCT GCTGAACTGG GCATTGCAAG
851 CCTTCGATAC GCCCAAATA TATCCGAAAG GCAAAACCGT TGCCCAAATC
901 CAAATTTCCG GAGGCAGCAA AAAAACCCTC CGCGCAGGCT TCCTCAAAGA
951 AGCCTACATC ACTCTGCCAC ATAAGGAAGC GAAAATGGCA GAACAAATTC
1001 TAGAAACCAT ACAGCCGATT CCCGCCCCAG TAAAAAAGG GCAAATTTTA
1051 GGAAAAATCA AAATCAGACA AAACGGATAC ACCATTGCCG AAAAAGAAAT
1101 CGTCGCACTG GAAAATGTAA AAAAAAGAAG CCGGTGGCAA AGGCTTTGGG
1151 CGTGTCTGAC AGGGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1630; ORF 554.a>:

```

a554 . pep
1   MTAHKILPVL LSIILGVSHA TAASPAPNRP TAHAAPTFTQ PETLTAAHIV
51  IDLQSKQILS AKNINTPVEP AALTQLMTAY LVFKNMKS GN IRSEENLKIP
101 ESAWASEGSR MFVRPGD TVS TDKLLKGMIA LSANDAAL TL AGR LGNGSIE
151 NFVQQMKEA RRLGMKNTVF KNPTGLSREG QVSTAKDLAQ LSEALMRDFP
201 EYYPLFSIKS FKFKNIEQNN RNILLYRDNN VNGLKAGHTE SGGYNLAVSY
251 SGNRHILVI TLGSESAETR ASDNSKLLNW ALQAFDTPKI YPKGKTVAQI
301 QISGGSKKT V RAGFLKEAYI TLPHEAKMA EQILETIQPI PAPVKKGQIL
351 GKIKIRQNGY TIAEKEIVAL ENVKKRSRWQ RLWACL TGQ*

```

m554/a554 99.2% identity in 389 aa overlap

```

           10      20      30      40      50      60
m554 . pep MTAHKILPVLLSIILGVSHATAASPAPNRP TVHAAPTFTQ PETLTAAHIVIDLQSKQILS
           |||||
a554      MTAHKILPVLLSIILGVSHATAASPAPNRP TAHAAPTFTQ PETLTAAHIVIDLQSKQILS
           10      20      30      40      50      60
           70      80      90     100     110     120
m554 . pep AKNINTPVEPAALTQLMTAYLVFKNMKS GN IQSEENLKIPESAWASEGSRMFVRPGD TVS
           |||||
a554      AKNINTPVEPAALTQLMTAYLVFKNMKS GN IRSEENLKIPESAWASEGSRMFVRPGD TVS

```

837

	70	80	90	100	110	120
	130	140	150	160	170	180
m554.pep	TDKLLKGMIALSANDAALTLAGRLGNGSIENFVQQMNKEARRLGMKNTVFKNPTGLSREG					
a554	TDKLLKGMIALSANDAALTLAGRLGNGSIENFVQQMNKEARRLGMKNTVFKNPTGLSREG					
	190	200	210	220	230	240
m554.pep	QVSTAKDLALLSEALMRDFPEYYPLFSIKSEFKFNIEQNNRNILLYRDNNVNLKAGHTE					
a554	QVSTAKDLAQLSEALMRDFPEYYPLFSIKSEFKFNIEQNNRNILLYRDNNVNLKAGHTE					
	250	260	270	280	290	300
m554.pep	SGGYNLAVSYSGNGRHILVITLGSESAETRASDNSKLLNWALQAFDTPKIYPKGKTVAQI					
a554	SGGYNLAVSYSGNGRHILVITLGSESAETRASDNSKLLNWALQAFDTPKIYPKGKTVAQI					
	310	320	330	340	350	360
m554.pep	QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIAPVKKGQILGKIKIRQNGY					
a554	QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIAPVKKGQILGKIKIRQNGY					
	370	380	390			
m554.pep	TIAEKEIVALENVKKRSRWQRLWACLTGQX					
a554	TIAEKEIVALENVKKRSRWQRLWACLTGQX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1631>:

g556.seq..

```

1  atggacaata agaccaaact gcgcttgggc ggcctgattt tactgaccac
51  cgccgtttta agcctcatta tcgtattgat tgcgattcc tggccgcttg
101 ccatacctgct tgccgccgctc atcgctcgccg ccgctgcggg cggctttggt
151 tggacatccc gccgacagca acgccagttt atcgacgctc tgaaaaaatt
201 cgacatcgat cccgaaaaag gcagaatcaa cgaggcaaac ctgcgccgta
251 tgtaccacag cggcgggacaa caccagaaag atgcgattac cctgatctgc
301 ctgtcgcaaa aatgttcggt ggacgaggcg cagctatgt tcaaaaaacg
351 cccgacacgt caggaaatca atcaaatggc ggcaaaacag tcgcgcggtc
401 agaaacgtcc gcaccgttaa

```

This corresponds to the amino acid sequence <SEQ ID 1632; ORF 556.ng>:

g556.pep.

```

1  MDNKTKLRLG GLILLTTAVL SLIIVLIVDS WPLAILLAIV IVAAAAGGFV
51  WTSRRQQRQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC
101 LSQKCSVDEA HAMFKKRPTTR QEINQMAAKQ SRGQKRPHR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1633>:

m556.seq..

```

1  ATGGACAATA AGACCAAACCT GCGCTTGGGC GGCCTGATTT TACTGACCAC
51  CGCCGTTTSTA AGCCTCATTA TCGTATTGAT TGTCGATTCC TGGCCGCTTG
101 CCATCCTGCT TGCAGCCGTC ATTGTCGCTG CCGCTGCGGG CGGTTTTGTT
151 TGGACATCCC GCCGACAGCA ACGCCAGTTT ATCGAACGCC TGAAAAAATT
201 CGACATCGAT CCCGAAAAAG GCAGAATCAA CGAGGCAAAC CTGCGCCGTA
251 TGTACCACAG CGGCGGACAA CACCAGAAAG ATGCGATTAC CCTGATCTGC
301 CTGTGCAAAA AATGTTTCGGT GGACGAGGCG CACGCTATGT TCAAAAAACG
351 CCCGACACGT CAGGAAATCA ATCAAATGGC GGCAAAACAG TCGCGCGGTC
401 AGAAACGTCC GCACCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1634; ORF 556>:

m556.pep..

```

1  MDNKTKLRLG GLILLTTAVL SLIIVLIVDS WPLAILLAIV IVAAAAGGFV
51  WTSRRQQRQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC

```

838

101 LSQKCSVDEA HAMFKKRPTR QEINQMAAKQ SRGQKRPHR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 556 shows 100.0% identity over a 139 aa overlap with a predicted ORF (ORF 556.ng) from *N. gonorrhoeae*:

m556/g556

	10	20	30	40	50	60
m556.pep	MDNKT	KLRLG	LILLT	TAVLS	LIIVL	IVDSW
g556	MDNKT	KLRLG	LILLT	TAVLS	LIIVL	IVDSW
	10	20	30	40	50	60
	70	80	90	100	110	120
m556.pep	IERLK	KFDID	PEKGR	INEAN	LRRMY	HSGGQ
g556	IERLK	KFDID	PEKGR	INEAN	LRRMY	HSGGQ
	70	80	90	100	110	120
	130	140				
m556.pep	QEINQ	MAAKQ	SRGQK	RPHRX		
g556	QEINQ	MAAKQ	SRGQK	RPHRX		
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1635>:

a556.seq

1	ATG	GACAATA	AGACCAA	ACT	GCGCT	TGGGC	GGCCT	GATTT	TACTG	ACCAC
51	CGC	CGTTT	TA	AGCCT	CATTA	TCGTAT	TGAT	TGTCG	ATTCC	TGGCC
101	CCAT	CCTGC	T	TGCCG	CCGTC	ATCGT	CGCCG	CCGCT	GCGGG	CGGCT
151	TGG	ACATCCC	GCCGAC	AGCA	ACGCC	AGTTT	ATCGA	ACGTC	TGAAAA	AATT
201	CGA	CATCG	AT	CCCGAAA	AAG	GCAGA	AATCA	CGAGG	CAAAC	CTGCG
251	TGT	ACCAC	AG	CGGCG	GACAA	CACCAA	AAAG	ATGCG	ATTAC	CCTGAT
301	CTGT	CGCAAA	AATGTT	CGGT	GGACG	AGGCG	CACGCT	TATGT	TCAAAA	AACG
351	CCC	GACAC	GT	CAGGA	AATCA	ATCAA	ATGGC	GGCAA	AACAG	TCGCG
401	AGAA	ACGTCC	GCACC	GTAA						

This corresponds to the amino acid sequence <SEQ ID 1636; ORF 556.a>:

a556.pep

1	MDNKT	KLRLG	GLILLT	TAVL	SLIIVL	IVDS	WPLAIL	LAIV	IVAAA	AGGFV
51	WTSRR	QQRQF	IERLK	KFDID	PEKGR	INEAN	LRRMY	HSGGQ	HQKDA	ITLIC
101	LSQK	CSVDEA	HAMFK	KRPTR	QEINQ	MAAKQ	SRGQK	RPHR*		

m556/a556 100.0% identity in 139 aa overlap

	10	20	30	40	50	60
m556.pep	MDNKT	KLRLG	LILLT	TAVLS	LIIVL	IVDSW
a556	MDNKT	KLRLG	LILLT	TAVLS	LIIVL	IVDSW
	10	20	30	40	50	60
	70	80	90	100	110	120
m556.pep	IERLK	KFDID	PEKGR	INEAN	LRRMY	HSGGQ
a556	IERLK	KFDID	PEKGR	INEAN	LRRMY	HSGGQ
	70	80	90	100	110	120
	130	140				
m556.pep	QEINQ	MAAKQ	SRGQK	RPHRX		
a556	QEINQ	MAAKQ	SRGQK	RPHRX		
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1637>:

g557.seq

```

1  atgaacaaaa tattccttac tgccgcagcc ttggtgctgg gcgcgtgcgg
51  tttccacctg aaaggtgcag acggcatttc tccgccgctg acctaccgga
101 gctggcacat cgaaggcggg caggcattgc aatttccttt ggaaaccgcg
151 ctgtatcagg cttcgggcag ggtggacgat gctgccggcg cgcagatgac
201 cctgcgtata gacagcgttt cccaaaacaa ggaaacctat accggttacc
251 gtgcggcagt catcaacgaa tatcttttga tattgacggt tgaagcgag
301 gtattgaaac gcggcgagcc ggtcggaaca ccgatgaccg tgtccgtccg
351 ccgcattttg gattatgccg acaacgaaat tttgggcaaa caggaagaag
401 aagaaacctt gtgggcggaa atgcggcagg atgttgccga acagattgtc
451 cgccgcctga cctttctgaa ggcggaatga

```

This corresponds to the amino acid sequence <SEQ ID 1638; ORF 557.ng>:

g557.pep..

```

1  MNKIFLTAAL LVLGACGFHL KGADGISPPL TYRSWHIEGG QALQFPLETA
51  LYQASGRVDD AAGAQMTRLI DSVSQNKETY TVTRAAVINE YLLILTVEAQ
101 VLKRGEFVGK PMTVSVRRIL DYADNEILGK QEEEEELWAE MRQDVAEQIV
151 RRLTFLKAE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1639>:

m557.seq..

```

1  ATGAACAAAC TGTTCCTTAC TGCCGCAGTG CTGATGCTGG GCGCGTGCGG
51  TTTCCACCTG AAAGGTGCAG ACGGCATTTC TCCGCCGCTG ACCTACCGGA
101 GCTGGCACAT CGAAGGCGGA CAGGCATTGC GGTTCCTTTT GGAAACCGCG
151 CTGTATCAGG CTCGGGCAG GGTGGACGAT GCTGCCGGCG CGCAGATGAC
201 CCTGCGTATA GACAGCGTTT CCCAAAACAA GGAAACCTAC ACCGTTACCC
251 GTGCGGCAGT CATCAACGAA TATCTTTTGA TATTGACGGT TGAAGCGCAG
301 GTATTGAAAC GCGGCGAGCC GGTGCGTAAA CCGATGACCG TGTCCGTCCG
351 CCGCGTCCTT GCTTATGCCG ACAACGAGAT CTTGGGCAAA CAGGAAGAGG
401 AAGCGGCATT GTGGGCGGAA ATGCGGCAGG ATGCCGCCGA ACAGATTGTC
451 CGCCGCCTGA CCTTCTGAA GCGGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1640; ORF 557>:

m557.pep..

```

1  MNKLFLTAAL LMLGACGFHL KGADGISPPL TYRSWHIEGG QALRFPLETA
51  LYQASGRVDD AAGAQMTRLI DSVSQNKETY TVTRAAVINE YLLILTVEAQ
101 VLKRGEFVGK PMTVSVRRVL AYADNEILGK QEEEAALWAE MRQDAAEQIV
151 RRLTFLKAE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 557 shows 94.3% identity over a 159 aa overlap with a predicted ORF (ORF 557.ng) from *N. gonorrhoeae*:

m557/g557

	10	20	30	40	50	60
m557.pep	MNKLFLTAALVLMGACGFHLKGADGISPPLTYRSWHIEGGQALRFPLETALYQASGRVDD					
	: :					
g557	MNKIFLTAALVLMGACGFHLKGADGISPPLTYRSWHIEGGQALQFPLETALYQASGRVDD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m557.pep	AAGAQMTRLIDSVSQNKETYTVTRAAVINEYLLILTVEAQVLKRGEFVGKPMTVSVRRVL					
g557	AAGAQMTRLIDSVSQNKETYTVTRAAVINEYLLILTVEAQVLKRGEFVGKPMTVSVRRIL					
	70	80	90	100	110	120
	130	140	150	160		
m557.pep	AYADNEILGKQEEEAALWAEMRQDAEQIVRRLTFLKAEX					
	:					
g557	DYADNEILGKQEEETLWAEMRQDVAEQIVRRLTFLKAEX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1641>:

840

```

a557.seq
  1 ATGAACAAAC TGTTTCTTAC TGCCGCAGTG CTGATGCTGG GCGCGTGCGG
 51 TTTCCACCTG AAAGGTGCAG ACGGCATTTC TCCGCCGCTG ACCTACCGGA
101 GCTGGCACAT CGAAGGCGGA CAGGCATTGC AGTTTCCTTT GGAAACCGCG
151 CTGTATCAGG CTTTCGGGTAG GGTGGACGAT GCTGCCGCGC CGCAGATGAC
201 CCTGCGTATA GACAGCGTTT CCAAAAACAA GGAAACCTAC ACCGTTACCC
251 GTGCGGCAGT CATCAACGAA TATCTTTTGA TATTGACGGT TGAAGCGCAG
301 GTATTGAAAC GCGGCGAGCC GGTCCGGCAA CCGATGACCG TGTCCTCCG
351 CCGCGTCCTT GCTTATGCCG ACAACGAGAT CTTGGGCAA CAGGAAGAGG
401 AAGCGGCATT GTGGGCGGAA ATGCGGCAGG ATGCCGCCGA ACAGATTGTC
451 CGCCGCCTGA CCTTCTGAA GCGGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1642; ORF 557.a>:

```

a557.pep
  1 MNKLFLTA AV LMLGACGFHL KGADGISPPL TYRSWHIEGG QALQFPLETA
 51 LYQASGRVDD AAGAQMTLRI DSVSQNKETY TVTRAAVINE YLLILTVEAQ
101 VLKRGE PVGK PMTVSVRRVL AYADNEILGK QEEEAALWAE MRQDAEQIV
151 RRLTFLKAE*

```

m557/a557 99.4% identity in 159 aa overlap

	10	20	30	40	50	60
m557.pep	MNKLFLTA	AVLMLGAC	GFHLKGAD	GISPPLTY	RSWHIEGG	QALRFPLE
a557	MNKLFLTA	AVLMLGAC	GFHLKGAD	GISPPLTY	RSWHIEGG	QALRFPLE
	10	20	30	40	50	60
	70	80	90	100	110	120
m557.pep	AAGAQMTL	RIDSVSQN	KETYTVTR	AAVINEYL	LLILTVEA	QVLKRGE
a557	AAGAQMTL	RIDSVSQN	KETYTVTR	AAVINEYL	LLILTVEA	QVLKRGE
	70	80	90	100	110	120
	130	140	150	160		
m557.pep	AYADNEIL	GKQEEEA	ALWAEMR	QDAEQIV	RRLTFLK	AEX
a557	AYADNEIL	GKQEEEA	ALWAEMR	QDAEQIV	RRLTFLK	AEX
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1643>:

```

g558.seq..
  1 ATGGATGCTT GTTTTTTCGT CATTCCCGCA CAGGCGGGAA TTCGGAGATT
 51 CGGGATTGTT TTCAAACGTT CGGGTCGGAT TCTTGCCGGT GCGGGAATGA
101 TGCCCTTATA TACTTTCTCC GAGCTTTATA TGCTTCAACA GGGGACGGCA
151 CATCAAGCAC CGCACTGCGT GTTGCCCGAA CGAGGCTGCC CTCCGATTAG
201 ATTCTATCGC TATAAACAGA CGGGTTTCAA CCGAAAAGGA ATGGGGATAA
251 AGTCCATTTT CGACACCTCT CGGGCGATGC CGTCTGAAAA CCAATCTCCA
301 CTTTCAGACG GCATTGTTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1644; ORF 558.ng>:

```

g558.pep..
  1 MDACFFVIPA QAGIRRFIV FKRSGRILAG AGMMPYTFE ELYMLQQGTA
 51 HQAPHCVLPE RGCPIRFYR YKQTGFNRKG MGIKSISDTS RAMPSNQSP
101 LSDGIV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1645>:

```

m558.seq..
  1 ATGAATGCTT GTTTTTTCGT CATTCCACAA CAGGCGGGAA TTCGGAGATT
 51 CGGGATTGTT TTCAAACGTT CGGGTCGGAT TCTTGCCGGT GCAGGAATGA
101 TGCCCTTATA TACTTTCTCC GAGCTTTATA TGTTTCAACA GGGGACGGCA
151 CATCAAGCAC CGCACTGCGT GTTGCCCGAA CGAGACTACC CTCCGATTAG
201 ATTCTATCGC CATAAACAGA CGGGTTTCAA CCGAAAAGGA ATGGGGATAA
251 AGTCCATTTT CGACATCTsT CGGGCGATGC CGTCTGAAAA CCAATCTCCA
301 CTTTCAGACG GCATTGTTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1646; ORF 558>:

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 558 shows 92.5% identity over a 106 aa overlap with a predicted ORF (ORF 558.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m558.pep	MNACFFVIPTQAGIRRFGIVFKRSGRILAGAGMMPLYTFSELYMFQQGT	AHQAPHCVLPE				
	:	:				
g558	MDACFFVIPAQAGIRRFGIVFKRSGRILAGAGMMPLYTFSELYMLQQGT	AHQAPHCVLPE				
	10	20	30	40	50	60
	70	80	90	100		
m558.pep	RDYPPIRFYRHKQTGFNRKGMGIKSISDIXRAMPSENQSPLSDGIVX					
g558	RGCPPIRFYRKQTGFNRKGMGIKSISDTSRAMPSENQSPLSDGIVX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1647>:

a558.seq

1	ATGAATGCTT	GTTTTTTCGT	CATTCCCACA	CAGGCGGGAA	TTCGGAGATT
51	CGGGATTGTT	TTCAAACGTT	CGGGTCGGAT	TCTTGCCGGT	GCGGGAATGA
101	TGCCCTTATA	TATAGTGGAT	TAAATTTAAA	TCAGGACAAG	GCGACGAAGC
151	CGCAGACAGT	ACAAATAGTA	CGGCAAGGCG	AGGCAACGCC	GTACTGGTTT
201	AAATTTAATC	CACTATACTT	TCTCCGAGCT	TTATATGTTT	CAACAGAGGA
251	CGGCACATCA	AGCACCGCAC	TGCGTGTTGC	CCGAACGAGA	CTGCCCTCCG
301	ATTAGATTCT	ATCGCTATAA	ACAGACGGGT	TTCAACCGAA	AAGGAATGGG
351	AATGAAGTCC	GTTTCCGACA	CCTCTCGGGC	GATGCCGTCT	GAAAACCAAT
401	CTCCACTTTC	AGACCGCATT	GTTTAG		

This corresponds to the amino acid sequence <SEQ ID 1648; ORF 558.a>:

a558.pep

1	MNACFFVIPT	QAGIRRFQIV	FKRSGRILAG	AGMMPLYIVD	*I*IRTRRRS
51	RRQYK*YGKA	RQRRTGLNLI	HYTFSELYMF	QORTAHQAPH	CVLPERDCPP
101	IRFYRYKQTG	FNRKGMGMKS	VSDTSRAMPS	ENQSPLSDGI	V*

m558/a558 70.2% identity in 141 aa overlap

```

                                10      20      30
m558.pep  MNACFFVIPTQAGIRRFGIVFKRSGRILAGAGMMPLY-----
          |||||
a558      MNACFFVIPTQAGIRRFGIVFKRSGRILAGAGMMPLYIVDXIXIRTRRRSRROYKXYGKA
          10      20      30      40      50      60

                                40      50      60      70      80
m558.pep  -----TFSELYMFQQGTAHQAPHCVLPERDYPPIRFYRHKQTGFNRKGMGIKS
          |||||
a558      RQRRTG LNL IHYTFSELYMFQQT AHQAPHCVLPERDC PPIRFYRYKQTGFNRKGMGMKS
          70      80      90      100     110     120

                                90      100
m558.pep  ISDIXRAMPSENQSPLSDGIVX
          :|| |||||
a558      VSDTSRAMPSENQSPLSDGIVX
          130     140

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEO ID 1649>:

g560.seq
1 atgctcatca tccgcaacct gatttactgg ctgatactct qttccagcct

842

```

51 gattttcctc tttcccttta tgctgctcgc ctcgcctttc cgggacgggg
101 cgcacaagat ggcgcgggtc tgggtcggca tcctcaactg gtcgctcaaa
151 cacatcgctc ggctcaaata ccgcatcatc ggcgcggaac acattccgga
201 ccgccccctc gtcattctgcg ccaaacacca aagcggctgg gaaacgctcg
251 cgctccaaga gattttttccg ccgcagggtt acgttgccaa gcgcgagttg
301 ttcaaaatcc cctttttcgg ctggggcttg aaactgggtc aaaccatagg
351 catagaccgc aacaaccgcc gcgaagccaa cgaacagctc ataaaacagg
401 gtttggcgcg caaaaacgaa ggttattgga ttaccatttt ccccgaaaggc
451 acgcgccttg cgcgggaaa acgcggcaaa tacaaactcg gcggcgcgcg
501 catggcgaaa atgtttgaga tggacatcgt ccccgctgcc ctcaacagcg
551 gcgaattttg gccgaaaaat tcctttctga aatatccggg ggaaatcacc
601 gtcattcatc gtccgaccat ccgcacgcga agcggcagcg aagccgaatt
651 gatggaaaaa tgcgaacacc tcattgaaac gcaacaaccg cttatttccg
701 gcgcaggccc gtttgccgcc gaaatgccgt ctgaaaccgc atga

```

This corresponds to the amino acid sequence <SEQ ID 1650; ORF 560.ng>:

g560.pep..

```

1 MLIIRNLIYW LILCSSLIFL FPFMLLASPF RDGAHKMARV WVGILNWSLK
51 HIVGLKYRII GAEHIPDRPS VICAKHQSGW ETLALQEIFP PQVYVAKREL
101 FKIPFFGWGL KLVKTIGIDR NNRREANEQL IKQGLARKNE GYWITIFPEG
151 TRLAPGKR GK YKLGGARMAK MFEMDIVPVA LNSGEFWPKN SFLKYPGEIT
201 VIICPTIPHA SGSEAELEMEK CEHLIETQQP LISGAGPFAA EMPSET*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1651>:

m560.seq

```

1 ATGCTCATCA TCCGCAACCT GATTTACTGG CTGATACTCT GTTCCACCCCT
51 GATTTTCCTC TTTCCCTTTA TGCTGCTCGC CTCGCCTTTC CGGGACGGGG
101 CGCACAAGAT GGC GCGGGT TGGGT CCGCA TTCTCAACTG GTCGCTCAAA
151 CACATCGT CG GGCTCAAATA CCGCATCATC GGC GCGGAAA ACATCCCGGA
201 CCGCCCCGCC GTCATCTGCG CCAAACACCA AAGCGGCTGG GAAACGCTCG
251 CCCTTCAGGA CATTTTTCGG CCGCAGGTTT ACGTTGCCAA ACGCGAGTTG
301 TTCAAAATCC CCTTTTTCGG CTGGGGCTTG AAAC TGGTCA AAACCATAGG
351 CATAGACCGC AACCAACGCC GCGAAGCCAA CGAGCAGCTC ATAAAACAGG
401 GGTTGGTGCG CAAAAACGAA GGCTATTGGA TTACCATTTT CCCC GAAGGC
451 ACGCGCCTTG CGCCCGGAAA ACGCGGCAAA TACAAACTCG GCGGCGCGCG
501 CATGGCGAAA ATGTTT GAGA TGGACATCGT CCCC GTCGCC CTCAACAGCG
551 GCGAATTTTG GCCGAAAAAC TCCTTTCTGA AATATCCGGG GGAAATCACC
601 GTCGTCATCT GTCCGACCAT CCCGCACGCA AGCGGCAGCG AAGCCGAATT
651 GATGGAAAAA TGCGAACATC TCATCGAAAC GCAACAACCG CTTATTCCG
701 GCGCAGGCCG GTTTGCCGCC AAAATGCCGT CTGAAACCGC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1652; ORF 560>:

m560.pep

```

1 MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVGILNWSLK
51 HIVGLKYRII GAENIPDRPA VICAKHQSGW ETLALQDIFP PQVYVAKREL
101 FKIPFFGWGL KLVKTIGIDR NNRREANEQL IKQGLVRKNE GYWITIFPEG
151 TRLAPGKR GK YKLGGARMAK MFEMDIVPVA LNSGEFWPKN SFLKYPGEIT
201 VVICPTIPHA SGSEAELEMEK CEHLIETQQP LISGAGPFAA KMPSETA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 560 shows 97.2% identity over a 246 aa overlap with a predicted ORF (ORF 560.ng) from *N. gonorrhoeae*:

m560/g560

```

          10      20      30      40      50      60
m560.pep  MLIIRNLIYWLILCSTLIFLFPFMLLASPF RDGAHKMARVWVGILNWSLK HIVGLKYRII
          |||||:|||||
g560      MLIIRNLIYWLILCSSLIFLFPFMLLASPF RDGAHKMARVWVGILNWSLK HIVGLKYRII
          10      20      30      40      50      60

          70      80      90     100     110     120
m560.pep  GAENIPDRPAVICAKHQSGWETLALQDIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g560      GAEHIPDRPSVICAKHQSGWETLALQEIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR

```

843

	70	80	90	100	110	120
	130	140	150	160	170	180
m560.pep	NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
	:					
g560	NNRREANEQLIKQGLARKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m560.pep	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMEKCEHLIETQQPLISGAGPFAA					
	:					
g560	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMEKCEHLIETQQPLISGAGPFAA					
	190	200	210	220	230	240
m560.pep	KMPSETAX					
	:					
g560	EMPSETX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1653>:

```

a560.seq
1   ATGCTCATCA TCCGCAACCT GATTACTGG CTGATACTCT GTTCCACCCT
51  GATTTTCCTC TTTCCCTTTA TGCTGCTCGC CTCGCCTTTC CGAGACGGGG
101 CGCACAAAGAT GGCGCGGGTC TGGGTCAAAA TCCTCAACCT CTCGCTCAA
151 CACATCGTCG GGCTCAAATA CCGCATCATC GGCGCGGAAA ACATCCCCGA
201 CCGCCCCGCC GTCATCTGCG CCAAACACCA AAGCGGCTGG GAAACGCTCG
251 CCCTTCAGGA CATTTTTCG CCGCAGGTTT ACGTTGCCAA ACGCGAGTTG
301 TTCAAATCC CCTTTTTCG CTGGGGCTTG AACTGGTCA AAACCATAGG
351 CATAGACCGC AACAACCGCC GCGAAGCCAA CGAGCAGCTC ATAAAACAGG
401 GGTGGCGCG CAAAAACGAA GGCTATTGGA TTACCATTTT CCCCGAAGGC
451 ACACGCCTTG CGCCCGGAAA ACGCGGCAAA TACAACTCG GCGCGCGCG
501 CATGGCGAAA ATGTTTGAGA TGGACATCGT CCGCGTCGCC CTCAACAGCG
551 GCGAATTTTG GCCGAAAAC TCCTTCTGA AATATCCGGG GGAAATCACC
601 GTCGTCATCT GTCCGACCAT CCCGACGCA AGCGGCAGCG AAGCCGAATT
651 GATGGGAAAA TGCGAACACC TCATCGAAAC GCAGCAGCCG CTCATTTCG
701 GCGCAGGCC GTTGGCGCC AAAATGCCGT CTGAAACCGC ATGA
  
```

This corresponds to the amino acid sequence <SEQ ID 1654; ORF 560.a>:

```

a560.pep
1   MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVKILNLSLK
51  HIVGLKYRII GAENIPDRPA VICAKHQSGW ETLALQDIFP PQVYVAKREL
101 FKIPFFGWGL KLVKTIGIDR NNRREANEQL IKQGLARKNE GYWITIFPEG
151 TRLAPGKRGK YKLGARMAMK MFEMDIVPVA LNSGEFWPKN SFLKYPGEIT
201 VVICPTIPHA SGSEAELEMGK CEHLIETQQP LISGAGPFAA KMPSETA*
  
```

m560/a560 98.4% identity in 247 aa overlap

	10	20	30	40	50	60
m560.pep	MLIIRNLIYWLILCSTLIFLFPFMLLASPF RDGAHKMARVWVGILNWSLKHIVGLKYRII					
a560	MLIIRNLIYWLILCSTLIFLFPFMLLASPF RDGAHKMARVWVKILNLSLKHIVGLKYRII					
	10	20	30	40	50	60
	70	80	90	100	110	120
m560.pep	GAENIPDRPAVICAKHQSGWETLALQDIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR					
a560	GAENIPDRPAVICAKHQSGWETLALQDIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m560.pep	NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
	:					
a560	NNRREANEQLIKQGLARKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					

844

	130	140	150	160	170	180
	190	200	210	220	230	240
m560.pep	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAE	LMKCEHLIETQQPLISGAGPFAA				
a560	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAE	LMGKCEHLIETQQPLISGAGPFAA				

m560.pep	KMPSETAX					
a560	KMPSETAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1655>:

```

m561.seq.
1   ATGATACTGC CAGCCCGTTT TTCAGACGGC ATCAGCCTTT CCCTGCGCCT
51  GAAACTCCTG ACCGGACTGT GGGTCGGGTT GGCGGCATTG TCTGTCGTTT
101 TGACACTGCT GCTCTCTTTG CGTCTGGAAA ACGCGGCCTC CGTCATCGAA
151 GAGGCGGGCA ACTTGAGAAT GCAGGCATAC CGTCTGGCAT ACATGGCGGG
201 TGAAGGCTCG CCCCCTGCGC AAATTGACAA TCAGGTTGCC GAATTTGAAA
251 AAAGTTTAAA ACGCATTGCC CAAAGCGATG CCATCCATCC GCTGATTCTT
301 TCGGACACCC CTCTTGCTTA TGATTGATA CAATCCATGC TGATTATAGA
351 TTGGCAGGCA CACATCCTCC CCCCCTCCA GTCCTACCGG CGACCGACTC
401 AGGTCGATCT CTACCGCTTT GCCGGAACA TCGAACTGTT TTTGCAGGCA
451 TTGGAATG CCAACGAAAA AAACACATGG TGGCTCAGGC GTTTTCAATG
501 GGCAATTATG TTGATGACGC TGGTGTCGTC TGTACTGATG CTGTTTTGGC
551 ACCAGATTG GGTATCCGG CCGCTGCAGG CGTTAAGGGA AGGTGCGGAA
601 CGCATCGGAC GGAGGTGTTT CGATATTCCG GTTCCCGAAG GCGGTACGCC
651 GGAATTCAA CAGGTCGGGC GTTGTTCAT TCAAATGGGC GGCAGGTTGA
701 AAATTTTATA TGATGATTG GAAGGACAAG TCGCCGAGCA GACACGCAGT
751 CTCGAAAAAC AAAATCAAAA CCTGACCCTG CTGTACCAA CTACACGGGA
801 CCTGCACCAA TCCTACATAC CGCAACAGGC TGCAGAACAT TTTCTAAACC
851 GTATCCTGCC CGCCGTAGGA GCAGATTCCG GCAGAGTTTG TTTGGACGGC
901 GGATCCGATG TTTATGTTT CATTATCAT GCGGATTGCG GCACAGCAGC
951 TTCGATTG GGGAAGTACC ATGAGGAAAT CTTCCCCATT GAGTACCAGA
1001 ACGAAACATT GGGCAGGCTG TTGCTCAGCT TTCCAAACGG CATTCTCTCT
1051 GATGAAGACG ACCGCATCCT GCTTCAAACA CTAGGCAGGC AATTGGCGCT
1101 ATCGCTTGCC GCGCAAAAC AGGAGGAAGA AAAACGCCTG CTTGCAGTAT
1151 TGCAGGAACG CAACCTGATT GCGCAAGGAT TACATGACAG CATCGCACAA
1201 GCATTAACGT TCCTAAACCT ACAGGTACAG ATGCTGGAAG CCGCCTTTGC
1251 CGAAACAAA CGGGAGGAAG CCGCAGAAAA CATCAGCTT ATCAAAACAG
1301 CCGTGCAGGA ATGTTATGAA GATGTCGCG AACTGCTGCT CAACTCCGT
1351 ACCAAAATCA GCAATAAGA ATTTCCCGAA GCCGTTGCCG ACCTATTCGC
1401 CCGCTTTACG CAACAAACCG GGATAACGCT CGAAACCGCC TGGGAAACG
1451 GTTCGTTTCT GCCGCTCAG GAAGCGCAGC TCCAAATGAT TTTTATCCTG
1501 CAGGAAAGCC TGTCCAACAT CCGCAAACAC GCCCGCGCCA CCCATCTAAA
1551 ATTACCCCTT TCCGAACAG GCGGACGCTT TACCATGACC ATCCAAGACA
1601 ACGGACAAGG TTTGACACG GAGAAAATAG GAGAACCAC GGGCAGCCAT
1651 GTCGACTGC ACATCATGCA GGAGCGTGCC AAACGCATCC ATGCCGTTT
1701 AGAAATCCGT TCCCAAGCTC AACAGGGAAC CACCGTCTCA TTGACGGTTG
1751 CATCTGAAGA AAGCTTGAAA TGA

```

This corresponds to the amino acid sequence <SEQ ID 1656; ORF 561>:

```

m561.pep
1   MILPARFSDG ISLSRLKLL TGLWVGLAAL SVVLTLTLLSL RLENAASVIE
51  EAGNLRMQAY RLAYMAGEGS PRAQIDNQVA EFEKSLKRIA QSDAIHPLIP
101 SDTPLAYDLI QSMLIIDWQA HILPPLQSYR RPTQVDLYRF AGNIELFLQA
151 LENANEKNTW WLRRFQWAIM LMTLVSSVLM LFHWQIHWIR PLQALREGAE
201 RIGRRCFDIP VPEGGTPEFK QVGRCFNQMG GRLKILYDDL EGQVAEQTRS
251 LEKQNQNLT LYTTRDLHQ SYIPQQAEEH FLNRILPAVG ADSGRVCLDG
301 GSDVYVSIHH ADCGTAASDL GKYHEEIFPI EYQNETLGR LLSFPNGISL
351 DEDDRILLQ LGRQLGVSLA GAKQEEERL LAVLQERNLI AQGLHDSIAQ
401 ALTFLNLQV MLETAFAENK REEAENISF IKTGVQECYE DVRELLNFR
451 TKISNKEFPE AVADLFARFT QQTGITVETA WENGSLFPQ EAQLQMFIL

```

845

501 QESLSNIRKH ARATHVKFTL SEHGGFRFTMT IQDNGQGFD T EKIGEPTGSH
 551 VGLHIMQERA KRIHAVLEIR SQAQOGTTVS LTVASEESLK *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m561/g561 89.7% identity in 223 aa overlap

	10	20	30	40	50	60
m561.pep	MILPARFSDGISLSRLKLLTGLWVGLAALSVVLTLLLSRL	ENAASVIEEAGNLRMQAY				
	:					
g561	MILPTRFSDGIPLSLRLKLLTGLWVGLAALSVVLTLLLSFR	LENAASVIEEAGNLKMQAY				
	10	20	30	40	50	60
	70	80	90	100	110	120
m561.pep	RLAYMAGEGSPRAQIDNQVAEFESLKRISQSDAIHPLIPSDTPLAYDLIQSMLIIDWQA					
g561	RLAYMAGEGSPRAQIDNQIAEFESLKRISQSDAIHPLIPSDNPLAYDLIQSMLIIDWQA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m561.pep	HILPPLQSYRRPTQVDLYRFAGNIELFLQALENANEKNTWWLRRFQWAIMLMTLVSSVLM					
	:	:	:	:	:	:
g561	NILPPLQAYRRPTQIELYRFAGNIELFLQALENAGEKNTWWLRRFQWVIMLMTLVSSVLM					
	130	140	150	160	170	180
	190	200	210	220	230	240
m561.pep	LFWHQIWVIRPLQALREGAERIGRRCFDIPVPEGGTPEFKQVGRCFNQMGGRKILYDDL					
					:	:
g561	LFWHQIWVIRPLQALREGAERIGRHFDPVPEDVRPNNSRSGGVSTKWRSGX					
	190	200	210	220	230	
	250	260	270	280	290	300
m561.pep	EGQVAEQTRSLEKQNQNLTLTYQTTTRDLHQSYIPQQAEEHFLNRLPAVGADSGRVCLDG					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1657>:

a561.seq

1	ATGATACTGC	CAGCCCGTTT	TTCAGACGGC	ATCAGCCTTT	CCCTGCGCCT
51	GAAACTCCTG	ACCGGACTGT	GGGTCGGGTT	GGCGGCATTG	TCTGTCTGTTT
101	TGACACTGCT	GCTCTCTTTG	CGTCTGGAAA	ACGCGGCCCTC	CGTCATCGAA
151	GAGGCGGGCA	ACTTGAGAAT	GCAGGCATAC	CGTCTGGCAT	ACATGGCGGG
201	TGAAGGCTCG	CCCCGTGCGC	AAATTGACAA	TCAGGTGCC	GAATTTGAAA
251	AAAGTTTAAA	ACGCATTGCC	CAAAGCGATG	CCATCCATCC	GCTGATTCCCT
301	TCGGACACCC	CTCTTGCTTA	TGATTTGATA	CAATCCATGC	TGATTATAGA
351	TTGGCAGGCA	CACATCCTCC	CCCCGCTCCA	GTCCTACCGG	CGACCGACTC
401	AGGTCGATCT	CTACCGCTTT	GCCGGAAACA	TCGAACGTGT	TTTGCAGGCA
451	TTGGAAAATG	CCAACGAAAA	AAACACATGG	TGGCTCAGGC	GTTTTCAATG
501	GGCAATTATG	TTGATGACGC	TGGTGTCTGC	TGTACTGATG	CTGTTTTGGC
551	ACCAGATTTG	GGTTATCCGG	CCGCTGCAGG	CGTTAAGGGA	AGGTGCGGAA
601	CGCATCGGAC	GGAGGTGTTT	CGATATTCCG	GTTCCCGAAG	GCGGTACGCC
651	GGAATTCAAA	CAGGTCGGGC	GTTGTTTCAA	TCAAATGGGC	GGCAGGTTGA
701	AAATTTTATA	TGATGATTTG	GAAGGACAAG	TCGCCGAGCA	GACACGCAGT
751	CTCGAAAAAC	AAAATCAAAA	CCTGACCCCTG	CTGTACCAAA	CTACACGGGA
801	TCTGCACCAA	TCCTACATAC	CGCAACAGGC	TGCAGAACAT	TTTCTAAACC
851	GTATCCTGCC	CGCCGTAGGA	GCAGATTCCG	GCAGAGTTTG	TTTGGACGGC
901	GGATCCGATG	TTTATGTTTC	CATTCATCAT	GCGGATTGCG	GCACAGCAGC
951	TTCGGATTTG	GGGAAGTACC	ATGAGGAAAT	CTTCCCCATT	GAGTACCAGA
1001	ACGAAACATT	GGGAGGCTG	TTGCTCAGCT	TTCCAAACGG	CATTTCTCTT
1051	GATGAAGACG	ACCGCATCCT	GCTTCAAACA	CTAGGCAGGC	AATTGGGCGT
1101	ATCGCTTGCC	GGCGCAAAAC	AGGAGGAAGA	AAAACGCCCTG	CTTGCAGTAT
1151	TGCAGGAACG	CAACCTGATT	GCGCAAGGAT	TACATGACAG	CATCGCACAA
1201	GCATTAACGT	TCCTAAACCT	ACAGGTACAG	ATGCTGAAAA	CCGCCTTTGC
1251	CGAAAAACAA	CGGGAGGAAG	CCGCAGAAAA	CATCGGCTTC	ATCAAAACAG
1301	GCGTGCAGGA	ATGTTATGAA	GATGTCCGCG	AACTGCTGCT	CAACTTCCGT
1351	ACCAAAATCA	GTAATAAAGA	ATTTCCCGAA	GCCGTTGCCG	ACCTATTCTC

846

```

1401 GCGCTTTACG CAACAGACCG GCACGACTGT CGAAACCGCT TGGGAAAACG
1451 GCACGCACCT GCCTACACAG GACGAGCAGC TCCAAATGAT TTTCATCCTG
1501 CAAGAAAGCT TGTCCAACAT CCGAAAACAT GCCCAGCCA CCCATATCAA
1551 ATTCAGACTG CTCAAACAGG ATGGAAGTTT TACAATGACC ATTCAGACA
1601 ACGGACAGGG TTTTGACACG GAAAACATTG GAGAACCATC GGGCAGCCAT
1651 GTCGGACTGC ATATCATGCA GGAGCGTGCC AAACGCATCC ATGCCGTTT
1701 AGAAATCCGT TCCCAAGCTC AACAGGGAAC CACCGTCTCA TTGACGGTTG
1751 CATCTGAAGA AAGCTTGAAA TGA

```

This corresponds to the amino acid sequence <SEQ ID 1658; ORF 561.a>:

```

a561.pep
  1 MILPARFSDG ISLSRLKLL TGLWVGLAAL SVVLTLLLSL RLENAASVIE
 51 EAGNLRMQAY RLAYMAGEGS PRAQIDNQVA EFEKSLKRIA QSDAIHPLIP
101 SDTPLAYDLI QSMLIIDWQA HILPPLQSYR RPTQVDLYRF AGNIELFLQA
151 LENANEKNTW WLRRFQWAIM LMTLVSSVLM LFWHQIWVIR PLQALREGAE
201 RIGRRCFDIP VPEGGTPEFK QVGRCFNQMG GRKILYDDL EGQVAEQTRS
251 LEKQNQNLTLYQTTRDLHQ SYIPQQAEEH FLNRILPAVG ADSGRVCLDG
301 GSDVYVSIHH ADCGTAASDL GKYHEEIFPI EYQNETLGRLLSFPNGISL
351 DEDDRILLQT LGRQLGVSLA GAKQEEKRL LAVLQERNLI AQGLHDSIAQ
401 ALTFNLQVQ MLETAFENK REEAENIGF IKTGVQECYE DVRELLNFR
451 TKISNKEFPE AVADLFSRFT QQTGTTVETA WENGTHLPTQ DEQLQMIFIL
501 QESLSNIRKH AHATHIKFRL LKQDGSFTMT IQDNGQGFD ENIGEPSGSH
551 VGLHIMQERA KRIHAVLEIR SQAQQTTSV LTVASEESLK *

m561/a561 96.9% identity in 590 aa overlap

      10      20      30      40      50      60
m561.pep MILPARFSDGISLSRLKLLTGLWVGLAALS SVVLTLLLSL RLENAASVIEEAGNLRMQAY
a561      10      20      30      40      50      60
MILPARFSDGISLSRLKLLTGLWVGLAALS SVVLTLLLSL RLENAASVIEEAGNLRMQAY

      70      80      90      100     110     120
m561.pep RLAYMAGEGSPRAQIDNQVAEFEKSLKRIAQSDAIHPLIPSDTPLAYDLIQSMLIIDWQA
a561      70      80      90      100     110     120
RLAYMAGEGSPRAQIDNQVAEFEKSLKRIAQSDAIHPLIPSDTPLAYDLIQSMLIIDWQA

      130     140     150     160     170     180
m561.pep HILPPLQSYRRPTQVDLYRFAGNIELFLQALENANEKNTWWLRRFQWAIMLMTLVSSVLM
a561      130     140     150     160     170     180
HILPPLQSYRRPTQVDLYRFAGNIELFLQALENANEKNTWWLRRFQWAIMLMTLVSSVLM

      190     200     210     220     230     240
m561.pep LFWHQIWVIRPLQALREGAERIGRRCFDIPVPEGGTPEFKQVGRCFNQMGGRKILYDDL
a561      190     200     210     220     230     240
LFWHQIWVIRPLQALREGAERIGRRCFDIPVPEGGTPEFKQVGRCFNQMGGRKILYDDL

      250     260     270     280     290     300
m561.pep EGQVAEQTRSLEKQNQNLTLLYQTTRDLHQSYIPQQAEEHFLNRILPAVGADSGRVCLDG
a561      250     260     270     280     290     300
EGQVAEQTRSLEKQNQNLTLLYQTTRDLHQSYIPQQAEEHFLNRILPAVGADSGRVCLDG

      310     320     330     340     350     360
m561.pep GSDVYVSIHHADCGTAASDLGKYHEEIFPIEYQNETLGRLLSFPNGISLDEDDRILLQT
a561      310     320     330     340     350     360
GSDVYVSIHHADCGTAASDLGKYHEEIFPIEYQNETLGRLLSFPNGISLDEDDRILLQT

      370     380     390     400     410     420
m561.pep LGRQLGVSLAGAKQEEKRL LAVLQERNLIAQGLHDSIAQALTFLNLQVQMLETAFENK
a561      370     380     390     400     410     420
LGRQLGVSLAGAKQEEKRL LAVLQERNLIAQGLHDSIAQALTFLNLQVQMLETAFENK

```

847

	370	380	390	400	410	420
	430	440	450	460	470	480
m561.pep	REEAAENISFIKTGVQECYEDVRELLLNFR TKISNKEFPEAVADLFARFTQQTGTVETA					
a561	REEAAENIGFIKTGVQECYEDVRELLLNFR TKISNKEFPEAVADLFSRFTQQTGTTVETA					
	430	440	450	460	470	480
	490	500	510	520	530	540
m561.pep	WENGSLFPQEAQLQMIFILQESLSNIRKHARATHVKFTLSEHGGRFTMTIQDNGQGFD					
a561	WENGTHLPTQDEQLQMIFILQESLSNIRKHAHATHIKFRLLKQDGSFTMTIQDNGQGFD					
	490	500	510	520	530	540
	550	560	570	580	590	
m561.pep	EKIGEPTGSHVGLHIMQERAKRIHAVLEIRSQAQQGTTVSLTVASEESLKK					
a561	ENIGEPSGSHVGLHIMQERAKRIHAVLEIRSQAQQGTTVSLTVASEESLKK					
	550	560	570	580	590	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1659>:

g562.seq..

1	atggcaagcc	cgctcgagtct	gcctttcaat	tcgggcaaga	ccaaaccgac
51	ggcttttgcc	gcgccggttt	tggtcggaat	catgttttcc	acgcccgctgc
101	ggcgcgccgc	caggtccttg	tgccgcacgt	cggtaacggt	ttggtcggtg
151	gtcagtgctg	ggatggtggt	cattgcgcct	ttgacgatgc	cgacgctttc
201	gctcaacact	ttggcaaccg	gcgagaggca	gttggtggtg	caggaagcgt
251	tggaaacgac	ggcatgtcgc	gcggtcagga	cgctgtcgtt	cacgccgtac
301	acgacggttg	catcgacatc	gtcgccgccc	ggtgcgga	tgaggacttt
351	tttcgcgccg	ctttcgaggt	ggattttggc	ttttctttg	ctggtgaacg
401	cgccggtgca	ttccatgacc	aaatcgacac	cgagttcttt	ccacggcagt
451	tcggcagggg	tgccgggtcg	gaagaagggg	atthttgtcg	cgttgacgat
501	gaggttgccg	ccgtcgtggg	atacgtcggc	ttcaaagcgt	ccgtgtacgg
551	tgtcgaattt	ggtcagatgg	gcgttggttt	caaggctgcc	gctggcggtg
601	acggcgacga	tttgaggttg	gtcttga		

This corresponds to the amino acid sequence <SEQ ID 1660; ORF 562.ng>:

g562.pep

1	MASPS	SLPFN	SGKTK	PFAFA	APVLV	GIMFS	TPLRARR	RRSL	WRTSV	TVWSL
51	VSAWM	VVIAP	LTMP	TL	SLNT	LATGE	RQLVV	QEALE	TTVMS	AVRTL
101	TVAST	SSPP	GAEMR	TF	FAP	LSRW	ILAFSL	LVNAP	VHSMT	KSTPS
151	SAGLR	VEKKG	ILSPL	TM	RLP	PSWDT	SASKR	PCTVS	NLVRW	ALVSR
201	TATI	WSWS*								

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1661>:

m562.seq

1	ATGGCAAGCC	CGTCGAGCCT	GCCTTTCAAT	TCGGGCAGTA	CCAAACCGAC
51	GGCTTTTGCC	GCGCCGTTT	TGGTCGGAAT	CATGTTTTC	ACGCCGCTGC
101	GGGCGCGCG	CAGGTCTTTG	TGGCGCACGT	CGGTAACGGT	TTGGTCGTTG
151	GTCAGCGCGT	GGATGGTGGT	CATCGCGCCT	TTGACGATGC	CGACGCTTTC
201	GCTCAACACT	TTGGCAACCG	GCGAGAGGCA	GTTGGTGGTG	CAGGAAGCGT
251	TGGAAACGAC	GGTCATGTCG	GCGGTCAGGA	CGCTGTCGTT	CACGCCGTAC
301	ACGACGGTTG	CATCGACATC	GTGCGCGCCC	GGTGCAGAAA	TGAGGACTTT
351	TTTCGCGCCG	CTTCGAGGT	GGATTTTGGC	TTTTCTTTG	CTGGTGAACG
401	CGCCGGTGCA	TTCCATGACC	AAATCGACAC	CGAGTTCTTT	CCACGGCAGT
451	TCGGCAGGGT	TGCGGGTCGA	GAAGAAGGGG	ATTTGTGCGC	CGTTGACGAT
501	GAGGTTGCCG	CCGTCGTGGG	ATACGTCGGC	TTCAAAGCGT	CCGTCACGGG
551	TGTCGAATTT	GGTCAGATGG	GCGTTGGTTT	CAAGGCTGCC	GCTGGCGTTG
601	ACGGCGACGA	GTTGGAGTTG	GTCTTGA		

This corresponds to the amino acid sequence <SEQ ID 1662; ORF 562>:

m562.pep

1	MASPS	SLPFN	SGSTK	PFAFA	APVLV	GIMFS	TPLRARR	RRSL	WRTSV	TVWSL
51	VSAWM	VVIAP	LTMP	TL	SLNT	LATGE	RQLVV	QEALE	TTVMS	AVRTL

848

```

101 TTVASTSSPP GAEMRTFFAP LSRWILAFSL LVNAPVHSMT KSTPSSFHGS
151 SAGLRVEKKG ILSPLTMLRP PSWDTASAKR PCTVSNLVRW ALVSRLPLAL
201 TATSWWS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m562/g562 99.0% identity in 208 aa overlap

```

              10      20      30      40      50      60
m562.pep      MASPSSLPFNSGSTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAWMVVIAP
              |||||:|||||
g562          MASPSSLPFNSGKTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAWMVVIAP
              10      20      30      40      50      60

              70      80      90      100     110     120
m562.pep      LTMPTLSLNTLATGERQLVVQEALETTVMSAVRTLSFTPYTTVASTSSPPGAEMRTFFAP
              |||||:|||||
g562          LTMPTLSLNTLATGERQLVVQEALETTVMSAVRTLSFTPYTTVASTSSPPGAEMRTFFAP
              70      80      90      100     110     120

              130     140     150     160     170     180
m562.pep      LSRWILAFSLLVNAPVHSMTKSTPSSFHGSAGLRVEKKGILSPLTMLRPSPWDTASAKR
              |||||:|||||
g562          LSRWILAFSLLVNAPVHSMTKSTPSSFHGSAGLRVEKKGILSPLTMLRPSPWDTASAKR
              130     140     150     160     170     180

              190     200     209
m562.pep      PCTVSNLVRWALVSRLPLALTATSWWSX
              |||||:|||||
g562          PCTVSNLVRWALVSRLPLALTATIWSWSX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1663>:

```

a562.seq
1  ATGGCAAGCC CGTCGAGTTT GTCTTTCAAT TCGGGCAGTA CCAAACCGAC
51 GGCTTTTGCC GCGCCAGTTT TGGTCGGAAT CATGTTTCC ACGCCGCTGC
101 GGGCGCGCG CAGGTCTTGT TGGCGCACGT CGGTAACGGT TTGGTCGTTG
151 GTCAGCGCGT GGATGGTGGT CATCGCGCCT TTGACGATGC CGACGCTTTC
201 GCTCAACACT TTGGCAACCG GCGAGAGGCA GTTGGTGGTG CAGGAAGCGT
251 TGGAAACGAC GGTCAATGTC GCGGTCAGGA TGCTGTCGTT CACGCCGTAC
301 ACGACGGTTG CATCGACATC GTCGCCGCC GGTGCGGAAA TGAGGACTTT
351 TTTCCGCGCG CTTTCCAGAT GAACTTTGGC TTTTCTTTG CTGGTGAACG
401 CGCCGGTGCA TTCCATGACC AAATCGACAC CGAGTTCTTT CCACGGCAGT
451 TCGGCAGGGT TGCGGGTCNA GAAGAANGGG ATTTTGTCGC CGTTGACGAT
501 GAGGTTGCCG CCGTCGTGGG ATACGTCGGC TTCAAAGCGT CCGTGCACGG
551 TGTCGAATTT GGTGAGGTGG GCGTTGGTTT CAAGGCTGCC GCTGGCGTTG
601 ACGGCGACGA TTTGAGGTTG GTCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1664; ORF 562.a>:

```

a562.pep
1  MASPSSLSFN SGSTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL
51 VSAWMVVIAP LTMPTLSLNT LATGERQLVV QEALETTVMS AVRMLSFPTY
101 TTVASTSSPP GAEMRTFFAP LSR*TLAFSL LVNAPVHSMT KSTPSSFHGS
151 SAGLRVXKXG ILSPLTMLRP PSWDTASAKR PCTVSNLVRW ALVSRLPLAL
201 TATIWSWS*

```

m562/a562 96.6% identity in 208 aa overlap

```

              10      20      30      40      50      60
m562.pep      MASPSSLPFNSGSTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAWMVVIAP
              |||||:|||||
a562          MASPSSLSFN SGSTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAWMVVIAP
              10      20      30      40      50      60

```


849

	70	80	90	100	110	120
m562 . pep	LTMP T L S L N T L A T G E R Q L V V Q E A L E T T V M S A V R T L S F T P Y T T V A S T S S P P G A E M R T F F A P					
a562	L T M P T L S L N T L A T G E R Q L V V Q E A L E T T V M S A V R M L S F T P Y T T V A S T S S P P G A E M R T F F A P					
	70	80	90	100	110	120
	130	140	150	160	170	180
m562 . pep	L S R W I L A F S L L V N A P V H S M T K S T P S S F H G S S A G L R V E K K G I L S P L T M R L P P S W D T S A S K R					
a562	L S R X T L A F S L L V N A P V H S M T K S T P S S F H G S S A G L R V X K X G I L S P L T M R L P P S W D T S A S K R					
	130	140	150	160	170	180
	190	200	209			
m562 . pep	P C T V S N L V R W A L V S R L P L A L T A T S W S W S X					
a562	P C T V S N L V R W A L V S R L P L A L T A T I W S W S X					
	190	200				

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1665>:

g563 . seq

```

1  ATGAACAAAA CCCTCTATCG TGTGATTTTC AACCGCAAAC GCGGTGCTGT
51  GGTAGCTGTT GCCGAAACCA CCAAGCGCGA AGGTAAAAGC TGTGCCGATA
101 GTGGTTTCGGG CAGCGTTTAT GTGAAATCCG TTTCTTTTCAT TCCTACTCAT
151 TCCAAAGCCT TTTGTTTTTC TGCATTAGGC TTTTCTTTAT GTTTGGCTTT
201 GGGTACGGTC AATATTGCTT TTGCTGACGG CATTATTACT GATAAAGCTG
251 CTCCTAAAC CCAACAAGCC ACGATTCTGC AAACAGGTAA CGGCATACCG
301 CAAGTCAATA TTCAAACCCc tACTTCGGCa ggGGTTTCTG TTAATCAATA
351 TGCCCAGTTT GATGTGGGTA ATcgCGGGC GATTTTAAAC AACAGTCGCA
401 GCAACACCCA AACACAGCTA GGCGGTGGA TTCAAGGCAA TCCTTG GTT
451 ACAAGGGGCG AAGCACGTGT GGTGTGTAAC CAAATCAACA GCAGCCATCC
501 TTCACAACG AATGGCTATA TTGAAGTGGG TGGACGACGT GCAGAAGTCG
551 TTATTGCCAA TCCGGCAGGG ATTGCAGTCA ATGGTGGTGG TTTTATCAAT
601 GCTTCCCGTG CCACTTTGAC GACAGGCCAA CCGCAATATC AAGCAGGAGA
651 CTTTAGCGGC TTAAAGATAA GGCAAGGCAA TGCTGTAATC GCCGGACACG
701 GTTTGGATGC CCGTGATACC GATTTACACG GTATTCTTTT GTATGCCAAC
751 AAAATCACCT TGATCAGTAC GGCCGAACAA GCAGGCATTC GTAATCAAGG
801 GCAGTTGTTT GCTTCTTCCG GTAATGTGGC GATTGATGCA AATGGCCGTT
851 TGCATAATAG TGGCAGCATG GCTGCCGCCA ATGTGCAAGA TATGAATAAT
901 ACAGCGGAAC ACAAAAGTCAA TATCCGCAGT CAAGCCTTTG AAAACAGCGG
951 TACGGCGGTA TCGCAACAAG GCACTCAAAT TCACAGTCAA TCGATTCAAA
1001 ACACTGGCAA ATTATTGTCG GCAGGAACAG AGGATTTAGC CGTTTCAGGC
1051 AGCCTGAACA ATCAAAATGG CGAAATAGCG ACCAATCAAC AACTGATTAT
1101 TCACGATGGT CAGCAATCTA CCGTTGTCAT TGATAATACG AATGGCACGA
1151 TACAATCAGG CCGTGATGTT GCCATTCAGG CAAAATCGTT ATCCAACAAC
1201 GGCACACTTG CCGCTGATAA TAAACTGGAT ATTGCGTTAC AAGATGATTT
1251 TTATGTAGAA CGCAAGATCG TGGCGGGCAA TGAATTGTCT CTCAGTACAC
1301 GAGGCAGCCT GAAAAATTCA CATACTTGC AAGCAGGAAA ACGCATTCCG
1351 ATTAAAGCAA ATAACCTTGA TAATGCAGTA CAAGGCAACA TTCAATCCGG
1401 CCGTACGACA GACATTGGCA CGCAGCACAA TTAAACCAAT AGAGGCTTGA
1451 TTGACGGACA ACAAACCAA ATCCAAGCCG GGCAAATGAA TAATATCGGT
1501 ACAGGTCGGA TTTATGGCGA CAATATCGCT ATTGCGGCTA CCCGCTTAGA
1551 CAATCAAGAT GAAAACGGTA CAGGTGCCGC CATTGCGGCA CGCGAAAACC
1601 TGAATTTAGG CATTGAACAA TTAAATAACC GTGAAAACAG TCTGATTTAC
1651 AGCGGTAACG ATATGGCGGT TGGCGGCGCA TTAGATACCA ATGACCAAGC
1701 CACAGGCAAA GCCCAAAGGA TACACAATGC CGGCGCAATC ATTGAAGCTG
1751 CAGGCAAAAT GCGTTTAGGT GTAGAAAAGC TGCACAATAC CAATGAGCAT
1801 TTGAAAACGC AGTTGGTAGA AACAGGGCGC GAGCGTATTG TTGATTACGA
1851 AGCATTGGA CGACACGAAT TATTGCGAGA AGGCACGCAA CATGAATTAG
1901 GCTGGTTTGT CTACAACAAT GAATCAGACC ACTTACGCAC CCCTGATGGA
1951 GTGGCGCATG AAAATTGGCA TAAATACGAT TATGAAAAAG TAACGCAAGA
2001 AACTCAAGTA ACCGGAACGT GGCCTGCTAA AATCATTGCA GGTAGCGATT
2051 TGATTATTGA TAGCAAAGCA GTCTTCAACA GCGACAGCCG AATCATTGCC

```

```

2101  GGCGGCCAAT  TGCTTGTGCA  AACAGAAAAA  GACGGTTTGC  ATAACGAGCA
2151  AACCTTTGGC  GAGAAGAAAG  TCTTCAGCGA  AAATGGTAAG  TTGCACAAC
2201  ACTGGCGTGC  GCGTCGTAAA  GGACATGATG  AAACAGGGCA  TCGTGAACAA
2251  AATTATACTT  TGCCGGAGGA  AATCACACGC  GACATTTTAC  TGGGTTCATT
2301  TGCCTATGAA  TCGCATAGCA  AAGCATTAAAG  CCGTCATGCG  CCCAGCCAAG
2351  GCACTAGATT  GCCACAAAGT  AACCAGGATA  ATATCCGTAC  TCGGAAAAGC
2401  AACGGTATTT  CGCTACCCTA  TACGCCCAAT  TCTTTTACCC  CATTACCCGG
2451  CAGCAGCTTA  TACATTATCA  ATCCTGCCAA  TAAAGGCTAT  CTTGTTGAAA
2501  CCGATCCACG  CTTTGCCAAC  TACCGTCAAT  GGTGCGGTAG  TGAATATATG
2551  CTGGGCAGCC  TCAAACCTAG  CCCAAACAAT  TTACATAAAC  GTTGGGTGA
2601  TGGTTATTAC  GAGCAACGTT  TAATCAATGA  ACAAATCGCA  GAGCTGACAG
2651  GGCATCGTCG  TTTAGACGGT  TATCAAAACG  ACGAAGAACA  ATTTAAAGCC
2701  TTAATGAGTA  ATGGCGCGAC  TGCGGCACGT  TCGATGAATC  TCAGCGTTGG
2751  CATTGCATTA  AGTGCCGAGC  AAGCAGCGCA  ACTGACCAGC  GATATTGTTT
2801  GGTGTTGACA  AAAAGAAGTT  AAACCTCCTG  ATGGCGGCAC  ACAAACCGTA
2851  TTGATGCCAC  AGGTTTATGT  ACGCGTTAAA  AATGGCGGCA  TAGACGGTAA
2901  AGGTGCATTG  TTGTCAGGCA  GCAATACACA  AATCAATGTT  TCAGGCAGCC
2951  TGAAAACTC  AGGCACGATT  GCAGGGCGCA  ATGCGCTTAT  TATCAATACC
3001  GATACGCTAG  ACAATATCGG  TGGCGGTATT  CATGCGCAAA  AATCAGCGGT
3051  TACGGCCACA  CAAGACATCA  ATAATATTGG  CGGCATTCTT  TCTGCCGAAC
3101  AGACATTATT  GCTCAATGCG  GGTAACAACA  TCAACAACCA  AAGCACGGCC
3151  AAGAGCAGTC  AAAATGCACA  AGGTAGCAGC  ACCTACCTAG  ACCGAATGGC
3201  AGGTATTTAT  ATCACAGGCA  AAGAAAAAGG  TGTTTTAGCA  GCGCAGGCAG
3251  GCAAAGACAT  CAACATCATT  GCCGGTCAA  TCAGCAATCA  ATCAGATCAA
3301  GGGCAAACCC  GGCTGCAGGC  AGGACGCGAC  ATTAACCTGG  ATACGGTACA
3351  AACCAGCAAA  TATCAAGAAA  TCCATTTTGA  TGCCGATAAC  CATACCATCC
3401  GAGTTTCAAC  GAACGAAGTC  GGCAGCAGCA  TTCAAACAAA  AGGCGATGTT
3451  ACCCtatTGT  CAGGGAATAA  TCTCAATGCC  AAAGCTGCCG  AAGTCGGCAG
3501  CGCAAAGGC  AACTTTGCCG  TGTATGCTAA  AAATGACATT  ACTATCAGCT
3551  CAGGCATCCA  TGCCGGCCAA  GTTGATGATG  CGTCCAAACA  TACAGGCAGA
3601  AGCGCGGCG  GTAATAAATT  AGTCATTACC  GATAAAGCCC  AAAGTCATCA
3651  CGAACTGCT  CAAAGCAGCA  CCTTTGAAGG  CAAGCAAGTT  GTATTGCAGG
3701  CAGGAAACGA  TGCCAACATC  CTTGGCAGTA  ATGTTATTTC  CGATAATGGC
3751  ACCCGGATT  AAGCAGGCAA  TCATGTTCCG  ATTGGTACAA  CCCAACTCA
3801  AAGCCAAAGC  GAAACCTATC  ATCAAACCCA  AAAATCAGGA  TTGATGAGTG
3851  CAGGTATCGG  CTTCATCTAT  GGCAGCAAGA  CAAACACACA  AGAAAACCAA
3901  TCCCAAAGCA  ACGAACATAC  AGGCAGTACC  GTAGGCAGCC  TGAAAGGCGA
3951  TACCACCATT  GTTGCAAGCA  AACACTACGA  ACAAACCGGC  AGCAACGTTT
4001  CCAGCCCTGA  GGGCAACAAC  CTTATCAGCA  CGCAAAGTAT  GGATATTGGC
4051  GCAGCACAAA  ACCAATTAAA  CAGCAAAACC  ACCCAAACCT  ACGAACAAAA
4101  AGGCTTAACG  GTGGGCATT  AGTTCGCCCG  TTACCGATTT  GGCACAACAA
4151  GCGATTGCCG  TAGCACACAA  AGCAGCAAAC  AAGTCGGACA  AAGCAAAAAC
4201  GACCGCGTTA  ATGCCATGGC  GGCTGCCAAT  GCAGGTTGGC  AGGCCTATCA
4251  AACAGGCAAA  GGCGCACAAA  ACTTAGCCAA  TGGTACAACC  AATGCCAAAC
4301  AAGTCAGCAT  CTCCATAACC  TACGGCGAAC  AGCAAAACCG  ACAAACCACC
4351  CAAGTTCAAG  CCAATCAAGC  CCAAGCGAGT  CAAATTCAAG  CAGGCGGCAA
4401  AACTACCCTT  TATTGCCGAA  GGTGCGGCGA  ACAATCCAAT  ATCAACATCA
4451  CAGGCTCAGG  TGTTTCAGGC  AGAGCAGGAA  CCGGCCTGAT  TGCCGATAAG
4501  CAAATCCATC  TGCAATCAGC  CGAGCAAAGC  AATACCGAAC  GCAGCCAAAA
4551  CAAATCAGCA  GGCTGGAACG  CAGGTGCTGC  CGTATCATTC  GGACAAGGAG
4601  GCTGGTCATT  AGGCGTTGCC  GCAGGCGGCA  ATGTCGGCAA  AGGCTACGGC
4651  TATGGCGATA  GCGTAACCCA  CCGCCATAGC  CATATTGGCG  ACAAAGGCAG
4701  CCAAACCTT  ATCCAAAGTG  GTGGCGATAC  CATCATCAAA  GGCGCGCAAG
4751  TACGCGGCAA  AGGCGTACAA  GTCAATGCCA  AAAACCTAAG  CATTCAAAGT
4801  GTACAAGATA  GAGAACTTA  TCAAAGCAAA  CAACAAAACG  CCGGTGCACA
4851  AGTTACCGTA  GGTATGCGCT  TCAGTGCCAG  TGGCGATTAC  AGCCAAAGCA
4901  AAATCCGAGC  CGACCATGCT  TCGGTAACCG  AGCAAAGCGG  TATTTATGCC
4951  GGAGAAGACG  GCTATCAAA  CAAGGTCGGA  AACCATACAG  GCCTCAAAGG
5001  CGGCATCATC  ACCAGCAGCC  AAAGCGCAAA  AGACAAGGGT  AAAAACCGAT
5051  TCAGCACAGG  CACACTCGCC  GGCAGTGATA  TTCAAATAA  CAGCCAATAC
5101  GAAGGAAAAA  GTTTTGGATT  GGGTGCCAGC  GTTGCCGTAA  GCGGCAAAAC
5151  ACTGGGACAG  GGCGCAAAAA  ATAAACCTCA  AGACAAACAC  CTGACAAGCA

```

5201 TAGCCGATAA AAACGGCGCA AGTTCATCAG TAGGGTACGG CAGCGACAGC
 5251 GACAGTCAAA GCAGCATCAC AAAAAGCGGC ATCAATACCC CCAAAAACAT
 5301 TCAAATCACA GACGAAGCCG CACAAATCAG GCTGACAGGC AAAATAGCGG
 5351 CACAAACCAA AGCCGATATT GATACAAACG TAACCACAGA CACCGCCGAA
 5401 CGACATTCGG GCAGCCTGAA AAACATATTT GACAAAGATA GAGTGCAAAG
 5451 TGAATGGAT TTACAAAgaa CCGTCAGCCA AGATTTTAGT AAAAATGTTC
 5501 AACAAACCAA TACCGAGATT AACCAACATT TAGACAAACT CAAAGCAGAC
 5551 AAAGAAGCAG CCGAAACAGC AGCAGCCGAG GCATTAGCCA ATGGCGATAT
 5601 GGAAACTGCC AAACGCAAAG CCCATGAAGC TCAAGATGCG GCAGCAAAG
 5651 CAGATAATTG GCAACAAGGC AAAGTCATTC TCAACATGTT AGCCTCAGGT
 5701 TTAGCTGAGC CGACCCAAAG CGGAGCgggc ATCGCTGCGG CTACCGCATC
 5751 GCCaagCGTA TCGTATGCGA TTGGACAGCA CTTTAAagaT TTAGCCGGTC
 5801 AAAACGCGAA TGGCAAATA ACCGCCAGTC AagaAACCGC TCACGTCTTT
 5851 GCCCACGCGG TATTAGGAGC AGCGGTTGCC GCAGCATGAG GCAACAATGC
 5901 CCCGCGAGGA GCATTGGGTG CGGGCGGGTc ggAagcggCC GCCCAATCA
 5951 TCGGCAAATG GCTGTACGGC AAAGGAGAcg gcggcagccT GAATgcggag
 6001 gaaaAAGaga CCGTTTCGGC GATTACAAGG ATGCTGggtta cGgctGCCGG
 6051 AGCAGCTGAG GGAAACTCGT CCGCCGATGC TGTGTGGGGT TGTTTcaaa
 6101 cggctTCaga TTTTCGCTTCC TCTTTTTCAT ATCCTATAAA CATGTGA

This corresponds to the amino acid sequence <SEQ ID 1666; ORF 563.ng>:
 g563.pep..

1 MNKTLRYVIF NRKRGAUVAV AETTKREGKS CADSGSGSVY VKSVSFIPTH
 51 SKAFCF~~S~~ALG FSLCLALGTV NIAFADGIIT DKAAPKTQQA TILQTGNGIP
 101 QVNIQTPTSA GVSVNQYAQF DVGNRGAILN NSRSNTQTQL GGWIQGNPWL
 151 TRGEARVVVN QINSSHPSQL NGYIEVGRR AEVVIANPAG IAVNGGGFIN
 201 ASRATLTGQ PQYQAGDFSG FKIRQGN~~A~~VI AGHGLDARDT DFTRILLYAN
 251 KITLISTAEQ AGIRNQQLF ASSGNVAIDA NGRLVNSGTM AAANVQDMNN
 301 TA~~E~~HKVNIRS QAFENSGTAV SQOQTQIHSQ SIQNTGKLLS AGTEDLAVSG
 351 SLNNQNGEIA TNQQLIIHDG QOSTVVIDNT NGTIQSGRDV AIQAKSLSNN
 401 GTLAADNKLD IALQDDFYVE RKIVAGNELS LSTRGSLKNS HTLQAGKRIR
 451 IKANNLDNAV QGNIQSGGTT DIGTQHNLTN RGLIDGQQT~~K~~ IQAGQMNNIG
 501 TGRIYGDNIA IAATRLDNQD ENGTGA~~A~~IAA RENLNLGIEQ LNNRENSLIY
 551 SGNDMAVGGA LDTNDQATGK AQRIHNAGAI IEAAGKMRLG VEKLHNTNEH
 601 LKTQLVETGR ERIVDYEAFG RHELLREGTQ HELGW~~F~~VYNN ESDHLRTPDG
 651 VAHENWHKYD YEKVTQETQV TGTAPAKIIA GSDLIIDSKA VFNSDSRIIA
 701 GGQLLVQTEK DGLHNEQTFG EKKVFSENGK LHN~~Y~~WRARRK GHDETGHREQ
 751 NYTLPEEITR DISLGSFAYE SHSKALSRHA PSQGT~~E~~LPOS NRDNIRTAKS
 801 NGISL~~P~~YTPN SFTPLPGSSL YIINPANKGY LVETDPRFAN YRQWLGS~~D~~YM
 851 LGS~~L~~KLD~~P~~NN LHKRLGDGYY EQRLINEQIA ELTGHRRLDG YONDEEQFKA
 901 LMDNGATAAR SMNLSVGIAL SAEQAAQLTS DIVWL~~V~~QKEV KLPDGGTQTV
 951 LMPQVYVRVK NGGIDGKGAL LSGSNTQINV SGSLKNSGTI AGRNALIINT
 1001 DTLDNIGGRI HAQKSAVTAT ODINNIGGIL SAEQTL~~L~~LNA GNNINNQSTA
 1051 KSSQNAQSS TYLDRMAGIY ITGKEKGVLA AQAGKDINII AQQISNQSDQ
 1101 GQTRLQAGRD INLDTVQTGK YQEIHFADN HTIRGSTNEV GSSIQT~~K~~GDV
 1151 TLLSGNNLNA KAAEVGSAKG TLAVYAKNDI TISSGIHAGQ VDDASKHTGR
 1201 SGGGNKL~~V~~IT DKAQSHHETA QSSTFEGKQV VLQAGNDANI LGSNVISDNG
 1251 TRIQAGNHVR IGT~~T~~QTQSQS ETYHQTQKSG LMSAGIGFTI GSKTNTQENQ
 1301 SQSNEHTGST VGSLKGD~~T~~TI VASKHYEQTG SNVSSPEGNN LISTQSM~~D~~IG
 1351 AAQNQLNSKT TQTYEQKGLT VGIQFARYRF GTTSDCRSTQ SSKQVGQSKN
 1401 DRVNAMA~~A~~AN AGWQAYQTGK GAQNLANGTT NAKQVSISIT YGEQQNRQTT
 1451 QVQANQAQAS QIQAGGKTTL YCRRCGEQSN INITGSGVSG RAGTGLIADK
 1501 QIHLQSAEQS NTERSQNKSA GWNAGAAVSF GQGGWSLGVA AGGNV~~G~~KGYG
 1551 YGDSVTHRHS HIGDKGSQTL IQSGGDTI~~I~~K GAQVRGKGVQ VNAKNLSIQS
 1601 VQDRETYQSK QQNAGAQVTV GYGFSASGDY SOSKIRADHA SVTEQSGIYA
 1651 GEDGYQIKVG NHTGLKGGII TSSQSAKDKG KNRFTGT~~L~~A GSDIQNYSQY
 1701 EGKSFGLGAS VAVSGKTLGQ GAKNKPQDKH LTSIADKNGA SSSVGYGSDS
 1751 DSQSSITKSG INTPKNIQIT DEAAQIRLTG KIAAQTKADI DTNVT~~T~~DTAE
 1801 RHSGSLKNIF DKDRVQSELD LQRTVSQDFS KNVQQT~~N~~TEI NQHLDK~~L~~KAD
 1851 KEAAETA~~A~~AE ALANGDMETA KRKAHEAQDA AAKADNWQ~~Q~~G KVILNMLASG
 1901 LAEPTQSGAG IAAATASPDV SYAIGQHFKD LAGQ~~N~~ANGKL TASQETAHVL
 1951 AHAVLGA~~A~~VA AAXGNNAPAG ALGAGGSEAA APIIGK~~W~~LYG KGDGGS~~L~~NAE
 2001 EKETVSAITR MLGTAAGAAE GNSSADAVWG CFQTASDFAS SFSYPINM*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1667>:

m563.seq..

```

1   ATGAATAAAA CTCTCTATCG TGTAATTTTC AACCGCAAAC GTGGGGCTGT
51  GGTAGCCGTT GCTGAAACTA CCAAGCGCGA AGGTAAAAGC TGTGCCGATA
101 GTGATTCAGG CAGCGCTCAT GTGAAATCTG TTCCTTTTGG TACTACTCAT
151 GCACCTGTTT GTCGTTCAAA TATCTTTTCT TTTTCTTTAT TGGGCTTTTC
201 TTTATGTTTG GCTGTAGGTA CGGCCAATAT TGCTTTTGCT GATGGCATT
251 TTGCTGATAA AGCTGCTCCT AAAACTCAAC AAGCCACGAT TCTGCAAACA
301 GGTAACGACA TACCGCAAGT CAATATTCAA ACCCTACTT CGGCAGGGGT
351 TTCTGTAAAT CAATACGCCC AGTTTGATGT GGGTAATCGC GGGGCGATTT
401 TAAACAACAG CCGCAGCAAC ACCCAAACAC AGCTAGGCGG TTGGATTCAA
451 GGTAATCCTT GGTGGCAAG GGGCGAAGCA CGTGTGGTTG TAAACCAAAT
501 CAACAGCAGC CATTCTTCAC AAATGAATGG CTATATTGAA GTGGGCGGAC
551 GACGTGCAGA AGTCGTTATT GCCAATCCGG CAGGGATTGC AGTCAATGGT
601 GGTGGTTTTA TCAATGCTTC CCGTGCCACT TTGACGACAG GCCAACCGCA
651 ATATCAAGCA GGAGACCTTA GCGGCTTTAA GATAAGGCAA GGCAATGTTG
701 TAATCGCCGG ACACGGTTTG GATGCCCCGTG ATACCGATT CACACGTATT
751 CTCAGTTATC ATTCCAAAAT TGATGCACCC GTATGGGGAC AAGATGTTTCG
801 TGTCGTGCGG GGACAAAACG ATGTGGTCCG AACAGGTAAT GCACATTTCG
851 CTATTCTCAA TAATGCTGCT GCCAATACGT CAAACAATAC AGCCAACAAC
901 GGCACACATA TCCCTTTATT TGCGATTGAT ACAGGCAAAT TAGGAGGTAT
951 GTATGCCAAG AAAATCACCT TGATCAGTAC GGCCGAGCAA GCAGGCATT
1001 GTAATCAAGG GCAGTTGTTT GCTTCTTCCG GTAATGTGGC GATTGATGCA
1051 AATGGCCGTT TAGTCAATAG TGGCACGATG GCTGCCGCCA ATGCGAAAGA
1101 TACGATAAAT ACAGCGGAAC ACAAGTCAA TATCCGAGT CAGGGCGTTG
1151 AAAACAGCGG TACGGCGGTA TCGCAACAAG GCACTCAAAT TCACAGTCAG
1201 TCGATTCAAA ACTTGGCAC ATTATTGTCC TCAGGCGAAA TATTGATTCA
1251 CAATTCGGGC AGCCTGAAAA ATGAAACATC AGGCACCAT GAAGCCGCTC
1301 GTTTGGCTAT TGATACCGAC ACACTTAATA ATCAAGGCAA ACTCTCTCAA
1351 ACAGGTTTCA AAAAACTCCA TATTGATGCA CAAGGCAAAA TGGATAACCG
1401 TGGCCGCATG GGTTTACAAG ATACCGCACC AACCGCGTCA AATGGTTCAA
1451 GCAATCAAAC CGGCAATAGT TACAATGCAT CTTTCCATTC ATCCACTACC
1501 ACACCAACAA CGGCAACAGG TACGGGTACT GCAACCGTTT CTATATCAAA
1551 CATAACTGCG CCTACCTTTG CTGATGGGAC AATTCGCACT CATGGTGCAC
1601 TGGATAATTC AGGCAGTATT ATTGCCAATG GTCAAACAGA TGTTAGTGCG
1651 CAACAAGGTT TAAATAATGC AGGACAAATA GACATTTCATC AGTTAAATGC
1701 AAAAGGTTTC GCGTTTGACA ATCACAATGG AACAAATTATC AGTGATGCGG
1751 TCCACATTCA AGCCGGCAGC CTGAATAATC AAAATGGCAA CATCACAACA
1801 CGCCAACAGT TAGAGATTGA AACCGATCAA CTGGATAACG CTCATGGCAA
1851 GTTATTATCA GCAGAAATAG CGGATTTAGC CGTTTCAGGC AGCCTGAACA
1901 ATCAAAATGG CGAAATAGCG ACCAATCAAC AACTGATTAT TCACGATGGT
1951 CAGCAATCTA CCGCTGTCAT TGATAATACG AATGGCACGA TACAATCAGG
2001 CCGTGATGTT GCTATTCAGG CAAAATCGTT ATCCAACAAC GGCACACTTG
2051 CCGCTGATAA TAACTGGAT ATTGCGTTAC AAGATGATT TATGTAGAA
2101 CGCAATATCG TGGCGGGCAA TGAATTGTCG CTCAGTACAC GAGGCAGCCT
2151 GAAAAATTCA CATACTTTGC AAGCAGGAAA ACGCATTCCG ATTAAGCAA
2201 ATAACCTTGA TAATGCAGCA CAAGGCAACA TTCAATCCGG CGGTACGACA
2251 GACATTGGCA CGCAGCACAA TTTAACCAAT AGAGGCTTGA TTGACGACA
2301 ACAAACCAAA ATCCAAGCCG GGCAATGAA TAATATCGGT ACAGGTCGGA
2351 TTTATGGCGA CAATATCGCT ATTGCGGCTA CCCGCTTAGA CAATCAAGAT
2401 GAAACGGTA CAGGTGCCGC CATTGCGGCA CGTGAAAACC TGAATTTAGG
2451 CATCGACAAA TTAAACAACC GTGAAAACAG TCTGATTTAC AGCGGTAACG
2501 ATATGGCGGT TGGCGGCGCA TTAGATACCA ATGGCCAAGC CACAGGCAAA
2551 GCCCAAAGGA TACACAATGC CGGCGCAACC ATTGAAGCTG CAGGCAAAAT
2601 CGCTTTAGGT GTAGAAAAGC TGCACAATAC CAATGAGCAT TTGAAAACGC
2651 AGTTGGTAGA AACAGGGCGC GAGCATATTG TTGATTACGA AGCATTGGGA
2701 CGACACGAAT TATTGCGAGA AGGCACGCAA CATGAATTAG GCTGGTCTGT
2751 CTATAACGAT GAATCAGACC ACTTACGCAC CCCTGATGGA GCGGCGCATG
2801 AAAATTGGCA TAAATACGAT TATGAAAAAG TCACCCAAAA AACCCAAGTT
2851 ACCCAAACCTG CGCCAGCCAA AATCATTTCA GGTAAATGATT TAACCATTGA
2901 TGGTAAAGAA GTATTTAATA CCGATAGCCA AATCATTGCT GGTGGCAATC
2951 TCATTGTACA AACAGAAAAA GACGGTTTGC ATAACGAGCA AACCTTTGGC

```

```

3001  GAAAAGAAAG  TATTCAGTGA  AAATGGCAAA  TTACACAGCT  ATTGGCGTGA
3051  GAAACATAAA  GGACGAGACT  CAACGGGACA  TAGCGAACAA  AATTACACTT
3101  TGCCGGAGGA  AATCACACGC  AACATTTTAC  TGGGTTTATT  TGCCTATGAA
3151  TCGCATCGCA  AAGCATTAA  CCATCATGCG  CCCAGCCAAG  GCACTGAGTT
3201  GCCGCAAAGC  AACGGTATTT  CGCTACCCTA  TACGTCCAAT  TCTTTTACCC
3251  CATTACCCAG  CAGCAGCTTA  TACATTATCA  ATCCTGTCAA  TAAAGGCTAT
3301  CTTGTTGAAA  CCGATCCACG  CTTTGCCAAC  TACCGTCAAT  GGTGGGTAG
3351  TGACTATATG  CTGGACAGCC  TCAAACATA  CCCAAACAAT  TTACATAAAC
3401  GTTTGGGTGA  TGGTTATTAC  GAGCAACGTT  TAATCAATGA  ACAAATCGCA
3451  GAGCTGACAG  GGCATCGTCG  TTTAGACGGT  TATCAAAACG  ACGAAGAACA
3501  ATTTAAAGCC  TTAATGGATA  ATGGCGCGAC  TGCGGCACGT  TCGATGAATC
3551  TCAGCGTTGG  CATTGCATTA  AGTGCCGAGC  AAGTAGCGCA  ACTGACCAGC
3601  GATATTGTTT  GGTTGGTACA  AAAAGAAGTT  AAGCTTCCTG  ATGGCGGCAC
3651  ACAAAACGTA  TTGGTGCCAC  AGGTTTATGT  ACGCGTTAAA  AATGGCGACA
3701  TAGACGGTAA  AGGTGCATTG  TTGTCAGGCA  GCAATACACA  AATCAATGTT
3751  TCAGGCAGCC  TGAAAAACTC  AGGCACGATT  GCAGGGCGCA  ATGCGCTTAT
3801  TATCAATACC  GATACGCTAG  ACAATATCGG  TGGGCGTATT  CATGCGCAAA
3851  AATCAGCGGT  TACGGCCACA  CAAGACATCA  ATAATATTGG  CGGCATGCTT
3901  TCTGCCGAAC  AGACATTATT  GCTCAACGCA  GGCAACAACA  TCAACAGCCA
3951  AAGCACCACC  GCCAGCAGTC  AAAATACACA  AGGCAGCAGC  ACCTACCTAG
4001  ACCGAATGGC  AGGTATTTAT  ATCACAGGCA  AAGAAAAAGG  TGTTTTAGCA
4051  GCGCAGGCAG  GAAAAGACAT  CAACATCATT  GCCGGTCAAA  TCAGCAATCA
4101  ATCAGAGCAA  GGGCAAACCC  GGCTGCAAGC  AGGGCGCGAC  ATTAACCTAG
4151  ATACGGTACA  AACCAGCAAA  CATCAAGCAA  CCCATTTTGA  TGCCGATAAC
4201  CATGTTATT  GCGGTTCAAC  GAACGAAGTC  GGCAGCAGCA  TTCAAACAAA
4251  AGGCGATGTT  ACCCTATTGT  CAGGGAATAA  CCTCAATGCC  AAAGCTGCCC
4301  AAGTCAGCAG  CGCAAACGGT  ACACTCGCTG  TGTCTGCCAA  AAATGACATC
4351  AACATCAGCG  CAGGCATCAA  CACGACCCAT  GTTGATGATG  CGTCCAAACA
4401  CACAGGCAGA  AGCGGTGGTG  GCAATAAATT  AGTCATTACC  GATAAAGCCC
4451  AAAGTCATCA  CGAAACCGCC  CAAAGCAGCA  CCTTTGAAGG  CAAGCAAGTT
4501  GTATTGCAGG  CAGGAAACGA  TGCCAACATC  CTTGGCAGCA  ATGTTATTTT
4551  CGATAATGGC  ACCCAGATTC  AAGCAGGCAA  TCATGTTTCG  ATTGGTACAA
4601  CCCAAACTCA  AAGCCAAAGC  GAAACCTATC  ATCAAACCCA  GAAATCAGGA
4651  TTGATGAGTG  CAGGTATCGG  CTTCACTATT  GGCAGCAAGA  CAAACACACA
4701  AGAAAACCAA  TCCCAAAGCA  ACGAACATAC  AGGCAGTACC  GTAGGCAGCT
4751  TGAAAGGCGA  TACCACCATT  GTTGCAGGCA  AACACTACGA  ACAAATCGGC
4801  AGTACCGTTT  CCAGCCCGGA  AGGCAACAAT  ACCATCTATG  CCCAAAGCAT
4851  AGACATTCAA  GCGGCACACA  ACAAAATAAA  CAGTAATACC  ACCCAAACCT
4901  ATGAACAAAA  AGGCCTAACG  GTGGCATTCA  GTTCGCCCGT  TACCGATTTG
4951  GCACAACAAG  CGATTGCCGT  AGCACAAGC  AGCAAACAAG  TCGGACAAAG
5001  CAAAACGAC  CGCGTTAATG  CCAATGGCGG  TGCCAATGCA  GGCTGGCAAG
5051  CCTATCAAAC  AGGTAAGAGT  GCACAAAAC  TAGCCAATGG  TACAACCAAT
5101  GCCAAACAAG  TCAGCATCTC  CATAACCTAC  GGCGAACAGC  AAAACCGACA
5151  AACCACCCAA  GTTCAAGCCA  ATCAAGCCCA  AGCGAGTCAA  ATTCAAGCAG
5201  GTGGTAAAC  CACATTAATC  GCCACAGGCG  CAGCAGAACA  ATCCAATATC
5251  AACATCGCAG  GCTCAGATGT  TGCCGGCAAA  GCAGGCACAA  TCCTGATTGC
5301  CGATAACGAC  ATCACACTCC  AATCAGCCGA  GCAAAGCAAT  ACCGAACGCG
5351  GCCAAACAA  ATCGGCAGGC  TGGAACGCAG  GTGCTGCCGT  ATCATTGCGA
5401  CAAGGAGGCT  GGTCAATTAG  CGTTACCGCA  GGCGGCAATG  TCGGCAAAGG
5451  CTACGGCAAT  GCGCAGAGCA  TCACCCACCG  CCATAGCCAT  ATCGGCGACA
5501  AAGGCAGCCA  AACCCTTATC  CAAAGCGGTG  GCGACACTAC  CATCAAAGGC
5551  GCGCAAGTAC  GCGGCAAAGG  CGTACAAGTC  AATGCCAAAA  ACCTAAGTAT
5601  TCAAAGCGTA  CAAGATAGAG  AAACCTATCA  AAGCAAACA  CAAAACGCCA
5651  GTGCACAAGT  TACCGTAGGT  TATGGCTTCA  GTGCCGGTGG  CGATTACAGC
5701  CAAAGCAAAA  TCCGAGCCGA  CCATGTTTCA  GTAACCGAGC  AAAGCGGTAT
5751  TTATGCCGGA  GAAGACGGCT  ATCAAATCAA  GGTGCGAAAC  CATACAGACC
5801  TCAAAGGCGG  CATCATCACC  AGTACCCAAA  GCGCAGAAGA  CAAGGGTAAA
5851  AACCCTTTT  AGACGGCCAC  CCTCACCCT  AGCGACATCA  AAAACCACAG
5901  CCAATACAAA  GGCGAAAGTT  TTGGATTGGG  CGCAAGTGG  TCCATAAGCG
5951  GCAAAACACT  GGGACAGGGC  GCACAAAATA  AACCTCAAAA  CAAACACCTG
6001  ACAAGCGTAG  CCGATAAAAA  CAGCGCAAGT  TCATCAGTGG  GTTATGGCAG
6051  CGACAGCGAC  AGTCAAAGCA  GCATCACAAA  AAGCGGCATC  AACACCCGCA

```

```

6101 ACATTCAAAT CACCGACGAA GCCGCACAAA TCCGGCTGAC AGGCAAAACA
6151 GCGGCACAAA CCAAAGCCGA TATTGATACA AACGTAACCA CAGACACCGC
6201 CGAACGACAT TCGGGCAGCT TGAAGAACAC CTTCAACAAA GAAGCGGTGC
6251 AAAGTGAAC TGGATTTACAA AGAACCGTCA GCCAAGATT TAGTAAAAAT
6301 GTTCAACAAG CCAATACCGA GATTAACCAA CATTTAGACA AACTCAAAGC
6351 AGACAAAAGAA GCAGCCGAAA CAGCAGCAGC CGAGGCATTA GCCAATGGCG
6401 ATATGGAAAC TGCCAAACGC AAAGCCCATG AAGCTCAAGA TGCGGCAGCA
6451 AAAGCAGATA ATTGGCAACA AGGCAAAGTC ATTCTCAACA TGTTAGCCTC
6501 AGGTTTAGCT GCGCCGACCC AAAGCGGAGC GGGCATCGCT GCGGCTACCG
6551 CATCGCCAGC CGTATCGTAT GCGATTGGAC AGCACTTTAA AGATTTAGCC
6601 GGTCAAAACG CGAATGGTAA ACTAACCGCC AGTCAAGAAA CCGCACACGT
6651 TCTTGCCAC GCGGTATTAG GAGCAGCGGT TGCCGCAGTA GGAGACAACA
6701 ATGCTCTAGC AGGAGCATTG AGTGC GGCG GGTGCGAAGC GGCTGCGCCT
6751 TACATCAGCA AATGGTTATA CGGCAAAGAA AAAGGAAGCG ACTTAACGGC
6801 GGAAGAGAAA GAGACTGTAA CAGCGATTAC AAATGTATTG GGTACGGCTA
6851 CGGGTGCGGC AGTCGGCAAC AGCGCAACAG ATGCAGCGCA AGGCAGCCTG
6901 AATGCGCAA GTGCGGTGGA GAATAATGAT ACTGTAGAGC AAGTGAAATT
6951 TGCTCTTAGG CACCCTAGAA TTGCTATTGC AATTGGATCT GTACATAAAG
7001 ATCCTGGCTC TACATTAGAG CCTAATATTT CAACAATTGC TTCAACTTTT
7051 CAATTAATTT TATTTCTTAA TAGTGAATTT GGTGGTGAAG GTGGAGTTGG
7101 CAATGCATTC AGGCACGTTT TATGGCAAGC AACCATCACA CGAGAATTTG
7151 GCAAAGATAT TGCTGTTAAA GTAGGAAATA GTCATGAAAG TGGGGAAAAA
7201 ATTAATTATT CTATAAGACG TAATCTTTCA TTAGATAAAG CAGATGAAAT
7251 GATTGATCAA CTAAATAACG AAATAGGAAG AGAAATAGCA TTAAATACCA
7301 ATAGGTTAAA CACAAAAGAG TTAGTTGGAT TAATTCTGGA AACTTATAAA
7351 AATAATGGTT TTTATCAAGC AGAAAGAAAC AGTAATGGAA ATTATGATGT
7401 TGTAAGAAAA AGATTATCTG AAAAAAGATTA CCAGAATACA AGCAATATAT
7451 TGATTCACTT AGATAATACT GGTGCCGGAT TAAAATTCA GCAGAGGAGA
7501 AAACAAATCA GAGCACAAAT TTCAGCCAGA CAATGGAGAA GATAA

```

This corresponds to the amino acid sequence <SEQ ID 1668; ORF 563>:

m563.pep..

```

1 MNKTLYRVIF NRKRGAVVAV AETTKREGKS CADSDSGSAH VKSVPFGTTH
51 APVCRSNIFS FSLLGFSLCL AVGTANIAFA DGIIADKAAP KTQQATILQT
101 GNGIPQVNIQ TPTSAGVSVN QYAQFDVGNR GAILNNSRSN TQTQLGGWIQ
151 GNPWLARGEA RVVNVQINSS HSSQMNGYIE VGGRRAEVVI ANPAGIAVNG
201 GGFINASRAT LTTGQPQYQA GDLSGFKIRQ GNVVIAGHGL DARDTDFTRI
251 LSYHISKIDAP VWQDVRVVA QONDVVATGN AHSPILNNA ANTSNNTANN
301 GTHIPLFAID TGKLGGMYAN KITLISTAEQ AGIRNQGLF ASSGNVAIDA
351 NGRLVNSGTM AAANAKDTDN TAEHKVNIRS QGVENSQTAV SQOQTQIHSQ
401 SIQNTGTLLS SGEILIHNSG SLKNETSGTI EAARLAIDTD TLNNQGLKLSQ
451 TGSQKLHIDA QGKMDNRGRM GLQDTAPTAS NGSSNQTGNS YNASFHSSTT
501 TPTTATGTGT ATVSISNITA PTFADGTIRT HGALDNSGSI IANGQTDVSA
551 QOGLNNAQOI DIHQLNAKGS AFDNHNGTII SDAVHIQAGS LNNQNGNITT
601 RQOLEIETDQ LDNAHGKLLS AEIADLAVSG SLNNQNGEIA TNQQLIIHDG
651 QQSTAVIDNT NGTIQSGRDV AIQAKSLSNN GTLAADNKLD IALQDDFYVE
701 RNIVAGNELS LSTRGSLKNS HTLQAGKRIR IKANNLDNAA QGNIQSGGTT
751 DIGTQHNLTN RGLIDGQQTQ IQAGQMNNIG TGRIYGDNIA IAATRLDNQD
801 ENGTGAAIAA RENLNLGIGQ LNNRENSLIY SGNDMAVGGA LDTNGQATGK
851 AQRIHNAGAT IEAAGKMRLG VEKLHNTNEH LKTQLVETGR EHIVDYEAFG
901 RHELLREGTQ HELGWSVYND ESDHLRTPDG AAHENWHKYD YEKVTQKTQV
951 TQTAPAKIIS GNDLTIDGKE VFNTDSQIIA GGNLIVQTEK DGLHNEQTFG
1001 EKKVFSENGK LHSYWREKHK GRDSTGHSEQ NYTLPEEITR NISLGSFAYE
1051 SHRKALSHHA PSQGTLPQS NGISLPYTSN SFTPLPSSSL YIINPVNKG Y
1101 LVETDPRFAN YRQWLGS DYM LDSLKLDPNN LHKRLGDGYY EORLINEQIA
1151 ELTGHRRLDG YQNDDEEQFKA LMDNGATAAR SMNLSVGIAL SAEQVAQLTS
1201 DIVWLQKEV KLPDGGTQTV LVPQVYVRVK NGDIDGKGAL LSGSNTQINV
1251 SGSLKNSGTI AGRNALIINT DTLDNIGGRI HAQKSAVTAT QDINNIGGML
1301 SAEQTLLENA GNNINSQSTT ASSQNTQGSS TYLDRMAGIY ITGKEKGVLA
1351 AQAGKDINII AGQISNQSEQ GQTRLQAGRD INLDTVQTSK HQATHFDADN
1401 HVIRGSTNEV GSSIQTGKDV TLLSGNNLNA KAAEVSSANG TLAVSAKNDI
1451 NISAGINTTH VDDASKHTGR SGGGNKLVIT DKAQSHHETA QSSTFEGKQV
1501 VLQAGNDANI LGSNVIDNG TQIQAGNHVR IGTQTQTSQS ETYHQTQKSG

```

855

```

1551 LMSAGIGFTI GSKTNTQENQ SQSNEHTGST VGSCLKGDTTI VAGKHYEQIG
1601 STVSSPEGNN TIYAQSIDIQ AAHNKLNST TQTYEQKGLT VAFSSPVTDL
1651 AQQAIAVAQS SKQVGQSKND RVNAMAANA GWQAYQTGKS AQNLANGTTN
1701 AKQVVISITY GEQQNRQTQ VQANQAQASQ IQAGGKTTLI ATGAAEQSNI
1751 NIAGSDVAGK AGTILIADND ITLQSAEQSN TERGQNKASG WNAGAAVSFG
1801 QGGWSLGVTA GGNVKGKGYGN GDSITHRSH IGDKGSQTLI QSGGDTTIKG
1851 AQVRGKGVQV NAKNLSIQSV QDRETYQSKQ QNASAQVTVG YGFSAGGDYS
1901 QSKIRADHVS VTEQSGIYAG EDGYQIKVGN HTDLKGGIIT STQSAEDK GK
1951 NRFQTATLTH SDIKNHSQYK GESFGLGASA SISGKTLGQG AQNKPNKHL
2001 TSVADKNSAS SSVGYGSDSD SQSSITKSGI NTRNIQITDE AAQIRLTGKT
2051 AAQTKADIDT NVTDTAERH SGSLKNTFNK EAVQSELDLQ RTVSQDFSKN
2101 VQQANTEINQ HLDKCLKADKE AAETAAAEAL ANGDMETAKR KAHEAQDAAA
2151 KADNWQQGV ILNMLASGLA APTQSGAGIA AATASPAVS Y AIGQHFCDLA
2201 QONANGKLT SQETAHVLAH AVLGAAVAAV GDNALAGAL SAGGSEAAAP
2251 YISKWLYGKE KGSDLTAEK ETVTAITNVL GTATGAAVGN SATDAAQGS L
2301 NAQSAVENND TVEQVKFALR HPRIAIAIGS VH KDPGSTLE PNISTIASTF
2351 QLNLPNSEF GEGGVGNF RHVLWQATIT REFGKDI AVK VGNSHESGEK
2401 INYSIRRNL LDKADEMIDQ LNNEIGREIA LNTNRLNTKE LVGLILETYK
2451 NNGFYQAERN SNGNYDVVRK RLSEKDYQNT SNILIHLDNT GAGFKIQRR
2501 KQIRAQISAR QWRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 563 shows 79.1% identity over a 2316 aa overlap with a predicted ORF (ORF 563.ng) from *N. gonorrhoeae*:

m563/g563

```

              10      20      30      40      50
g563 . pep  MNKTL YRVIFNRKRGAVVAVAETTKREGKSCADSGSGSVYVKSVSFIPTH-----SKAFC
              |||||
m563 . pep  MNKTL YRVIFNRKRGAVVAVAETTKREGKSCADSDSGSAHVKSVPFGTTHAPVCRSNIFS
              10      20      30      40      50      60

              60      70      80      90      100     110
g563 . pep  FSALG FSLCLALGTVNIAFADGIITDKAAPKTQQATILQTGNGIPQVNIQTPTSAGVSVN
              |||||
m563 . pep  FSLLG FSLCLAVGTANIAFADGIADKAAPKTQQATILQTGNGIPQVNIQTPTSAGVSVN
              70      80      90      100     110     120

              120     130     140     150     160     170
g563 . pep  QYAQFDVGNRGAILNNSRSNTQTQLGGWIQGNPWLTRGEARVVVNQINSSHPSQLNGYIE
              |||||
m563 . pep  QYAQFDVGNRGAILNNSRSNTQTQLGGWIQGNPWLARGEARVVVNQINSSHSQMNGYIE
              130     140     150     160     170     180

              180     190     200     210     220     230
g563 . pep  VGGRRAEVVIANPAGIAVNGGGFINASRATLTGQPQYQAGDFSGFKIRQGNVIAIGHGL
              |||||
m563 . pep  VGGRRAEVVIANPAGIAVNGGGFINASRATLTGQPQYQAGDLSGFKIRQGNVIAIGHGL
              190     200     210     220     230     240

              240
g563 . pep  DARDTDFTRIL-----
              |||||
m563 . pep  DARDTDFTRILSYHSKIDAPVWQDVRVVGQNDVVATGNAHSPILNNAANTSNTANN
              250     260     270     280     290     300

              250     260     270     280     290
g563 . pep  -----LYANKITLISTAEQAGIRNQGLFASSGNVAIDANGRLVNSGTM
              :|||
m563 . pep  GTHIPLFAIDTGKLGMYANKITLISTAEQAGIRNQGLFASSGNVAIDANGRLVNSGTM
              310     320     330     340     350     360

```

856

	300	310	320	330	340
g563 . pep	AAANVQDMNNTAEHKVNIRSQAFENSGTAVSQQGTQIHSQSIQNTGKLLSAGT-----				
	:: : :				
m563 . pep	AAANAKDTDNTAEHKVNIRSQGVENSGTAVSQQGTQIHSQSIQNTGTLSSGEILIHNSG				
	370	380	390	400	410 420
g563 . pep	-----				
m563 . pep	SLKNETSGTIEAARLAIDTDTLNNQGKLSQTSQKLHIDAQGMKMDNRGRMGLQDTAPTAS				
	430	440	450	460	470 480
g563 . pep	-----				
m563 . pep	NGSSNQTGNSYNASFHSSTTTPTTATGTGTATVSIENITAPTTFADGTIRTHGALDNSGSI				
	490	500	510	520	530 540
g563 . pep	-----				
m563 . pep	IANGQTDVSAQQGLNNAQIDIHQLNAKGSADFNDHNGTIIISDAVHIQAGSLNNQNGNITT				
	550	560	570	580	590 600
g563 . pep	-----EDLAVSGSLNNQNGEIATNQQLIIHDGQQSTVVIDNT				
m563 . pep	RQOLEIETDQLDNAHGKLLSAEIALAVSGSLNNQNGEIATNQQLIIHDGQQSTAVIDNT				
	610	620	630	640	650 660
g563 . pep	390	400	410	420	430 440
	NGTIQSGRDVAIQAKSLNNGTLAADNKLDIALQDDFYVERKIVAGNELSLSTRGSLKNS				
m563 . pep	NGTIQSGRDVAIQAKSLNNGTLAADNKLDIALQDDFYVERNIVAGNELSLSTRGSLKNS				
	670	680	690	700	710 720
g563 . pep	450	460	470	480	490 500
	HTLQAGKRIRIKANNLDNAVQGNIQSGGTTDIGTQHNLNTRGLIDGQQTQKIAGQMNNIG				
m563 . pep	HTLQAGKRIRIKANNLDNAAQGNIQSGGTTDIGTQHNLNTRGLIDGQQTQKIAGQMNNIG				
	730	740	750	760	770 780
g563 . pep	510	520	530	540	550 560
	TGRIYGDNIAIAATRLDNQDENGTTGAAIAARENLNLGIEQLNNRENSLIYSGNDMAVGGA				
m563 . pep	TGRIYGDNIAIAATRLDNQDENGTTGAAIAARENLNLGIGQLNNRENSLIYSGNDMAVGGA				
	790	800	810	820	830 840
g563 . pep	570	580	590	600	610 620
	LDTNDQATGKAQRIHNAGATIEAAGKMRLGVEKLHNTNEHLKTQLVETGRERIVDYEAFG				
m563 . pep	LDTNGQATGKAQRIHNAGATIEAAGKMRLGVEKLHNTNEHLKTQLVETGREHIVDYEAFG				
	850	860	870	880	890 900
g563 . pep	630	640	650	660	670 680
	RHELLREGTQHELGFVYNNESDHLRTPDGAHENWHKYDYKVTQETQVTTGAPAKIIA				
m563 . pep	RHELLREGTQHELGWSVYNDES DHLRTPDGAHENWHKYDYKVTQKTQVTTGAPAKIIS				
	910	920	930	940	950 960
	690	700	710	720	730 740

859

	1950	1960	1970	1980	1990	2000
g563 . pep	TASQETAHVLHAHVLGA AVAAAXGNNAPAGALGAGGSEAAAPIIGKWLYGKGDGGSLSNAE					
	: : : : :: :					
m563 . pep	TASQETAHVLHAHVLGA AVAVGDNNALAGALSAGGSEAAAPYISKWLYGKEKGSIDLTAE					
	2210	2220	2230	2240	2250	2260

	2010	2020	2030	2040	2049	
g563 . pep	EKETVSAITRMLGTAAGAAEGNSSADAVWGCFTASDFASSFSYPINMX					
	: : : : : ::					
m563 . pep	EKETVTAITNVLTATGA AVGNSATDAAQGSLSNAQSAVENNDTVEQVKFALRHPRIAIAI					
	2270	2280	2290	2300	2310	2320

m563 . pep	GSVHKDPGSTLEPNISTIASTFQLNLPNSEFGGEGGVGNAFRHLVWQATITREFGKDIA					
	2330	2340	2350	2360	2370	2380

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1669>:

```

m564 . seq
1   ATGAACCGCA CCCTGTACAA AGTTGTATTT AACAAACATC GAAACTGCAT
51  GATAGCCGTT GCTGAAAATG CCAAACGCGA GGGCAAAAAC ACAGCCGACA
101 CCCAAGCTGT AGGTATTTTG CCAATGATA TTGCGGGCTT TGCGGGTTTT
151 ATCCATTCTA TCTCTGTTAT CTCATTCTCC CTTTCATTAC TGCTCGGTTC
201 TGCCCTTATC CTGACTTCTT CTCTGCTAC TGCCCAAGGT ATCGTTGCCG
251 ACAAATCCGC ACCTGCACAG CAACAGCCTA CCATCCTGCA AACAGGTAAC
301 GGCATACCGC AAGTCAATAT TCAAACCCCT ACTTCGGCAG GGGTTTCTGT
351 TAATCAATAC GCCCAGTTTG ATGTGGGTAA TCGCGGGGCG ATTTTAAACA
401 ACAGTCGCAG CAACACCCAA ACACAGCTAG GCGGTTGGAT TCAAGGCAAT
451 CCTTGGTTGG CAAGGGGCGA AGCACGTGTG GTTGTAACC AAATCAACAG
501 CAGCCATTCT TCACAATGTA ATGGCTATAT TGAAGTGGG GAGACAGGTG
551 CAGAAGTCGT TATTGCCAAT CCGGCAGGGA TTGCAGTCAA TGGTGGTGGT
601 TTTATCAATG CTTCCCGTGC CACTTTGACG ACAGCCCAAC CGCAATATCA
651 AGCAGGAGAC CTTAGCGGCT TTAAGATAAG GCAAGGCAAT GTTGTAAATC
701 CCGGACACGG TTTGGATGCA CGTGATACCG ATTACACACG TATTCTCAGT
751 TATCATTCCA AAATTGATGC ACCCGTATGG GGACAAGATG TTCGTGTCGT
801 CGCGGGACAA AACGATGTGG CCGCAACAGG TGATGCACAT TCGCCTATTC
851 TCAATAATGC TGCTGCCAAT ACGTCAAACA ATACAGCCAA CAACGGCACA
901 CATATCCCTT TATTTGCGAT TGATACAGGC AAATTAGGAG GTATGTATGC
951 CAACAAAATC ACCTTGATCA GTACGGTCGA GCAAGCAGGC ATTCGTAATC
1001 AAGGGCAATG GTTTGCCTCA GCCGGCAATG TGGCAGTGAA TGCTGAGGGT
1051 AAAGTGGTCA ACACGGGCAT GATTGCAGCG ACGGGAGAAA ATCATGCGGT
1101 TTCATTCTAT GCCCGCAATG TTCATAATAG CGGTACGGTT GCCTCACAGG
1151 ATGATGCCAA TATTCACAGC CAGACGCTGG ACAATTCAGG TACGGTCTTA
1201 TCCTCAGGTC GATTGACTGT TCGTAATTTA GGCCGTCTGA AAAACCAAAA
1251 CAACGGTACG ATCCAGGCTG CCCGCTTAGA TATGTCAACA GGTGGTTTGG
1301 ATAACACAGG TAATATTACT CAAACAGGTT CACAAGCATT GGATTTGGTA
1351 TCTGCCGGCA AATTCGATAA CAGTGGCAAG ATTGGTGTA GTGACGTTCC
1401 ACAGACCGGT TTGAATCCCA ATCCATCAGT CATACCACAG ATTCCGAGTA
1451 CTGCAACAGG TTCAGGCAGC AGCACTGTCT CGGTATCTAA GCCTGGTTCA
1501 AACAATCCCG TTTCACCTAC AGCACCTGCA AAAAATACG CCGTAGGACG
1551 CATTCAAACA ACAGGAGCAT TTGACAATGC AGGATCAATT AATGCGGGTG
1601 GGCAAAATGA CATTGCCGCC CAAAACGGTT TGGGAAATTC GGGTAGTCTG
1651 AATGCGGCTA AACTACGAGT ATCAGGCGAT TCATTTAACA ATACGGTAAA
1701 AGGCAAACTC CAGGCACAGC ATCTGGCTGT TAACACTCAA ACTGCTAAAA
1751 ACAGCGGTCA CTTATTAAT CAAACCGGCA AGATTGATAA CCGTGAAGTG
1801 CATAATGCCG GAGAAATTGC CGCCAACAAT CTGACACTCA TTCATTGGG
1851 CCGCTTGAGC AATGATAAAA AAGGCAATAT TCGAGCTGCA CATTTACAGC
1901 TTGATACCGC CGGTTTACAT AATGCAGGTA ACATTCTTGC CGATAGTGG
1951 ACCGTTACCA CCAAGAATAA TCTTCGCAAT ACAGGAAAAG TTTCTGTTGC
2001 ACGACTGAAT ACCGAAGGTC AGACTCTAGA TAATACGCGC GGACGTATAG
2051 AGGCTGAAAC GGTAAACATC CAAAGTCAGC AACTGACTAA CCAAAGCGGC
2101 CATATTACTG CTACCGAACA ACTGACTATC AATAGTCGAA ATGTAGACAA
2151 CCAAAACGGC AAATCCTAT CTGCAACCCA AGCACAATTA GCTGTTTCAG
2201 ACGGCCTATA CAACCAACAT GGTGAAATTG CCACCAACCG GCAGTTGTCT

```

2251 ATTCACGATA AAAATCAAAA CACTTTGGCG TTAAACAATG CGGATGGCAC
 2301 GATTCAATCT GCCGGTAATG TATCGCTACA AGCCAAATCA CTCGCCAACA
 2351 ATGGCACATT AACAGCCGGT AACAACTGG ATATTGCTTT GACGGACGAT
 2401 TTCGTCGTAG AGCGCGACCT CACTGCAGGC AAACAATTAA ATCTAAGCAT
 2451 AAAAGGCCGT CTGAAAAATA CCCATACCCT ACAAGCAGGC CATACGCTCA
 2501 AACTCAATGC CGGCAATATA GATAACCAAG TTACAGGCAA AATTATTGGT
 2551 GGAGAACAAA CGGACATCAC ATCCGAACAG CATGTTGACA ACAGGGGCTT
 2601 GATCAACAGC GACGGTTTGA CCCACATCGG TGCAGGTCAA ACCCTGACCA
 2651 ACACCGGGAC AGGCAAAATC TATGGCAACC ATATTGCCCT GGACGCGCAA
 2701 ATACTGCTTA ACCGGGAAGA AACGACGGAA GGCAGTACCA AAGCGGGGGC
 2751 AATAGCTGCA AGGAAACGTT TGGATATTGG AGCGAAAGAG ATTCATAACC
 2801 AAGAAGGTGC CCTACTATCC AGCGAAGGTA TTTTGGCCGT AgGTAATCGA
 2851 CTGGATGAAC AACATCATGC GGCAGGCATG GCCGATACCT TTGTTAATGG
 2901 CAGTGCCGGT TTGGAAGTAC AAGGTGATGC ATTGATGTCC GTTCGGAATA
 2951 TGCAGAATAT CAATAATCAC TTTAAACAG AGACATACTT AGCCAAAGCG
 3001 GAAAAGCAAG TCCGCGACTA CACCGTACTG GGGCAAAATA CCTACTATCA
 3051 GCGGGGAAAA GACGGTTTAT TCGACAACTC GCAAGGACAA AAAGACCAAA
 3101 CTAATGCTAC GTTCCATTAA AAAAATGGTT CTCGTATTGA GGCCAACCAA
 3151 TGGCATGTCC GAGACTACCA CATCGAGACT TATAAAGAAC GCATCATCGA
 3201 AAACCGGCCG GCACACATTA CTGTGGGCGG TGATTGACT GCCTCAGGTC
 3251 AAAATTGGCT GAACAAAGAC AGCCGGATTG TAGTAGGCGG GCGTATTATC
 3301 ACTGATGATT TAAACCAGAA AGAAATTACC AATCAAAGTA CAACAGGCAA
 3351 AGGTCGCACA GATGCTGTCT GCACACAGTG GGATTGAGT AAAAAAAG
 3401 GATGGTACAG CGGTAGAAAA AGACAACGCC GTACTGAAAG AAACCATACT
 3451 CCTTACCATG ATACCCAAT ATTTACCCAC GACTTCGACA CGCCTGTATC
 3501 CGTCATCCAA CAGAATGCCG CCTCCCCTTC CTTTCAACCC GCCCGTACTG
 3551 CAATCAAAT GATTGACGGA GTATCCACGG CAGCCGTCAA TGGTCAGCGC
 3601 ATCCATACCG GTAATGTGGT CTCGTAAAT AACGCTACTG TTACTCTGCC
 3651 TAACAGCAGC CTCTATACCA CCCATCCTGA CAATAAAGGC TGGTTGGTTG
 3701 AAACCGATCC TCAATTTGCA GACTACCGCC GCTGGTTGGG CAGCGACTAC
 3751 ATGTTGCAAC AACTGCAATT GGACACCAAT CATCTACACA AACGGCTTGG
 3801 CGACGGCTAC TACGAACAAA AACTTGTTAA TGAACAAATC CATCAGTTAA
 3851 CAGGCTACCG CCGACTCGAC GGCTACAGGA GTGATGAAGA ACAATTCAAA
 3901 GCTCTGATGG ACAACGGCCT TACTGCTGCC AAAACATTCG GTCTCACCCC
 3951 AGGTATCGCC TTGAGTGCAG AGCAAGTTGC CCGCTTAACT TCAGATATCG
 4001 TTTGGATGGA AAATCAAACC GTCACCCGTG CTGACGGTTC GACTCAAACC
 4051 GTACTGGTTC CTAAAGTCTA TGCCCTGGCG CGCAAAGGTG ATCTCAATAC
 4101 CTCCGGTGGC CTGATTAGTG CCGAACAGT CTTACTTAAA CTGCAAAACG
 4151 GCAACCTGAC TAACAGCGGT ACCATTGCGG GGCGACAGGC CGTACTCATC
 4201 CAGGCACGGA ATATTAACAG CAACGGTAAC ATTCAAGCCG ACCAAATCGG
 4251 CTTAAAGCT GAAAAAGTA TCAATATCGA CGGCGGGCAG GTACAAGCAG
 4301 GCAGACTGCT GACTGCCCAA GCGCAAAATA TCAACCTTAA CGGTACAACC
 4351 CAAACTTCCG GTAATGAACG TAACGGCAAT ACCGCCATCG ATCGTATGGC
 4401 CGGCATTAAC GTGGTCGGAA GCCATACTGA ACAAGTAGAT AACAGAAGTT
 4451 CAGACGGCAT CCTATCCCTG CATGCCAGCA ACGATATCAA CCTCAATTGCG
 4501 GCCACCGTCT CTAACCAAGT TAAAGACGGC ACTACCCAAA TTACCGCCGG
 4551 CAATAATCTC AACCTCGGCA CCATCCGTAC CGAACATCGC GAAGCCTATG
 4601 GTACATTAGA TGACGAGAAC CATCGCCATG TCCGCCAAAG TACCGAAGTC
 4651 GGCAGCAGTA TCCGCACGCA AAACGGCGCA CTGCTTAGAG CCGGTAACGA
 4701 CTTAAAAATC CGCCAAGGCG AACTGGAGGC CGAAGAAGGC AAAACCGTCC
 4751 TTGCCGAGG ACGTGATGTC ACTATCAGCG AAGGACGCCA AATAACCGAA
 4801 CTGGATACCT CGGTAAGCGG AAAAAGCAAA GGCAATCCTT CCAGTACCAA
 4851 AACACACGAC CGCTACCGCT TCAGTCATGA TGAAGCAGTC GGCAGCAACA
 4901 TCGGCGGCGG CAAAATGATT GTTGACGCCG GGCAGGATAT CAATGTACGC
 4951 GGCAGCAACC TTATTTCTGA TAAGGGCATT GTTTTAAAAG CAGGACACGA
 5001 CATCGATATT TCTACTGCCC ATAATCGCTA TACCGGCAAT GAATACACG
 5051 AGAGCAAAAA ATCAGGCGTC ATGGGTACTG GCGGATTGGG CTTTACTATC
 5101 GGTAACCGGA AAATAACCGA TGACACTGAT CGTACCAATA TTGTCCATAC
 5151 AGGCAGCATT ATAGGCAGCC TGAATGGAGA CACCGTTACA GTTGACAGAA
 5201 ACCGCTACCG ACAAACCGGC AGTACCGTCT CCAGCCCCGA GGGGCGCAAT
 5251 ACCGTCACAG CCAAAAGCAT AGATGTAGAG TTCGCAAAACA ACCGGTATGC
 5301 CACTGACTAC GCCCATACCC AGGAACAAAA AGGCCTTACC GTCGCCCTCA
 5351 ATGTCCCGGT TGTCCAAGCT GCACAAACT TCATACAAGC AGCCCAAAAT
 5401 GTGGGCAAAA GTAAAAATAA ACGCGTTAAT GCCATGGCTG CAGCCAATGC
 5451 TGCATGGCAG AGTTATCAAG CAACCAACA AATGCAACAA TTTGCTCCAA
 5501 GCAGCAGTGC GGGACAAGGT CAAAACAACA ATCAAAGCCC CAGTATCAGT

```

5551 GTGTCCATTA CCTACGGCGA ACAGAAAAGT CGTAACGAGC AAAAAAGACA
5601 TTACACCGAA GCGGCAGCAA GTCAAATTAT CGGCAAAGGG CAAACCACAC
5651 TTGCGGCAAC AGGAAGTGGG GAGCAGTCCA ATATCAATAT TACAGGTTCC
5701 GATGTCATCG GCCATGCAAG TACTGCCCTC ATTGCCGACA ACCATATCAG
5751 ACTCCAATCT GCCAAACAGG ACGGCAGCGA GCAAAGCAAA AACAAAAGCA
5801 GTGGTTGGAA TGCAGGCGTA GCCGTCAAAA TAGGCAACGG CATCAGGTTT
5851 GGAATTACCG CCGGAGGAAA TATCGGTAAA GGTAAGAGC AAGGGGGAAG
5901 TACTACCCAC CGCCACACCC ATGTCGGCAG CACAACCGGC AAAACTACCA
5951 TCCGAAGCGG CGGGGATACC ACCCTCAAAG GTGTGCAGCT CATCGGCAAA
6001 GGCATACAGG CAGATACGCG CAACCTGCAT ATAGAAAGTG TTCAAGATAC
6051 TGAAACCTAT CAGAGCAAAC AGCAAAACGG CAATGTCCAA GTTACTGTCG
6101 GTTACGGATT CAGTGCAAGC GGCAGTTACC GCCAAAGCAA AGTCAAAGCA
6151 GACCATGCCT CCGTAACCGG GCAAAGCGGT ATTTATGCCG GAGAAGACGG
6201 CTATCAAATC AAAGTCAGAG ACAACACAGA CCTCAAGGGC GGTATCATCA
6251 CGTCTAGCCA AAGCGCAGAA GATAAGGGCA AAAACCTTTT TCAGACGGCC
6301 ACCCTTACTG CCAGCGACAT TCAAAACAC AGCCGCTACG AAGGCAGAAG
6351 CTTCCGCATA GCGGCGAGT TCGACCTGAA CCGCGGCTGG GACGGCACGG
6401 TTACCGACAA ACAAGGCAGG CCTACCGACA GGATAAGCCC GGCAGCCGGC
6451 TACGGCAGCG ACGGAGACAG CAAAAACAGC ACCACCCGCA GCGGCGTCAA
6501 CACCCACAAC ATACACATCA CCGACGAAGC GGGACAACCT GCCCGAACAG
6551 GCAGGACTGC AAAAGAAACC GAAGCGCGTA TCTACACCGG CATCAGACCC
6601 GAAACTGCGG ATCAACACTC AGGCCATCTG AAAACAGCT TCGACAAAGA
6651 CGCGGTCGCC AAAGAGATCA ACCTGCAAAG GGAAGTAACG AAGGAGTTCC
6701 GCAGAAACGC CGCCCAAGCC GTAGCGGCCG TTGCCGACAA ACTCGGCAAT
6751 ACCCAAAGTT ACGAACGGTA TCAGGAAGCC CGAACCTGCT TGGAGGCCGA
6801 ACTGCAAAAC ACGGACAGCG AAGCCGAAAA AGCCGCCTTC CGCGCATCCC
6851 TCGGCCAAGT AAACGCCTAT CTTGCCGAAA ACCAAAGCCG CTACGACACC
6901 TGGAAGAAG GCGGCATAGG CAGGAGCATA CTGCACGGGG CGGCAGGCGG
6951 ACTGACGACC GGCAGCCTCG GCGGCATACT GGCCGGCGGC GGCATTCCC
7001 TTGCCGCACC GTATTTGGAC AAAGCGGCGG AAAACCTCGG TCCGGCGGGC
7051 AAAGCGGCGG TCAACGCACT GGGCGGTGCG GCCATCGGCT ATGCAAGTGG
7101 TGGTAGTGGT GGTGCTGTGG TGGGTGCGAA TGTAGATTGG AACAAAGGC
7151 AGCTGCATCC GAAAGAAATG GCGTTGGCCG ACAAATATGC CGAAGCCCTC
7201 AAGCGCGAAG TTGAAAAACG CGAAGGCAGA AAAATCAGCA GCCAAGAAGC
7251 GGCAATGAGA ATCCGCAGGC AGATACTGCG TTGGGTGGAC AAAGGTTCCC
7301 AAGACGGCTA TACCGACCAA AGCGTCATAT CCCTTATCGG AATGAAAGGC
7351 GAAGACAAAG CCTTGGGTTA TACTTGGGAC TACCGCGACT ACGGCGCAAG
7401 AAATCCGCAA ACCTACAACG ATCCGAAGCT GTTTGAGGAA TACCGCCGAC
7451 AGGACAAACC CGAATACCGC AACCTGACCT GGCTGCACAG CGGGACGAAA
7501 GACACCAAAA TCAGGCAGGG AGAGCGGAAA AACGAAGAGT TTGCACTGAA
7551 GCTTGCCGAA GGAAGTACGA GCCTTGTCAG CCCCAATCCG AGGATAAAAG
7601 TCCCGATTCT TGCAGGCATC CGCAACCTGA AAAACATCAA GCCGACAGTT
7651 ACCGGCAGCG ATCCCTTATT GCGGGTGCG GGAATATCC GTATCCCTGC
7701 AAACGGCAAT GTTGCGAAGG GGGACAGGAT TCCGGATACG GCATTGGCTA
7751 GCAAGGGAAT CAAACATAAA GATCGTAAAG ATCAACTGGA GAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1670; ORF 564>:

```

m564.pep
1  MNRTLYKVVF NKHRNCMIIV AENAKREGKN TADTQAVGIL PNDIAGFAGF
51  IHSISVISFS LSLLLGSALI LTSSSATAQG IVADKSAPAQ QQPTILQTGN
101 GIPQVNIQTP TSAGVSVNQY AQFDVGNRGA ILNNSRSNTQ TQLGGWIQGN
151 PWLARGEARV VVNQINSSHS SQLNGYIEVG GRRAEVVIAN PAGIAVNGGG
201 FINASRATLT TAQPQYQAGD LSGFKIRQGN VVIAGHGLDA RDTDYTRILS
251 YHSKIDAPVW GQDVRVVAGQ NDVAATGDAH SPILNNAAN TSNNTANNGT
301 HIPLFAIDTG KLGGMYANKI TLISTVEQAG IRNQGWQFAS AGNVAVNAEG
351 KLVNTGMIAA TGENHAVSLH ARNVHNSGTV ASQDDANIHS QTLDNSGTVL
401 SSGRLTVRNL GRLKNQNNGT IQAARLDMST GGLDNTGNIT QTSQALDLV
451 SAGKFDNSGK IGVSDVPQTG LNPNPSPVPIQ IPSTATGSGS STVSVPKPGS
501 NNPVSPTAPA KNYAVGRIQT TGAFDNAGSI NAGGQIDIAA QNGLGNSGSL
551 NAAKLRVSGD SFNNTVKGKL QAHD LAVNTQ TAKNSGHLLT QTKIDNREL
601 HNAGEIAANN LTLIHSGRLS NDKKGNIIRAA HLQLDTAGLH NAGNILADSG
651 TVTTKNLNRN TGKVSVARLN TEGQTLDNTR GRIEAEVNI QSQQLTNQSG
701 HITATEQLTI NSRNVDNQNG KLLSANQAQL AVSDGLYNQH GEIATNRQLS
751 IHDKNQNTLA LNNADGTIQS AGNVSLQAKS LANNGTLTAG NKLDIALTDD
801 FVVERDLTAG KQLNLSIKGR LKNTHTLQAG HTLKLNAGNI DNQVTGKIIG
851 GEQTDITSEQ HVDNRGLINS DGLTHIGAGQ TLTNTGTGKI YGNHIALDAQ

```

```

901 ILLNREETTE GSTKAGAIAA RKRLDIGAKE IHNQEGALLS SEGIFAVGNR
951 LDEQHHAGM ADTFVNGSAG LEVQGDALMS VRNMQNINNH FKTETYLAKA
1001 EKQVRDYTEVL GQNTYYQAGK DGLFDNSQGG KDQTTATFHL KNGSRIEANQ
1051 WHVRDYHIET YKERIENRP AHITVGGDLT ASGQNLWLNKD SRIVVGGRII
1101 TDDLNQKEIT NQSTTGKGRD DAVGTQWDSV TTKGWYSGRK RQRRTERNHT
1151 PYHDTQLFTH DEDTPVSVIQ QNAASPSFQP AASAIKLIDG VSTAAVNGQR
1201 IHTGNVVS LN NATVTLPNSS LYTHPDNKG WLVEDPQFA DYRRWLGS DY
1251 MLQQLQLDTN HHLKRLGDGY YEQLVNEQI HQLTGYRRLD GYRSDEEQFK
1301 ALMDNGLTAA KTFGLTPGIA LSAEQVARLT SDIVWMENQT VTLSDGSTQT
1351 VLVPKVYALA RKGD LNTSGG LISAEQVLLK LQNGNLNLSG TIAGRQAVLI
1401 QARNINSNGN IQADQIGLKA EKSINIDGGQ VQAGRLLTAQ AQNLNLNGTT
1451 QTSNGERNNGN TAIDRMAGIN VVGSHTQVD NRTSDGILSL HASNDINLNA
1501 ATVSNQVKDG TTQITAGNNL NLGTIRTEHR EAYGLDDEN HRHVRQSTEV
1551 GSSIRTQNGA LLRAGNDLKI RQGELEAEEG KTVLAAGR DV TISEGRQITE
1601 LDTSVSGKSK GILSSTKTHD RYRFSHDEAV GSNIGGGKMI VAAGQDINVR
1651 GSNLISDKGI VLKAGHDIDI STAHNRYTGN EYHESKSGV MGTGGLGFTI
1701 GNRKTTDDTD RTNIVHTGSI IGS LNGDVT VAGNRYRQTG STVSSPEGRN
1751 TVTAKSIDVE FANNRYATDY AHTQEQKGLT VALNVPVQA AQNFIAAQN
1801 VGKSKNKR VN AMAAANA AWQ SYQATQOMQ FAPSSSAGQG QNNNQSPSIS
1851 VSITYGEQKS RNEQKRHYTE AAASQIIGK QTTLAATGSG EQSNINITGS
1901 DVIGHAGTAL IADNHIRLQS AKQDGEQSK NKSSGWNAGV AVKIGNGIRF
1951 GITAGGNIGK GKEQGGSTTH RHTHVGSTTG KTTIRSGGDT TLKGVLIGK
2001 GIQADTRNLH IESVQDTETY QSKQNGNVQ VTVGYGFSAS GSYRQSKVKA
2051 DHASVTGQSG IYAGEDGYQI KVRDNTDLKG GIITSSQSAE DKGK NLFQTA
2101 TLTASDIQNH SRYEGRSFGI GGSFDLNGGW DGTVTDKQGR PTDRISPAAG
2151 YGSDGDSKNS TTRSGVNTHN IHITDEAGQL ARTGRTAKET EARIYTGIDT
2201 ETADQHSGLH KNSFDKDAVA KEINLQREVT KEFGRNAAQA VAAVADKLGN
2251 TQSYERYQEA RTLLEAELQN TDSEAEKAAF RASLGQVNAY LAENQSRDYT
2301 WKEGGIGRSI LHGAAGGLTT GSLGGILAGG GTSLAAPYLD KAAENLG PAG
2351 KAAVNALGGA AIGYATGGSG GAVVGANVDW NNRQLHPKEM ALADKYAEAL
2401 KREVEKREGR KISSQEAAMR IRRQILRWVD KGSQDGYTDQ SVISLGMKG
2451 EDKALGYTWD YRDYGARNPQ TYNDPKLFEE YRRQDKPEYR NLTWLHSGTK
2501 DTKIRQGERK NEEFALNVAE GLTSLVNP NP RIKVPILAGI RNLKNIKPTV
2551 TGS DPLLAGA GNIRIPANGN VAKGD RIPDT ALASKGIKHK DRKDQLEKK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with fha

m564/fha

```

ID FHAB_BORPE STANDARD; PRT; 3591 AA.
AC P12255;
DT 01-OCT-1989 (REL. 12, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE FILAMENTOUS HEMAGGLUTININ. . . .

```

SCORES Init1: 190 Initn: 524 Opt: 594
 Smith-Waterman score: 866; 21.7% identity in 2427 aa overlap

```

              10      20      30      40      50      60
m564 .pep  MNRTLYKVVENKHNRCMIAVAENAKREGKNTADTQAVGILPNDIAGFAGFIHSISVISFS
             || :||:| |:: |: :: |:|: | || :: | : :| : |:: ::
fhab_borpe MNTNLYRLVFSHVGRMLVPVSEHCTV-G-NTFCGRTRG---QARSGARATSLSVAPNALA
              10      20      30      40      50

              70      80      90     100     110     119
m564 .pep  LSLLLG-SALILTSSSATAQGIVADKSAPAAQQOPTILQTGNGIPQVNIQTPTSAGVSVNQ
             :|:|: ::| |:: |||:| | | | :| | | | | | | :|:| | | :
fhab_borpe WALMLACTGLPLVTH---AQGLV-----P-QGQTQVLQGGNKVPVVNIADPNSGGVSHNK
              60      70      80      90     100

              120     130     140     150     160     170     179
m564 .pep  YAQFDVGNRGAILNNSRSNTQTQLGGWIQGNPWLARGEARVVVNQINSSHSSQLNGYIEV
             : ||:|:| |::| |:: ::||: | || |:| :| :: :::: :| | | :|
fhab_borpe FQQFNVANPGVVFNNGLTGVSRI GGALTKPNLNR-QASAILAEVTDTSPSRLAGTLEV
              110     120     130     140     150     160

```

863

	180	190	200	210	220	230	239
m564 .pep	GRRRAEVVIANPAGIAVNGGGFINASRATLTTAQPQYQAGDLGFKIRQGNVVIAGHGLD						
	: :: : : : : : : :						
fhab_borpe	YGKGADLIIANPNGISVNGSLTNASNLTLTTGRPSVNGGRI-GLDVQQGTVTIERGGVN						
	170	180	190	200	210	220	
	240	250	260	270	280	290	
m564 .pep	ARDTDYTRILSYHSKIDAPV---WGQ---DVRVVAGQNDVAATGDAHSPILNNAANTSN						
	: : : : : : : : : : : : : : : : :						
fhab_borpe	ATGLGYFDVVARLVKLQGA VSSKQKPLADIAVVAGANRYDHATRRATPI----AAGARG						
	230	240	250	260	270	280	
	300	310	320	330	340	350	
m564 .pep	NTANNGTHIPLFAIDTGKLGMYANKITLISTVEQAGIRNQGWQFASAGNVAVNAEGKLV						
	: : : : : : : : : : : : : : :						
fhab_borpe	AAAGA-----YAIDGTAAGAMYGKHITLVSSDSGLGVRQLGS-LSSPSAITVSSQGEIA						
	290	300	310	320	330		
	360	370	380	390	400	410	
m564 .pep	NTGMIAATGENHAVSLHARNVHNSGTVASQDDANIHSQTLDNSGTVLSSGRLTVRNLGRL						
	: : : : : : : : : : : : : : : :						
fhab_borpe	---LGDATVQRGPLSLKGAGVVSAGKLASGGGAV---NVAGGGAVKIA---SASSVGNL						
	340	350	360	370	380		
	420	430	440	450	460	470	
m564 .pep	KNQNNGTIQAARLDMSTGGLDNTGNITQTGSQALDLVSAGKFDNSGKIGVSDVPQTGLNP						
	: : : : : : : : : : : : : : :						
fhab_borpe	AVQGGGKVQATLLNAG-----GTLVSGRQAVQLGAASSRQALSVNAGGALKADKLSA						
	390	400	410	420	430		
	480	490	500	510	520	530	
m564 .pep	NPSV-IPQIPSTATGSGSSTVSVPKPGSNNPVSPAPAKNYAVGRIQTTGAFD-NAGSIN						
	: : : : : : : : : : : : : : : :						
fhab_borpe	TRRVVDVGKQAVALGSASSNALSVRAGGA-----LKAGKLSATGRLDVDGKQAVTLGSA						
	440	450	460	470	480	490	
	540	550	560	570	579		
m564 .pep	AGGQIDIAAQNLGNSGSLNAAKL RVSG-----DSFNNT-----VKGKLQAHDLAVNT						
	: : : : : : : : : : : : : : : :						
fhab_borpe	SDGALSVSAGGNLRANELVSSAQLEVRGQREVALDDASSARGMTVVAAGALAARNLQSKG						
	500	510	520	530	540	550	
	580	590	600	610	620	630	
m564 .pep	QTAKNSGHLTQTGKIDNRELH--NAGEIAANNLTLIHSGRLSNDKKGNIRAAHLQLDTA						
	: : : : : : : : : : : : : : : : : :						
fhab_borpe	AIGVQGGAEVSVANANSDAELRVGRGQVDLHDLAARGADISGEGRVNI GRARSDSDVK						
	560	570	580	590	600	610	
	640	650	660	670	680	690	
m564 .pep	GLHNAGNILADSGTVTTKNNLRNTGKVSVARLNTGQTLDNTRGRIEAE TVNIQSQQLTN						
	: : : : : : : : : : : : : : : : : :						
fhab_borpe	-VSAHGALSIDSMTALGAIGVQAGGSVSAKDMRSRGAVTVSGGG-----AVNLGDVQ---						
	620	630	640	650	660		
	700	710	720	730	740	750	
m564 .pep	QSGHITATEQLTINSRNVDNQNGKLLSANQAQLAVSDGLYNQHGEIATNRQLSIHDKNQ						
	: : : : : : : : : : : : : : : :						
fhab_borpe	SDGQVRATSAGAMTVRDV-----AAAADLALQAGDALQAGFLKSAGAMTVNGRDAV						
	670	680	690	700	710		

m564	.pep	760	770	780	790	800	810
		TLALNNADGTIQSAGNVS	LQAKSLANNGT	LTAGNKLDIAL	TDDFFVVERDL	TAGKQL-NLS	
fhab_borpe			: :: : :: :	: : : : : :	: :	: :	
		RL-----DGA-HAGGQ	LRVSSDGQAALG	SLAAKGELT	VSAAARAATVA	-EL---KSLDNIS	
		720	730	740	750	760	
m564	.pep	820	830	840	850	860	870
		IKGRLK-NTH	TLQAGHTLKLNA	-GNIDNQVTG	KIIGGEQTDIT	SEQHVDNRGL	INSDGLT
fhab_borpe		: : ::::: : : :	: : :	: : : : :	: : : :	: : : :	
		VTGGERVSVQSVNS	SASRVAISAHG	ALD---VGKV--	SAKSGIGLE---	GWGAVGADSL	
		770	780	790	800	810	
m564	.pep	880	890	900	910	920	930
		HIGAGQTLTNTGT	GKIYGNHIALD	AQILLNREET	TGEGSTKAGAI	AARKRLDI-G	AKEIHN
fhab_borpe		: :: : : : : : :	: : : :	: : : :	: : : :	: : : :	
		--GSDGAISVSGR	DAVRVDQARSL	ADISLG----	AEGGATLGAVE	AAGSIDVRG	SGSTV--
		820	830	840	850	860	
m564	.pep	940	950	960	970	980	990
		QEGALLSSEGI	FAVGNRLDEQ	HHAAGMADTF	VNGSAGLEVQ	GDALMSVRN	MQNINNHFKT
fhab_borpe		: : : : : :	: : : : :	: : : : :	: : : : :	: : : : :	: : : :
		AANSLHANRDV	RVSQK--DAVR	VTAAATSGG	LHVSSGRQLD	LGAVQA-RG	ALALDGGAGV
		870	880	890	900	910	920
m564	.pep	1000	1010	1020	1030	1040	1050
		ETYLAKAEK--	QVRDYTVLGQ	NTYYQAGKD	GLFDNSQGQ	KDQTATFHL	KNGSRIEANQ-
fhab_borpe		: : :	: : :	: : :	: : :	: : :	: : :
		ALQSAKASGTL	HLVQGGEHL	DLGLTAAV	GAVDV----	NGTGDVRV	AKLVSDAGADLQAGRS
		930	940	950	960	970	
m564	.pep	1060	1070	1080	1090	1100	
		--WHVRDYHI	ETYKERIIE	NRPAHITV	GGDLTASGQ	NWLNKDSR	IVVGGRIITDDL
fhab_borpe		: : : : : :	: : : : :	: : : :	: : : :	: : : :	: : : :
		MTLGIVDTT	GDLOARAQQ	KLELGSVK	SDGGLQAA	AGGALS	LAAAEVAGALELS---
		980	990	1000	1010	1020	1030
m564	.pep	1110	1120	1130	1140	1150	1160
		ITNQSTTGK	RTDAVGTQ	WDSVTKK	GWY--SGR	KRQRRTERN	NHTPYHDTQLFTHDFDTPV
fhab_borpe		: : : : : :	: : :	: : :	: : :	: : :	: : :
		TVDRASAR	IDSTGS	VGIGALK	AGAVEAAS	PRRARRALR-----	QDFFTPG
		1040	1050	1060	1070	1080	
m564	.pep	1170	1180	1190	1200	1210	1220
		SVI---QQA	ASPSFQPA	ASAIKLID	GVSTA	AVNGQRIHT	GNVVS
fhab_borpe		: : :	: : :	: : :	: :	: : :	: : :
		SVVVRAQ	GNVTVGR	GDPHQGV	LAQGD	IIMDA--KGG	TLLRNDALTENGTVTISADSAVL
		1090	1100	1110	1120	1130	1140
m564	.pep	1230	1240	1250	1260	1270	1280
		THPDNKGW	LVETD-PQ	FADYRRW	LGSDYMLQ	LQLDTNH	LHKRLG
fhab_borpe		: : : :	: :	: :	: : :	: :	: : :
		EHSTIESK	ISQSVL	AAKGDKG	KPAVSVK	VAKKLF--	NGTLRAVNDN--
		1150	1160	1170	1180	1190	
m564	.pep	1290	1300	1310	1320	1330	1340
		LTGYRRLD	GYRSDEE	QFKALMD	NGLTAAK	TFGLT	PG-I
fhab_borpe		: : : :	: :	: : :	: : :	: :	: :
		VDGRPQI----	TDAVTGE	ARKDES	SVVSDA	ALVADGG	PIVVEAGELVSHAGGIGNGRNK--
		1200	1210	1220	1230	1240	1250

865

		1350	1360	1370	1380	1390	1400
m564	.pep	TLDGSTQTVLVPKYYALARKGDLNTSGGLISAEQVLLKLQNGNLNTSGTIAGRQAVLIQ					
		: :: :	: : : : : : :	: : : : :	: : : : :	: : : : :	: : : : :
fhab_borpe		--ENGASVTVRTT-----GNLVNKGYSAGKQGVLEV-GGALTNEFLVGSDDGTQRIE					
		1260		1270	1280	1290	1300
		1410	1420	1430	1440	1450	
m564	.pep	ARNINSNGNIQ-----ADQIGLKAESINIDGGQVQAGRLLTAQ----AQNINLNGTT					
		: : : : :	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :
fhab_borpe		AQRIENRGTFQSQAPAGTAGALVVKAAEAIVHDGVMATKGEMQIAGKGGSPFTVTAGAKA					
		1310	1320	1330	1340	1350	1360
		1460	1470	1480	1490	1500	
m564	.pep	QTSGNERNGNTAI-DRMAGINVV-GSHTEQVDNRTSD-GILSLHASNDINLNAATVSNQV					
		: : : : :	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :
fhab_borpe		TTSANKLSVDVASWDNAGSLDIKKGGAQVTVAGRYAEHGEVSIQGDYTVSADAIALAAQV					
		1370	1380	1390	1400	1410	1420
		1510	1520	1530	1540	1550	
m564	.pep	--KDGTQTITAGNNLNLGT-IRTE---HREAYGTLDDENHRHVRQST-----EVGS					
		: : : : :	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :
fhab_borpe		TQRGGAANLTSRHDTRFSNKIRLMGPLQVNAGGPVSNTGNLKVREGVTVTAASFDNETGA					
		1430	1440	1450	1460	1470	1480
		1560	1570	1580	1590	1600	
m564	.pep	SIRTQNGALLRAGNDLKIRQGELEAEKGKTVLAAGRDV--TISEGRQITELDTS---VSG					
		: : : : :	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :
fhab_borpe		EVMAKSATLTTSGAARN--AGKMQVKEAATIVAASVSNPGTFTAGKDITVTSRGGFDNEG					
		1490	1500	1510	1520	1530	
		1610	1620	1630	1640	1650	1660
m564	.pep	K---SKGILSSTKTHDRYRF---SHDEAV-GSNIGGGKMIVAAGQDINVRSNLSIDKGI					
		: : : : :	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :
fhab_borpe		KMESNKDIVIKTEQFSNGRVLDAKHDLTVTASGQADNRGSLKAGHDFTVQAQRI--DNSG					
		1540	1550	1560	1570	1580	1590
		1670	1680	1690	1700	1710	
m564	.pep	VLKAGHDIDISTAHNRYTG-----NEYHESKSGVMGTGGLGFTIGNRKTTDDTDRTNIV					
		: : : : :	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :
fhab_borpe		TMAAGHDATLKAPHLRNTGQVVAGHDIHIINSKLENTGRV--DARNIDIALDVADFTN--					
		1600	1610	1620	1630	1640	1650
		1720	1730	1740	1750	1760	1770
m564	.pep	HTGSIIGSLNGDVTVAGNRYRQT---GSTVSSPEGRNTVTAKSIDVEFANNRYATDYA					
		: : : : :	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :
fhab_borpe		-TGSLYAEHDA-TLTLAQGTQRDLVVDQDHILPVAEGTLRVKAKSLTTEIETGNPGLIA					
		1660	1670	1680	1690	1700	1710
		1780	1790	1800	1810	1820	1830
m564	.pep	HTQEOKGLTVALNVPVQAAQNFIAQAQNVGKSKNKRNVNMAAANAA-WQSYQATQQMQQ					
		: : : : :	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :
fhab_borpe		EVQE-----NIDNKQA----IVVGKDLTSL-SAHGNVANEANALLWAAGELTVKAQN					
		1720	1730	1740	1750		
		1840	1850	1860	1870	1880	1890
m564	.pep	FAPSSSAGQGQNNNQSPSISVSITYGEQKSRNEQKRHYTEAAASQIIGKQTTLAATGSG					
		: : : : :	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :
fhab_borpe		ITNKRAALIEAGGNARLTAVALLNKLGRIRAGEDMHLD---APRI----ENTAKLSGEV					
		1760	1770	1780	1790	1800	1810
		1900	1910	1920	1930	1940	1950
m564	.pep	EQSNINITGSDVIGHAGTALIADNHIRLQSAKQDGEQSKNKSSGWNAGVAVKIGNGIRF					
		: : : : :	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :
fhab_borpe		QRKGVQDVGGGEHGRWSGIGYVNYWLRAGNGKKAGT-----IAAPWYGGDLTAEQSLIEV					
		1820	1830	1840	1850	1860	

866

		1960	1970	1980	1990	2000	2010
m564	.pep	GITAGGNIGKGKEQGGSTTHRHTHVGSTTGKTTIRSGGDTTLKGVQLIGKGIQADTRNLH					
				::		::	::::
fhab_borpe		GKDLYLNAGARKDE-----HRHL-----LNEGVIQAGGHGHIGG-----DVDNRSV-					
		1870	1880	1890	1900		

		2020	2030	2040	2050	2060
m564	.pep	IESVQDTETYSKQQNGNVQVTVGYGFSASGSYRQSKVKA-----DHASVTGQSGIYAGE				
		:::	::	::	:	:
fhab_borpe		VRTVSAMEYFKTLPVSLTALDNRAGLSPATWNFQSTYELLDYLLDQNRYEYIWGLYPTY				
		1910	1920	1930	1940	1950

		2070	2080	2090	2100	2110	2120
m564	.pep	DGYQIKVRDNTDLKGGIITSSQSAEDKGKGNLFQTATLTASDIQNHS--RYEGRSFGIGGS					
		:::	::	::	:	:	:
fhab_borpe		TEWSVNTLKNLDL-GYQAKPAPTAPMPKA-----PELDLRGHTLESAEGRKI-FGEY					
		1970	1980	1990	2000	2010	

		2130	2140	2150	2160	2170
m564	.pep	FDLNGGWDGT-----VTDKQGRPTDRISPAAGYGSDDSKNSTTRSGVNTNHIHITDEAG				
		:	:	:	:	:
fhab_borpe		KKLQGEYEKAKMAVQAVEAYGEATRVRVDQLG-----QRYGKALGGMDAETKEVDGIIQ				
		2020	2030	2040	2050	2060

		2180	2190	2200	2210	2220	2230
m564	.pep	QLARTGRTAKETEARIYTGIDTETADQHSGHLKNSFDKDAVAKEINLQREVTKEFGRNAA					
		::	:	:	:	:	:
fhab_borpe		EFAADLRTVYAKQADQAT-IDAET-DKVAQRYKSQID--AVRLQAIQPGVRT--LAKALS					
		2080	2090	2100	2110	2120	

		2240	2250	2260	2270	2280	2290
m564	.pep	QAVAAVADKLGNTQSYERYQEARTLLE-AELQNTDSEAEKAAFRASLGQVNAYL-----					
		:	:	:	:	:	:
fhab_borpe		AALGADWRALGHSQLMQRWKDFKAGKRGAEIAFYPKQTVLAAGAGLTLSNGAIHNGENA					
		2130	2140	2150	2160	2170	2180

		2300	2310	2320	2330	2340	2350
m564	.pep	AENQSRDYDTWKEGGIGRSILHGAAGGLTTGSLGGILAGGGTSLAAPYLDKAAENLGPAGK					
		:	:	:	:	:	:
fhab_borpe		AQNRGRPEGLKIGAHSATSVSGSFDALRDVGLEKRLDIDDALA AVLNPHIFTRIGAAQT					
		2190	2200	2210	2220	2230	2240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1671>:

```

g565.seq
1  atggacagca cattgtctaa aacgtgttgc gtttcgtgca tattgttgag
51  cgtaaccacc accatthttcg ccggtcccag accggcggct tccaatactt
101 ccctgcgttt cgcacgcgcg aacgacaccg gctcgctgca acttctggct
151 acctgcacgc gtgcgatgac caagtcgagc gcgaaatacg gaataccttc
201 tttgggcgaa gacgcgtccg accgtctgcc cgcccctgcc gaagccgaca
251 atcagcacat gatcagactt gctcatcgct tccaccaaca tgctgtgcag
301 atcgagcgac ttcattgtccc agcttgga

```

This corresponds to the amino acid sequence <SEQ ID 1672; ORF 565.ng>:

```

g565.pep
1  MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
51  TCTRAMSKSS AKYGISSLGE DASDRLPAPA EADNQHMIRL AHRFHQHAVQ
101 IERLHVPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1673>:

```

m565.seq
1  ATGGACAGCA CATTGTCTAA AACGTGTTGC GTTTCGTGCA TATTGTTGAG
51  CGTAACCACC ACCATTTTCG CCCGTCCCAG ACCGGCGGCT TCCAATACTT
101 CCCTGCGTTT CGCATCGCCG AACGACACCG GTTCGCCCCG ACTTCTGGCA
151 ACCTGCACCC GCGCAATGTC CAAGTCGAGC GCGAAATACG GAATATCCTC
201 TTGGGCAAGG ACGCGTCCGA CCGTCTGCCC GCCCCTGCCG AAGCCGACAA

```

867

```

251 TCAGCACATG GTCGGACTTG CTCATGGTTT CTACCAGCAT ACTGTGCAGA
301 TCGAGCGACT TCATGTCCCA GCTTGACTTG ACCAAACGCC CGACCAGCGC
351 ATCGCTGCCG CCCAAGAGGA AGGGCGCGAT AATCATCGAC AGCAGAACCG
401 CCGCCGTCGC CGCCTGTTCC CATTCTGGCG AAACCATATC AAGCTGCCCC
451 GCAATGGCCA GCATCACGAA GCCGAACGCG CCGCCCTGCG CGAGATACAA
501 AGCCGTTTGG AGGCTGTCGC CGACCGAATG TTTCATTTTG AAGGCAATGG
551 CAAACACAAC CAGTGCCTTC AACACCAGCA GCATTGCCAA CAGCATCAAT
601 ACCTGCCGCC AGCCGCCGAT CAATGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1674; ORF 565>:

```

m565.pep
  1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
 51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTSILCR
101 SSDFMSQLDL TKRPTSASLP PKRKGAIID SRTAAVAACS HSGETISSCP
151 AMASITKPNS PPCARYKAVL RLSPTTECFIL KAMANTTSF NTSSIANSIN
201 TCRQPPINA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m565/g565 100.0% identity in 67 aa overlap

```

                10      20      30      40      50      60
m565.pep      MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
                |||||
g565           MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
                10      20      30      40      50      60

                70      80      90      100     110     120
m565.pep      AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSILCRSSDFMSQLDLTKRPTSASLP
                |||||
g565           AKYGISSLGEDASDRLPAPAEADNQHMIRLAHRFHQHAVQIERLHVPAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1675>:

```

a565.seq
  1 ATGGACAGCA CATTGTCTAA AACGTGTTGC GTTTCGTGCA TATTGTTGAG
 51 CGTAACCACC ACCATTTTCG CCGTCCCAG ACCGGCGGCT TCCAATACTT
101 CCCTGCGTTT CGCATCGCCG AACGACACCG GTTCGCCCCG ACTTCTGGCA
151 ACCTGCACCC GCGCAATGTC CAAGTCGAGC GCGAAATACG GAATATCCTC
201 TTGGGCAAGG ACGCGTCCGA CCGTCTGCCC GCCCCTGCCG AAGCCGACAA
251 TCAGCACATG GTCGGACTTG CTCATGGTTT CTACCAGCAT ACTGTGCAGA
301 TCGAGCGACT TCATGTCCCA GCTTGACTTG ACCAAACGCC CGACCATGTC
351 ATCGCTGCCG CCCAAGAGGA AGGGCGCGAT AATCATCGAC AGCAGAACCG
401 CCGCCGTCGC CGCCTGTTCC CATTCTAGCG AAACCATATC AAGCTGCCCC
451 GCAATGGCCA GCATCACGAA GCCGAACGCG CCGCCCTGCG CGAGATACAA
501 AGCCGTTTGG AGGCTGTCGC CGACCGAATG TTTCATTTTG AAGGCAATGG
551 CAAACACAAC CAGTGCCTTC AACACCAGCA GCATTGCCAA CAGCATCAAT
601 ACCTGCCGCC AGCCGCCGAT TAATGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1676; ORF 565.a>:

```

a565.pep
  1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
 51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTSILCR
101 SSDFMSQLDL TKRPTSASLP PKRKGAIID SRTAAVAACS HSSETISSCP
151 AMASITKPNS PPCARYKAVL RLSPTTECFIL KAMANTTSF NTSSIANSIN
201 TCRQPPINA*

```

m565/a565 99.5% identity in 209 aa overlap

```

                10      20      30      40      50      60
m565.pep      MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
                |||||

```

868

```

a565      MDSTLSKTCVSCILLSVTTTIFARPRPAASNTSLRFASPNDTGPALLATCTRAMSKSS
           10      20      30      40      50      60
           70      80      90      100     110     120
m565.pep  AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSIILCRSSDFMSQLDLTKRPTSASLP
           |||||
a565      AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSIILCRSSDFMSQLDLTKRPTSASLP
           70      80      90      100     110     120
           130     140     150     160     170     180
m565.pep  PKRKGAIIDSRTAAVAACSHSGETISSCPAMASITKPNSPPCARYKAVLRLSPTECFIL
           |||||
a565      PKRKGAIIDSRTAAVAACSHSSETISSCPAMASITKPNSPPCARYKAVLRLSPTECFIL
           130     140     150     160     170     180
           190     200     210
m565.pep  KAMANTTSAFNTSSIANSLNCRQPPINAX
           |||||
a565      KAMANTTSAFNTSSIANSLNCRQPPINAX
           190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1677>:

```

g566.seq..
1  atgccgtctg aacaatatct tttcagacgg cattttgtat ggggggttaac
51  ggttggtcag cccgagtagc tcctgcatat cgtacaaacc cgttttgccg
101 tttacccaaa ctgcggcgcg gacggcaccg gcggcaaagg tcatgcggct
151 gccggccttg tgggtgattt ccacgcgttc gccgtcgggt gcgaagaggg
201 cgggtgtggtc gccgactatg tcgcctgcgc ggacggtggc aaagccgatg
251 gtggaaggat cgcgcggacc agtgtggcct tcgcggccgt aaacggcgca
301 ttgtttgagg tcgcggccga gcgcgccggc gatgacttcg cccattcgta
351 a

```

This corresponds to the amino acid sequence <SEQ ID 1678; ORF 566.ng>:

```

g566.pep..
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFAVYPNCGA DGTGGKGHAA
51  AGFVGDFHAF AVGGEEGGVV ADYVACADGG KADGGRIART SVAFAAVNGA
101 LFEVAAERAG DDFAH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1679>:

```

m566.seq..
1  ATGCCGTCTG AACAAATATCT TTTCAGACGG CATTTTGTAT GGGGGTTAAC
51  GGTGTGTTAG CCCGAGTACG TCCTGCATAT CGTACAAACC CGTTTTGCCG
101 TTGACCCAAA CTGCGGCGCG GACGGCACC GCGGCAAAGG TCATGCGGCT
151 GCTGGCCTTG TGGGTGATTT CCACGCGCTC GCCGTCGGTG GCGAAGAGGG
201 CGGTGTGGTC GCCGACGATG TCGCCTGCGC GGACGGTGGC AAAGCCGATG
251 GTCGACGGAT CGCGCGGACC GGTGTGGCCT TCGCGGCCGT AAACGGCGCA
301 TTGTTTGAGG TCTCTGCCGA GCGCGCCGGC GATGACTTCG CCCATGCGTA
351 A

```

This corresponds to the amino acid sequence <SEQ ID 1680; ORF 566>:

```

m566.pep..
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFAVDPNCGA DGTGGKGHAA
51  AGLVGDFHAL AVGGEEGGVV ADDVACADGG KADGRRIART GVAFAAVNGA
101 LFEVSAERAG DDFAH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m566/g566 93.1% identity in 116 aa overlap

```

           10      20      30      40      50      60
m566.pep  MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVDPNCGADGTGGKGHAAAGLVGDFHAL
           |||||

```

869

```

g566      MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVYPNCGADGTGGKGHAAAGFVGDFHAF
           10          20          30          40          50          60
           70          80          90          100         110
m566.pep  AVGGEEGGVVADDVACADGGKADGRRRIARTGVAFAAVNGALFEVSAERAGDDFAHAX
           |||||
g566      AVGGEEGGVVADYVACADGGKADGGRIARTSVAFAAVNGALFEVAAERAGDDFAHSX
           70          80          90          100         110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1681>:

```

a566.seq
1  ATGCCGCTCTG AACAAATATCT TTTCAGACGG CATTGTGTAT GGGGGTTAAC
51  GGTGTTCAG CCCGAGTACG TCCTGCATAT CGTACAAACC CGTTTACCG
101 TTTACCCAAA CTGCGGCGCG GACGGCGCCG GCGGCAAAGG TCATGCGGCT
151 GCTTGCCTTG TGGGTGATTT CCACGCGCTC GCCGTGCGTG GCGAAGAGGG
201 CGGTGTGGTC GCCGACGATG TCGCCCGCGC GGACGGTGGC AAAGCCGATG
251 GTGGACGGAT CGCGCGGGCC GGTGTGGCCT TCGCGGCCGT AAACGGCGCA
301 TTGTTTGAGG TCTCTGCCGA GCGCGCCGGC GATGACTTCG CCCATGCGTA
351 A

```

This corresponds to the amino acid sequence <SEQ ID 1682; ORF 566.a>:

```

a566.pep
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFTVYPNCGA DGAGGKGHAA
51  ACLVGDFHAL AVGGEEGGVV ADDVARADGG KADGGRIARA GVAFAAVNGA
101 LFEVSAERAG DDFAHAX*

```

m566/a566 94.0% identity in 116 aa overlap

```

           10          20          30          40          50          60
m566.pep  MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVDPNCGADGTGGKGHAAAGLVGDFHAL
           |||||
a566      MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFTVYPNCGADGAGGKGHAAACLVGDFHAL
           10          20          30          40          50          60
           70          80          90          100         110
m566.pep  AVGGEEGGVVADDVACADGGKADGRRRIARTGVAFAAVNGALFEVSAERAGDDFAHAX
           |||||
a566      AVGGEEGGVVADDVARADGGKADGGRIARAGVAFAAVNGALFEVSAERAGDDFAHAX
           70          80          90          100         110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1683>:

```

g567.seq.
1  atgcgacgac gggcagcggc atcgacaagg cgggtttgca gtccggcggtt
51  tatcaggtct tattgggcga tgcggacgtg cagtcggcgg cggtacgcag
101 caaagagggc ggatacggcg tgttgggtgc gaacgcgcgc gcttgccggc
151 gcggaaatcg agctggtgca ggaaatcgcc cgggaagtgc gtttgaaaaa
201 cgcgctcaag gcagtgccgg aagattacga ctttatcctg atcgactgtc
251 cgccttcgct gacgtgttg acgcttaacg gcttggtggc ggcgggcggc
301 gtgattgtgc cgaatgttg cgaatattac gcgctggaag ggatttcga
351 tttgattgcy accgtgcgca aaatccgtca ggcggtcaat cccgatttgg
401 acatcacggg catcgtgcgt acgatgtacg acagccgcag caggctgggt
451 gccgaagtca gcgaacagtt gcgcagccat ttcggggatt tgctttttga
501 aaccgccatc ccgcgcaata tccgccttgc ggaagcgccg agccacggta
551 tgccggtgat ggcttacgac gcgcaggcaa agggtgccaa ggcgtatcct
601 gccttggcgg acgaactggc ggcgaggggtg tcggggaaat ag

```

This corresponds to the amino acid sequence <SEQ ID 1684; ORF 567.ng>:

```

g567.pep
1  MRRRAAATR RVCSPAFIRS YWAMRTCSRR RYAAKRADTA CWVRTRALAG
51  AEIELVQEIA REVRLKNALK AVAEDYDFIL IDCPPSLTLL TLNGLVAAGG
101 VIVPMLCEYY ALEGISDLIA TVRKIRQAVN PDLDITGIVR TMYDSRSLV
151 AEVSEQLRSH FGDLLFETAI PRNIRLAEAP SHGMPVMAYD AQAKGAKAYL
201 ALADELAARV SGK*

```

870

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1685>:

```
m567.seq..
  1 ATGAGTGCGA ACATCCTTGC CATCGCCAAT CAGAAGGGCG GTGTGGGCAA
 51 AACGACGACG ACGGTAAATT TGGCGGCTTC GCTGGCATCG CGCGGCAAAC
101 GCGTGCTGGT GGTCGATTTC GATCCGCAGG GCAATGCGAC GACGGGCAGC
151 GGCATCGACA AGGCGGGTTT GCAGTCCGGC GTTTATCAGG TCTTATTGGG
201 CGATGCGGAC GTGCAGTCGG CGGCGGTACG CAGCAAAGAG GGCGGATACG
251 CTGTGTTGGG TGCGAACCGC GCGCTGGCCG GCGCGGAAAT CGAACTGGTG
301 CAGGAAATCG CCCGGGAAGT GCGTTTGAAA AACGCGCTCA AGGCAGTGGA
351 AGAAGATTAC GACTTTATCC TGATCGACTG CCCGCCTTCG CTGACGCTGT
401 TGACGCTTAA CGGGCTGGTG GCGGCGGGCG GCGTGATTGT GCCGATGTTG
451 TGCGAATATT ACGCGCTGGA AGGGATTTCG GATTTGATTG CGACCGTGCG
501 CAAATCCGT CAGGCGGTCA ATCCCGATT TGGACATCACG GGCATCGTGC
551 GCACGATGTA CGACAGCCGC AGCAGGCTGG TTGCCGAAGT CAGCGAACAG
601 TTGCGCAGCC ATTTCCGGGA TTTGCTTTT GAAACCGTCA TCCCGCGCAA
651 TATCCGCCTT GCGGAAGCGC CGAGCCACGG TATGCCGGTG ATGGCTTACG
701 ACGCGCAGGC AAAGGTACC AAGGCGTATC TTGCCTTGCG GGACGAGCTG
751 GCGGCGAGGG TGTCGGGGAA ATAG
```

This corresponds to the amino acid sequence <SEQ ID 1686; ORF 567>:

```
m567.pep..
  1 MSANILAIAN QKGGVGKTTT TVNLAASLAS RGKRVLVVDL DPQGNATTGS
 51 GIDKAGLQSG VYQVLLGDAD VQSAAVRSKE GGYAVLGANR ALAGAEIELV
101 QEIAREVRLK NALKA VEEDY DFILIDCPPS LTLTLNGLV AAGGVIVPML
151 CEYYALEGIS DLIATVRKIR QAVNPDLIT GIVRTMYDSR SRLVAEVSEQ
201 LRSHFGDLLF ETVIPRNIRL AEAPSHGMPV MAYDAQAKGT KAYLALADEL
251 AARVSGK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

```
m567/g567 98.2% identity in 168 aa overlap

m567.pep      60      70      80      90      100      110      119
               GVIQVLLGDADVQSAAVRSKEGGYAVLGANRALAGAEIELVQEIAREVRLKNALKAVEED
g567          AFIRSYWAMRTCSRRRYAAKRADTACWVRTRALAGAEIELVQEIAREVRLKNALKAVEED
               20      30      40      50      60      70

m567.pep      120      130      140      150      160      170      179
               YDFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDI
g567          YDFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDI
               80      90      100      110      120      130

m567.pep      180      190      200      210      220      230      239
               TGIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAG
g567          TGIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETAIPRNIRLAEAPSHGMPVMAYDAQAG
               140      150      160      170      180      190

m567.pep      240      250
               TKAYLALADELAARVSGKX
g567          AKAYLALADELAARVSGKX
               200      210
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1687>:

```
a567.seq
  1 ATGAGTGCGA ACATCCTTGC CATCGCCAAT CAGAAGGGCG GTGTGGGCAA
 51 AACGACGACG ACGGTAAATT TGGCGGCTTC GCTGGCATCG CGCGGCAAAC
101 GCGTGCTGGT GGTCGATTTC GATCCGCAGG GCAATGCGAC GACGGGCAGC
151 GGCATCGACA AGGCGAGTTT GCAGTCCGGC GTTTATCAGG TCTTATTGGG
201 CGATGCGGAC GTGAAATCGG CGGCGGTACG CAGCAAAGAG GGCGGATACG
```

871

```

251 GCGTGTGGG TCGAACC GCCTGGCCG GCGCGGAAAT CGAGCTGGTG
301 CAGGAAATCG CCCGGGAAGT GCGTTTGAAA AACGCGCTCA AGGCAGTGGC
351 GGAAGATTAC GACTTTATCC TGATCGACTG CCCGCCTTCG CTGACGCTGT
401 TGACGCTTAA CGGCTTGGTG GCGGCAGGCG GCGTGATTGT GCCGATGTTG
451 TCGGAATATT ACGCGCTGGA AGGGATTTCC GATTTGATTG CGACCGTGCG
501 CAAAATCCGT CAGGCGGTCA ATCCCGATTG GGATATCACG GGCATCGTGC
551 GTACGATGTA CGACAGCCGC AGCAGGCTAG TTGCCGAAGT CAGCGAACAG
601 TTGCGCAGCC ATTTCCGGGA TTTGCTGTTT GAAACCGTCA TCCCGCGCAA
651 TATCCGCCTT GCGGAAGCGC CGAGCCACGG TATGCCGGTG ATGGCTTATG
701 ATGCGCAGGC AAAGGGTGCC AAGGCGTATC TTGCCTTGGC GGACGAGCTG
751 ATGGCGAGGG TGTCGGGGAA ATAG

```

This corresponds to the amino acid sequence <SEQ ID 1688; ORF 567.a>:

```

a567.pep
1 MSANILAIAN QKGGVGKTTT TVNLAASLAS RGKRVLVVDL DPQGNATTGS
51 GIDKASLQSG VYQVLLGDAD VKSAAVRSKE GYGVLGANR ALAGAEIELV
101 QEIAREVRLK NALKAVAEDY DFILIDCPPS LTLLTLNGLV AAGGVIVPML
151 CEYYALEGIS DLIATVRKIR QAVNPDLIT GIVRTMYDSR SRLVAEVSEQ
201 LRSHFGDLLF ETVIPRNIRL AEAPSHGMPV MAYDAQAKGA KAYLALADEL
251 MARVSGK*

m567/a567 97.7% identity in 257 aa overlap

10 20 30 40 50 60
m567.pep MSANILAIANQKGGVGKTTT TVNLAASLASRGKRVLVVDLDPQGNATTGSGIDKASLQSG
|||||
a567 MSANILAIANQKGGVGKTTT TVNLAASLASRGKRVLVVDLDPQGNATTGSGIDKASLQSG
10 20 30 40 50 60

70 80 90 100 110 120
m567.pep VYQVLLGDADVQSAAVRSKEGGYAVLGNRALAGAEIELVQEIAREVRLKNALKAVEEDY
|||||
a567 VYQVLLGDADVQSAAVRSKEGGYAVLGNRALAGAEIELVQEIAREVRLKNALKAVEEDY
70 80 90 100 110 120

130 140 150 160 170 180
m567.pep DFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLIT
|||||
a567 DFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLIT
130 140 150 160 170 180

190 200 210 220 230 240
m567.pep GIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKGT
|||||
a567 GIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKGA
190 200 210 220 230 240

250
m567.pep KAYLALADELAARVSGKX
|||||
a567 KAYLALADELMARVSGKX
250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1689>:

```

g568.seq
1 atgtctcaggg tcagaccggt attatttgcc gtcaaggctt ccgcctcttc
51 gataccttgc agaattctgcc gattaaagcg ttcgcggctg cccaatat
101 tcaggcgcac attgttttcg tgcaggcggc gtacctgtt ttgcaaagcc
151 tgtaaaaaca gcccacatcag gaacgaaact tcgtcttcg ggcgacgcca
201 gttttcgggt gaaaaggcaa acacggtcag atattgcacg cccagtttgg
251 cgcaatgctt caccatat tccaacgcgt ccaagccgcg tttgtgtccc
301 attatacgcg ggagaaaacg ttttttcgcc caacggcgt tgccgtccat
351 aattacggcg atgtgcctcg ggatggcggg gtgttccaaa atgggtctgcg

```

872

401 tgctgctctt catatctgcc ttctcgcggtt cggcggttcaa atgccgtctg
451 aacgccgcgc cgtga

This corresponds to the amino acid sequence <SEQ ID 1690; ORF 568.ng>:

g568.pep
1 MLRVRPVLFA VKASASSIPC RICRLKRSRL PNIFRRILFS CRRRTCFCCKA
51 CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP
101 IIRGRKRFFA QRPLPSIITA MCLGMAVCSK MVCVLLFISA FRGSAFKCRL
151 NAAP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1691>:

m568.seq
1 ATGCTCAGGG TCAGGCCGGT ATTGTTTGCC GTCAACGCTT CCGCCTCTTC
51 GATGCCTTGC AGAATCTGCC GGTGAAGCG TTCGCGGCTG CCCAATATCT
101 TCAGGCGCAT ATTGTTTTCG TGCAGGCGGC GTACCTGTTT TTGCAAAGCC
151 TGTA AAAACA GCCCCATCAG GAACGAACT TCGTCTTCGG GCGGCGGCCA
201 GTTTTCGGTT GAAAAGGCAA ACACGGTCAG ATATTGCACA CCCAGTTTGG
251 CGCAATGCTT CACCATATTT TCCAATGCGT CCAAACCGCG TTGTGTGCC
301 ATTATGCGCG GGAGGAAACG TTTTTCGCC CAACGGCCGT TGCCGTCCAT
351 AATCACGGCG ATATGCTTGG GAATGGCGGT GTGTTCCAAA ACGGCCTGCG
401 TGCTGCTTTT CATGTCTGCC TTTCGCGGTT CCGCATTCAA ATGCCGTCTG
451 AACGCCGAAC CGTGCAGGTT AAATTGCCAT CAAATCTTCT TCTTTGGCAG
501 TCAGGAGTTT GTCGGCTTCG GTAATGTATT TGTCCGTCAG TTTTGAACC
551 GCTTCTTCGC CGCGACGTGC CTCGTCTTCG GAAATTTCTT TGTCTTTGAG
601 GAGTTTTTTG ATGTGGTCGT TGGCATCGCG GCGCACGTTG CGGATAGAGA
651 CGCGGCCTTC TTCCGCTTCG CCGCGTACGA CTTTAATCAG GTCTTTGCGG
701 CGTTCCTCGG TCAGCATGGG CATCGGCACG CGGATCAGGT CGCCGACAGC
751 TGCCGGGTTT AGTCCCAAGT TTGA

This corresponds to the amino acid sequence <SEQ ID 1692; ORF 568>:

m568.pep..
1 MLRVRPVLFA VNASASSMPC RICRLKRSRL PNIFRRILFS CRRRTCFCCKA
51 CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP
101 IMRGRKRFFA QRPLPSIITA ICLGMAVCSK TACVLLFMSA FRGSAFKCRL
151 NAEPCLNCH QIFFFGSQEF VGFGNVFVGQ FLNRFFAATC LVFGNFFVFE
201 EFFDVVVGIA AHVADRDAAF FRFAAYDFNQ VFAAFLGQHG HRHADQVADS
251 CRVQSQV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m568/g568 94.8% identity in 154 aa overlap

m568.pep	10	20	30	40	50	60
	MLRVRPVLFAVNASASSMPCRICRLKRSRLPNIFRRILFSCRRRTCFCCKACKNSPIRNET					
g568	MLRVRPVLFAVKASASSIPCRICRLKRSRLPNIFRRILFSCRRRTCFCCKACKNSPIRNET					
	10	20	30	40	50	60
m568.pep	70	80	90	100	110	120
	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIMRGRKRFFAQRPLPSIITA					
g568	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIIRGRKRFFAQRPLPSIITA					
	70	80	90	100	110	120
m568.pep	130	140	150	160	170	180
	ICLGMVCSKTACVLLFMSAFRGSFAFKCRLNAEPCLNCHQIFFFGSQEFVGFGNVFVGQ					
g568	MCLGMVCSKMVCVLLFISAFRGSFAFKCRLNAAPX					
	130	140	150			
m568.pep	190	200	210	220	230	240
	FLNRFFAATCLVFGNFFVFEEFFDVVVGIAAHVADRDAAFFRFAAYDFNQVFAAFLGQHG					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1693>:

```
a568.seq
1  ATGCTCAGGG TCAGGCCGGT ATTGTTTGCC GTCAAGGCTT CCGCCTCTTC
51  GATGCCCTTC AGGATTTGAC GGTGAAGCG TTCGCGGCTG CCCAGTATTT
101 TCAGGCGCAT ATTGTTTTTC TGCAGGCGGC GTACCTGTTT TTGCAAAGCC
151 TGTA AAAACA GCCCATCAG GAACGAAACT TCGTCTTCGG GCGGCGCCA
201 GTTTTTCGGT GAAAAGGCAA ACACGGTCAG ATATTGCACA CCCAGTTTGG
251 CGCAATGCTT CACCATATTT TCCAATGCGT CCAAACCGCG TTTGTGTCCC
301 ATTATGCGCG GGAGGAAACG TTTTTCGCC CAACGGCCGT TGCCGTCCAT
351 AATCACGGCG ATATGCTTGG GAATGGCGGT GTGTCCAAA ACGGCCTGCG
401 TGCTGCTTTT CATGTCTGCC TTTCGCGGTT CCGCATTCOA ATGCCGCTCTG
451 AACGCCGAAC CGTGCAGGTT AAATTGCCAT CAAATCTTCT TCTTTGGCAG
501 TCAGGAGTTT GTCGGCTTCG GTAATGTATT TGTCGGTCAG TTTTGAACC
551 GCTTCTTCGC CGCGACGTGC CTCGTCTTCG GAAATTTCTT TGTCTTTGAG
601 GAGTTTTTTG ATGTGGTCGT TGGCATCGCG GCGCACGTTG CGGATGGAGA
651 CGCGGCCTTC TTCCGCTTCG CCGCGTACGA CTTTAATCAG GTCTTTGCGG
701 CGTTCCTCGG TCAGCATGGG CATCGGCACG CGGATCAGGT CGCCGACAGC
751 TGCCGGGTTC AGTCCCAAGT TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1694; ORF 568.a>:

```
a568.pep
1  MLRVRPVLFA VKASASSMPF RI*RLKRSRL PSIFRRILFS CRRRTCFCCKA
51  CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP
101 IMRGRKRFFA QRPLPSIITA ICLGMAVCSK TACVLLFMSA FRGSFAKRL
151 NAEPCLNCH QIFFFGSQEF VGFGNVFVGQ FLNRFFAATC LVFGNFFVFE
201 EFDVVVGIA AHVADGDAF FRFAAYDFNQ VFAAFLGQHG HRHADQVADS
251 CRVQSQV*
```

m568/a568 98.1% identity in 257 aa overlap

	10	20	30	40	50	60
m568.pep	MLRVRPVLFAVNASASSMPFRI*RLKRSRLPSIFRRILFS CRRRTCFCCKACKNSPIRNET					
a568	MLRVRPVLFAVKASASSMPFRIXRLKRSRLPSIFRRILFS CRRRTCFCCKACKNSPIRNET					
	10	20	30	40	50	60
m568.pep	70	80	90	100	110	120
a568	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNAKPRLCPIMRGRKRFFAQRPLPSIITA					
	70	80	90	100	110	120
m568.pep	130	140	150	160	170	180
a568	ICLGMVCSKTACVLLFMSAFRGSFAKRLNAEPCLNCHQIFFFGSQEFVGFGNVFVGQ					
	130	140	150	160	170	180
m568.pep	190	200	210	220	230	240
a568	FLNRFFAATCLVFGNFFVFEEFFDVVVGIAAHVADRDAAFFRFAAYDFNQVFAAFLGQHG					
	190	200	210	220	230	240
m568.pep	250	HRHADQVADSCRVSQVX				
a568	HRHADQVADSCRVSQVX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1695>:

```
g569.seq..
1  atgctgaaac aacgggtaat aaccgctatg tggctgctgc cgctgatgct
51  gggcatgctg ttttacgctg cgcaatggct gtgggctgca ttttgcgggc
101 tgattgccct gaccgccttg tgggagtatg cccgatggc cggtttgctg
```

874

```

151 aaaaccgaaa ccaaccatta cctcgccgca accttggttt tcggcgtagt
201 tgcctatgcg ggcggctgga tgctgcctaa tttggtttgg tatgttggtt
251 tggcattttg gctcgccggt atgcctttgt gggtgagatt caaatggagg
301 ctcaacggcg gttggcaggt ttatgccgct ggctggcttt tgctcatgcc
351 gttttgggtc gcgctcgat ccctggcgcc cgcacccga tga

```

This corresponds to the amino acid sequence <SEQ ID 1696; ORF 569.ng>:

g569.pep

```

1 MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALTAL WEYARMAGLC
51 KTETNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
101 LNGGWQVYAV GWLLMPFWF ALVSLAPASR *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1697>:

m569.seq..

```

1 ATGCTGAAAC AACGGGTAAT AACCGCCATG TGGCTGCTGC CGCTGATGCT
51 GGGCATGCTG TTTTACGCGC CGCAATGGTT GTGGGCTGCA TTTTGGCGAC
101 TGATTGCCCT GATTGCCTTG TGGGAATATG CCCGTATGGG CGGTTTGTGC
151 AAAATTAAAA CCAACCATT A CCTCGCCGCA ACCTTGTTTT TCGGCGTGGT
201 TGCCTATGCG GCGGCTGGA TGCTGCCTAA TTTGGTTTGG TATGTTGTTT
251 TGGCATTTTG GCTCGCCGTT ATGCCTTTAT GGTTGAGATT CAAATGGAGG
301 CTCAACGGCG GTTGGCAGGT TTATGCCGTC GGCTGGCTTC TGGTCATGCC
351 GTTTTGGTTC GCGCTCGTAT CCCTGCGCCC GCATCCCGAT GATGCCCTGC
401 CGCTGATCGC CGTGATGGGT TTGGTGTGGG TTGCCGATAT TTGCGCGTAT
451 TTCAGCGGCA AGGCGTTCGG CAAACACAAA ATCGCGCCGG CAATCAGCCC
501 CGGCAAAAGC TGGGAAGGTG CAATCGGCGG CGCGGTTTGC GTGGCAGTGT
551 ACATGACCGC CGTACGAAGT GCCGGCTGGC TGGCATTCTA TACAGGCTGG
601 TTCGATACCG TGTTAATCGG TTTGGTGTG ACCGTGTGCA GCGTATGCGG
651 CGACCTTTTG GAAAGCTGGC TCAAGCGCGC GGCAGGCATC AAAGACAGCA
701 GCAAGCTGCT GCCCGACAC GCGGCGTGT TCGACCGTAC CGACAGCCTG
751 ATTGCCGTGA TCAGCGTCTA TGCAGCGATG ATGTCGGTTT TAAATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1698; ORF 569>:

m569.pep..

```

1 MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALIAL WEYARMGGLC
51 KIKTNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
101 LNGGWQVYAV GWLLMPFWF ALVSLRPHPD DALPLLAVMG LVWVADICAY
151 FSGKAFGKHK IAPAI SPGKS WEGAIGGAVC VAVYMTAVRS AGWLAFTDGTW
201 FDTVLIGLVL TVVSVCGDLL ESWLKRAAGI KDSSKLLPGH GGVFDRDTSI
251 IAVISVYAAM MSVLN*

```

m569/g569 95.3% identity in 127 aa overlap

	10	20	30	40	50	60
m569.pep	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGLCKIKTNHYLAA					
	10	20	30	40	50	60
g569	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALTALWEYARMAGLCKTETNHYLAA					
	70	80	90	100	110	120
m569.pep	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNNGGWQVYAVGWLLMPFWF					
	70	80	90	100	110	120
g569	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNNGGWQVYAVGWLLMPFWF					
	130	140	150	160	170	180
m569.pep	ALVSLRPHPD DALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKS WEGAIGGAVC					
	130					
g569	ALVSLAPASRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1699>:

a569.seq

```

1 ATGCTGAAAC AACGGGTGAT AACCGCCATG TGGCTGCTGC CGCTGATGCT
51 GGGCATGCTG TTTTACGCGC CGCAATGGTT GTGGGCTGCA TTTTGGCGAC
101 TGATTGCCCT GATTGCCTTG TGGGAATATG CCCGTATGGG CGGTTTGTGC

```

875

```

151 AAAATTAAAA CCAACCATTA CCTCGCCGCA ACCTTGTTT TCGGCGTGGT
201 TGCCTATGCG GCGGCTGGA TGCTGCCTAA TTTGGTTTGG TATGTTGTTT
251 TGGCATTTTG GCTCGCCGTT ATGCCTTTAT GGTTGAGATT CAAATGGAGG
301 CTAACGGCG GTTGGCAGGT TTATGCCGTC GGCTGGCTTC TGGTCATGCC
351 GTTTTGGTTC GCGCTCGTAT CCCTGCGCCC GCATCCCGAT GATGCCCTGC
401 CGCTGCTCGC CGTGATGGGT TTGGTGTGGG TTGCCGATAT TTGCGCGTAT
451 TTCAGCGGCA AGGCGTTCGG CAAACACAAA ATCGCACCCG CAATCAGCCC
501 CGGCAAAAGC TGGGAAGGTG CAATCGGCGG CGCGGTTTGC GTGGCCGTGT
551 ACATGACCGC CGTACGAAGT GCCGGCTGGC TGGCATTCTA TACAGGCTGG
601 TTCGATACCG TGTTAATCGG TTTGGTGTG ACCGTTGTCA GCGTATGCGG
651 CGACCTTTTG GAAAGCTGGC TCAAGCGCGC GGCAGGCATC AAAGACAGCA
701 GCAACCTGCT GCCCGGACAC GCGGCGTGT TCGACCGCAC CGACAGCCTG
751 ATTGCCGTTA TCAGCGTCTA TGCAGCGATG ATGTCGGTTT TAAATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1700; ORF 569.a>:

```

a569.pep
1  MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALIAL WEYARMGGLC
51  KIKTNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
101 LNGGWQVYAV GWLLVMPFWF ALVSLRPHPD DALPLLAVMG LVWVADICAY
151 FSGKAFGKHK IAPAI SPGKS WEGAIGGAVC VAVYMTAVRS AGWLA FDTGW
201 FDTVLIGLVL TVVSVCGDLL ESWLKRAAGI KDSSNLLPGH GGVFDRTDSL
251 IAVISVYAAM MSVLN*

m569/a569 99.6% identity in 265 aa overlap

              10      20      30      40      50      60
m569.pep  MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGLCKIKTNHYLAA
a569      MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGLCKIKTNHYLAA
              10      20      30      40      50      60

              70      80      90      100     110     120
m569.pep  TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWF
a569      TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWF
              70      80      90      100     110     120

              130     140     150     160     170     180
m569.pep  ALVSLRPHPD DALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKS WEGAIGGAVC
a569      ALVSLRPHPD DALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKS WEGAIGGAVC
              130     140     150     160     170     180

              190     200     210     220     230     240
m569.pep  VAVYMTAVRSAGWLA FDTGW FDTVLIGLVLTVVSVCGDLL ESWLKRAAGI KDSSKLLPGH
a569      VAVYMTAVRSAGWLA FDTGW FDTVLIGLVLTVVSVCGDLL ESWLKRAAGI KDSSNLLPGH
              190     200     210     220     230     240

              250     260
m569.pep  GGVFDRTDSL IAVISVYAAMMSVLNX
a569      GGVFDRTDSL IAVISVYAAMMSVLNX
              250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1701>:

```

g570.seq..
1  atgatccgtt tgaccgcgc gtttgccgcc gccctgatcg gtttatgctg
51  caccacagcg gcgcagccg acacctcca aaaaatcggc tttatcaaca
101 ccgagcgcat ctacctcgaa tccaagcagg cgcgcaacat ccaaaaaacg
151 ctggacggcg aattttccgc ccgtcaggac gaattgcaaa aactgcaacg
201 cgaagccttg gatttggaag ggagctcgc cggcggaaca ctaaggagcg
251 caaaaaagcg gcaagccgaa gaaaaatggc gcgggctggt cgaagcgctc
301 cgcaaaaaac aggcgcagtt tgaagaagac tacaacctcc gccgcaacga
351 agagtgttgc tccctccagc aaaacgcaa ccgcgtcatc gtcaaaatcg

```

876

```

401 ccaaacagga aggttacgat gtcattttgc aggacgtgat ttacgtcaac
451 acccaatacg acgttaccga cagcgtcatt aaagaaatga acgcccgtg
501 a

```

This corresponds to the amino acid sequence <SEQ ID 1702; ORF 570.ng>:

g570.pep..

```

1 MIRLTRAFAA ALIGLCCTTG AHADTFQKIG FINTERIYLE SKQARNIQKT
51 LDGEFSARQD ELQKLQREGL DLERQLAGGK LKDAKKAQAE EKWRGLVEAF
101 RKKQAQFEED YNLRNNEEFA SLQQNANRVI VKIAKQEGYD VILQDVIYVN
151 TQYDVTDSVI KEMNAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1703>:

m570.seq..

```

1 ATGACCCGTT TGACCCGCGC GTTTGCCGCG GCTCTGATCG GTTTGTGCTG
51 CACCGCAGGC GCGCACGCGG ACACCTTCCA AAAAATCGGC TTTATCAACA
101 CCGAGCGCAT CTACCTCGAA TCCAAGCAGG CGCGCAAGAT TCAAAAAACG
151 CTGGACAGCG AATTTTCCGC TCGTCAGGAC GAATTGCAAA AACTGCAACG
201 CGAAGGTCTG GATTTGAAAA GGCAGCTTGC CGAAGGCAAA CTCAGAAACG
251 CAAAAAAGGC GCAAGCCGAA GAAAAATGGC GCGGGCTGGT CGCAGCGTTC
301 CGCAAAAAAC AGGCGCAGTT TGAAGAAGAC TACAACCTCC GCCGCAACGA
351 AGAGTTTGCC TCCCTCCAGC AAAACGCCAA CCGCGTCATC GTCAAAATCG
401 CCAAACAGGA AGGTTACGAT GTCATTTTGC AGAACGTGAT TTACGTCAAC
451 ACCCAATACG ACGTTACCGA CAGCGTCATT AAAGAAATGA ACGCCCGCTG
501 A

```

This corresponds to the amino acid sequence <SEQ ID 1704; ORF 570>:

m570.pep

```

1 MTRLTRAFAA ALIGLCCTAG AHADTFQKIG FINTERIYLE SKQARKIQKT
51 LDSEFSARQD ELQKLQREGL DLERQLAEGK LRNAKKAQAE EKWRGLVAAF
101 RKKQAQFEED YNLRNNEEFA SLQQNANRVI VKIAKQEGYD VILQNVIIYN
151 TQYDVTDSVI KEMNAR*

```

m570/g570 94.6% identity in 166 aa overlap

	10	20	30	40	50	60
m570.pep	MTRLTRAFAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLDSEFSARQD					
g570	MIRLTRAFAAALIGLCCTTGAAHADTFQKIGFINTERIYLESKQARNIQKTLDGEFSARQD					
	10	20	30	40	50	60
m570.pep	ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRNNEEFA					
g570	ELQKLQREGLDLERQLAGGKLKDAKKAQAEKWRGLVEAFRKKQAQFEEDYNLRNNEEFA					
	70	80	90	100	110	120
m570.pep	ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRNNEEFA					
g570	ELQKLQREGLDLERQLAGGKLKDAKKAQAEKWRGLVEAFRKKQAQFEEDYNLRNNEEFA					
	70	80	90	100	110	120
m570.pep	SLQQNANRVIVKIAKQEGYDVILQNVIIYVNTQYDVTDSVIKEMNARX					
g570	SLQQNANRVIVKIAKQEGYDVILQDVIYVNTQYDVTDSVIKEMNARX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1705>:

a570.seq

```

1 ATGACCCGTT TGACCCGCGC GTTTGCCGCG GCTCTGATCG GTTTGTGCTG
51 CACCGCAGGC GCGCACGCGG ACACCTTCCA AAAAATCGGC TTTATCAACA
101 CCGAGCGCAT CTACCTCGAA TCCAAGCAGG CGCGCAAGAT TCAAAAAACG
151 CTGGACAGCG AATTTTCCGC CCGCCAGGAC GAATTGCAAA AACTGCAACG
201 CGAAGGTCTG GATTTGAAAA GGCAGCTTGC CGAAGGCAAA CTCAAAGACG
251 CAAAAAAGGC GCAAGCCGAA GAAAAATGGT GCGGGCTGGT CGCAGCGTTC
301 CGCAAAAAAC AGGCGCAGTT TGAAGAAGAC TACAACCTCC GCCGCAACGA
351 AGAGTTTGCC TCCCTCCAGC AAAACGCCAA CCGCGTCATC GTCAAAATCG
401 CCAAACAGGA AGGTTACGAT GTCATTTTGC AGGACGTGAT TTACGTCAAC
451 ACCCAATACG ACGTTACCGA CAGCGTCATT AAAGAAATGA ACGCCCGCTG

```

877

501 A

This corresponds to the amino acid sequence <SEQ ID 1706; ORF 570.a>:

```

a570.pep
  1  MTRLTRAFAA ALIGLCCTAG AHADTFQKIG FINTERIYLE SKQARKIQKT
 51  LDSEFSARQD ELQKLQREGL DLERQLAEGK LKDAKKAQAE EKWCGLVAAF
101  RKKQAQFEED YNLRNNEEFA SLQQNANRVI VKIAKQEGYD VILQDVIYVN
151  TQYDVTDSVI KEMNAR*

m570/a570  97.6% identity in 166 aa overlap

              10      20      30      40      50      60
m570.pep    MTRLTRAFAAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLTLDSEFSARQD
              |||||||
a570        MTRLTRAFAAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLTLDSEFSARQD
              10      20      30      40      50      60

              70      80      90      100     110     120
m570.pep    ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRNNEEFA
              |||||||:|||||
a570        ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRNNEEFA
              70      80      90      100     110     120

              130     140     150     160
m570.pep    SLQQNANRVIVKIAKQEGYDVILQNVIVNTQYDVTDSVIKEMNARX
              |||||||:|||||
a570        SLQQNANRVIVKIAKQEGYDVILQNVIVNTQYDVTDSVIKEMNARX
              130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1707>:

```

g571.seq (partial)
  1  atgcgcgttt tccgagtaaa ccgatttggt gttaccggtt tcggcggcgg
 51  tataggttct ccggtcccac acgctgcctg cgtcggcaaa caggctcagg
101  cggacggtgc gtgcgtcttt cgcaccgggc atcgggaaga gcagctcggc
151  ggagacgttg gcttttttgt tgccgccgta gctgattttt tcgccgtatt
201  cgtcatacac ttteggggccg agcgtgccgc tttcgtagcc gcgcaccgaa
251  cccaggccgc cgcgtagaa gttttcaaag aaggggattt ctttggttct
301  gccgtagccg cccgcaatgc cgacttcgcc gccgagcatc agcgtgaagg
351  ttttgc...

```

This corresponds to the amino acid sequence <SEQ ID 1708; ORF 571.ng>:

```

g571.pep (partial)
  1  MRVFRVNRFV VTVFGGGIGS AVPHAACVGK QAQADGACVF RTGHREEQLG
 51  GDVGFFVAAV ADFFAVFVIH FRAERAAFVA AHRTQAAAVE VFKEGDFFGS
101  AVAARNADFA AEHQREGFA...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1709>:

```

m571.seq
  1  ATGGGTATTG CCGGCGCCGT AAATGTTTTG AACCTGCCG CCGGTGCGCG
 51  AACTGCTGTT GTCGTCGTAG GTTTTGCCGT CCCACACGCT GCCTGCGTCG
101  GCAAACAGGC TCAGGCGGAC GGTGCGCGCG TCTTTCGCGC CGGGCATCGG
151  GAAGAGCAGC TCGGCGGAGA CGTTGGCTTT TTTGTTGCCG CCGTAGCTGA
201  TTTTTCGCC GTATTCGTCA TAGACTTTCG GACCGAGCGT GCCGCTTTCG
251  TATCCGCGCA CCGAACCAG GCGGCCCGG TAGAAGTTTT CAAAGAAGGG
301  GATTTCCTTG GTTCTGCCGT AGCGGCCCGC AATGCCGACT TCGCCGCCGA
351  GCATCAGCGT GAAGGTTTTG CTCAGGGGGA AGAACCAGGT TTGGTTGTGG
401  GTGGCGGAGT AGTATTGCAG TTTGCTGCCA GGCAGGGCGA TTTCGGCGTT
451  CACGCCCGTC AGGTAGCCGC GCGTCGGCCA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1710; ORF 571>:

```

m571.pep
  1  MGIAGAVNVL NPAAGRGTAV VVVGFAVPHA ACVGKQAQAD GARVFRAGHR
 51  EEQLGGDVGF FVAAVADFFA VFVIDFRTER AAFVSAHRTQ AAAVEVFKEG
101  DFFGSAVAAR NADFAAEHQR EGFAQGEEPG LVVGGGVVLQ FAARQGDFGV
151  HARQVAARRP *

```

878

m571/g571 93.1% identity in 102 aa overlap

	10	20	30	40	50	60
m571.pep	MGIAGAVNV	LNPAAAGRG	TAVVVVGFA	VPHAAACVG	KQAQADGAR	VFRAGHREEQLGGDVGF
			:			
g571	MRVFRVNR	FVVTVFGG	GIGSAVPHA	ACVGKQAQ	ADGACVFR	TGHREEQLGGDVGF
	10	20	30	40	50	
	70	80	90	100	110	120
m571.pep	FVAAVADFF	FAVFVIDFR	TERAAAFV	SAHRTQAA	AVEVFKEG	DFFGSAVAARNADFAAEHQ
g571	FVAAVADFF	FAVFVIHF	RAERAA	FVAHRTQ	AAAVEVFKEG	DFFGSAVAARNADFAAEHQ
	60	70	80	90	100	110
	130	140	150	160		
m571.pep	EGFAQGEE	PGLVVGG	VVLQFAAR	QDGFVHAR	QVAARRPX	
g571	EGFA					
	119					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1711>:

```

a571.seq
1  ATGGGTATTG  CCGCGCCCGT  AAATGTTTGG  AACCTGCCG  CCGGTCCGCG
51  AACTGCTGTT  GTCGTCGTAG  GTTTTGCCGT  CCCACACGCT  GCCTGCGTCG
101  GCAAACAGGC  TCAGGCGGAC  GGTGCGCGCG  TCTTTCGCGC  CGGGCATCGG
151  GAAGAGCAGC  TCGGCGGAGA  CGTTGGCTTT  TTTGTGCCG  CCGTAGCTGA
201  TTTTTCGCC  GTATTCGTCA  TACACTTTCG  GACCGAGCGT  GCCGCTTTCG
251  TATCCGCGCA  CCGAACCCAG  GCCGCCGCCG  TAGAAGTTT  CAAAGAAGGG
301  GATTTCTTTG  GTTCTGCCGT  AGCCGCCCGC  AATGCCGACT  TCGCCGCCGA
351  GCATCAGCGT  GAAGGTTTGG  CTTAAGGGGA  AGAACCAGGT  TTGGTTGTGG
401  GTGGCGGAGT  AGTATTGCAG  TTTGCTGCCG  GGCAGGGCGA  TTTCGGCGTT
451  CACGCCCGTC  AGGTAGCCGC  GCGTCGGCCA  TAA

```

This corresponds to the amino acid sequence <SEQ ID 1712; ORF 571.a>:

```

a571.pep
1  MGIAGAVNVL  NPAAGRGTA  VVVVGFAVPH  A  ACVGKQAQAD  GARVFRAGHR
51  EEQLGGDVGF  FVAAVADFF  A  VFVIHFRT  ER  AAFVSAHRTQ  AAAVEVFKEG
101  DFFGSAVAAR  NADFAAEHQ  R  EGFA*GEEPG  LVVGGGVVLQ  FAAGQGDFGV
151  HARQVAARRP  *

```

m571/a571 98.1% identity in 160 aa overlap

	10	20	30	40	50	60
m571.pep	MGIAGAVNV	LNPAAAGRG	TAVVVVGFA	VPHAAACVG	KQAQADGAR	VFRAGHREEQLGGDVGF
a571	MGIAGAVNV	LNPAAAGRG	TAVVVVGFA	VPHAAACVG	KQAQADGAR	VFRAGHREEQLGGDVGF
	10	20	30	40	50	60
	70	80	90	100	110	120
m571.pep	FVAAVADFF	FAVFVIDFR	TERAAAFV	SAHRTQAA	AVEVFKEG	DFFGSAVAARNADFAAEHQ
a571	FVAAVADFF	FAVFVIHF	RTERRAA	FVSAHRTQ	AAAVEVFKEG	DFFGSAVAARNADFAAEHQ
	70	80	90	100	110	120
	130	140	150	160		
m571.pep	EGFAQGEE	PGLVVGG	VVLQFAAR	QDGFVHAR	QVAARRPX	
a571	EGFAQGEE	PGLVVGG	VVLQFAAR	QDGFVHAR	QVAARRPX	
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1713>:

g572.seq..

```

1  atgtgcgcca tcgtcggggc ggcggggctg ccttcgcgcg tcgcagcggc
51  gcaaaaaggc aaaaccattt atctggcaaa caaagaaacg ctggtggttt
101 cccgcgcggt gtttatggaa accgcccgcg caaacggcgc ggcagtgttg
151 cccgtcgaca gcgaacacaa cgccattttc caagttttgc cgcgcgatta
201 cacagaccgt ctgaacgaac acggcatcga ttcgattatc ctgaccgctt
251 cccgcggccc gtttttaaca accgatttaa gcacgttcga cagcattacg
301 cccgagcagg cggtaaaaca cccaattggg cgtatggggc gcaaaatctc
351 cgtcgattca gccactatgg caaacaaggg cttggaactg attgaagcgc
401 attggctggt caactgtccg cccgacaaac tcgaagtcgt catccatccc
451 caatccgtga tacacagtat ggtgcgctac cgcgacggct ccgtgctggc
501 gcaactgggc aatcccgata tgcgaacgcc catcgccctat tgtttgggct
551 tgcccgcgag catcgattcg ggtgtcggca aactcgattt cggcgcattg
601 tccgcgctga ccttccaaaa gcccgacttc ggccgcttcc cctgcctgaa
651 gttcgcctat gaaaccataa acgcaggcgg agccgcgccc tgcgtattga
701 acgcgcgcaa cgaaccgccg gtcgcgcgct ttttggacgg acagattaag
751 tttaccgaca ttgcaaaaac cgtcgcccac tgtcttgac aagacttttc
801 aaacggcatg ggcgatatag aaggactgtt ggcgcaagat gcccggaac
851 gcgcacaagc gcgggcattt atcggcacac tgcgctga

```

This corresponds to the amino acid sequence <SEQ ID 1714; ORF 572.ng>:

g572.pep..

```

1  MCAIVGAAGL PSALAAQKG KTIYLANKET LVVSGALFME TARANGAAVL
51  PVDSEHNAIF QVLPRDYTDRLNEHGIDSII LTASGGPFLT TDLSTFDSIT
101 PEQAVKHPNW RMGRKISVDS ATMANKGLEL IEAHWLFNCP PDKLEVVIHP
151 QSVIHSVMRY RDGSVLAQLG NPD MRTPIAY CLGLPERIDS GVGKLDLFDAL
201 SALTFQKPDF GRFPCLKFAY ETINAGGAAP CVLNAANETA VAAFLDGQIK

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1715>:

m572.seq..

```

1  ATGTGCGCCA TCGTCGGGGC GGTGGGGCTG CCTTCGCGC TCGCAGCGGC
51  GCAAAAAGGC AAAACCATT TATCTGGCAA CAAAGAAACG CTGGTGTTT
101 CCGGCGCGTT GTTTATGGAA ACCGCCGTG CAAACGGCGC GGCAGTGCTG
151 CCCGTCGACA GCGAACACAA CGCCGTTTTC CAAGTTTTCG CGCGCGATTA
201 CGCCGCGCGT CTGAACGAAC ACGGCATCGC TTCGATTATC CTGACCGCTT
251 CCGCGCGCCC GTTCTTGACC GCCGATTAA ACACGTTTCA CCGCATTACG
301 CCGGCCCAAG CCGTCAAAACA CCCCATTGG CGTATGGGAC GCAAAATCTC
351 CGTCGATTCC GCCACCATGA TGAACAAAGG TTTGGAGCTG ATTGAAGCGC
401 ATTGGCTGTT CAATGTGCCG CCCGACAAAC TCGAAGTCGT CATCCATCCG
451 CAATCCGTGA TACACAGCAT GGTGCGCTAC CGCGACGGCT CCGTGCTGGC
501 GCAACTGGGC AATCCCGATA TCGGAACGCC CATCGCTTAT TGTTTGGGTT
551 TGCCCGAGCG CATCGATTCT GGTGTCGGCG ACCTGGATT TCGACGATTG
601 TCCGCGCTGA CCTTCCAAA GCGCGACTTT GACCGCTTCC CCTGCCTGAG
651 GCTCGCCTAT GAAGCCATGA ACGCAGGCG AGCCGCGCCC TCGGTATTGA
701 ACGCCGCCAA CGAAGCCGCC GTCGCGCCT TTTTGGACGG ACAGATTAA
751 TTTACCGACA TTGCCAAAAC CGTCGCCCAC TGTCTTGCAC AAGACTTTTC
801 AGACGCGATA GCGCATATAG GGGGGCTCTT GCGCAAGAT GCCCGGACAC
851 GCGCACAAAG CCGAGCATTT ATCGGCACAC TCGCTGTA

```

This corresponds to the amino acid sequence <SEQ ID 1716; ORF 572>:

m572.pep..

```

1  MCAIVGAVGL PSALAAQKG KTIYLANKET LVVSGALFME TARANGAAVL
51  PVDSEHNAIF QVLPRDYAGR LNEHGIASII LTASGGPFLT ADLNTFDRIT
101 PAQAVKHPNW RMGRKISVDS ATMMNKGLEL IEAHWLFNCP PDKLEVVIHP
151 QSVIHSVMRY RDGSVLAQLG NPD MRTPIAY CLGLPERIDS GVGDLDFDAL
201 SALTFQKPDF DRFPCLRLAY EAMNAGGAAP CVLNAANEA VAAFLDGQIK
251 FTDIKTVAH CLAQDFSDGI GDIGLLAQD ARTRAQARAF IGTLR*

```

m572/g572 92.9% identity in 295 aa overlap

```

          10      20      30      40      50      60
m572.pep  MCAIVGAVGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVLPVDSEHNAIF
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g572       MCAIVGAAGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVLPVDSEHNAIF
          10      20      30      40      50      60

          70      80      90     100     110     120
m572.pep  QVLPRDYAGR LNEHGIASII LTASGGPFLTADLNTFDRITPAQAVKHPNWRMGRKISVDS
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g572       QVLPRDYTDRLNEHGIDSII LTASGGPFLTDLSTFDSITPEQAVKHPNWRMGRKISVDS

```

880

	70	80	90	100	110	120
m572 . pep	130	140	150	160	170	180
	ATMMNKGLELIEAHWLFNCP	PPDKLEVVIHPQSVIHSMVRYR	DG	SVLAQLGNPDMRTPIAY		
g572	ATMANKGLELIEAHWLFNCP	PPDKLEVVIHPQSVIHSMVRYR	DG	SVLAQLGNPDMRTPIAY		
	130	140	150	160	170	180
m572 . pep	190	200	210	220	230	240
	CLGLPERIDSGVGDLDFDALS	ALT	FTQKPDFRFPCLRLAYEAMNAGGAAP	CVLNAANEAA		
g572	CLGLPERIDSGVGKLD	FGALSALT	FTQKPDFRFPCLKFAYETINAGGAAP	CVLNAANETA		
	190	200	210	220	230	240
m572 . pep	250	260	270	280	290	
	VAAFLDGGQIKFTDI	AKTVAHCLAQDFSDGIGD	IGLLAQDARTRAQARAF	IGTLRX		
g572	VAAFLDGGQIKFTDI	AKTVAHCLAQDFSDG	MGDIEGLLAQDARTRAQARAF	IGTLRX		
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1717>:

a572 . seq	1	ATGTGCGCCA	TCGTGCGGGC	GGTGGGGCTG	CCTTCCGCGC	TCGCAGCGGC
	51	GCAAAAAGGC	AAAACCATTT	ATCTGGCGAA	CAAAGAGACG	CTGGTGGTTT
	101	CCGGCGCGTT	GTTTATGGAA	ACCGCCCGTG	CAAACGGCGC	GGCAGTGCTG
	151	CCCGTCGACA	GCGAACACAA	CGCCGTTTTT	CAAGTTTTGC	CGCGCGATTA
	201	CACAGGTCGC	CTGAACGAAC	ACGGCATCGC	TTGATTATC	CTGACCGCTT
	251	CCGGCGGCCC	GTTTCTGACC	GCCGATTTAA	ACACGTTTCA	CAGCATTACG
	301	CCCGACCAAG	CGGTCAAACA	CCCCAATTGG	CGTATGGGAC	GCAAAATCTC
	351	CGTCGATTCC	GCCACCATGA	TGAACAAAGG	TTTGGAGCTG	ATTGAAGCGC
	401	ATTGGCTGTT	CAACTGTCCG	CCCACAAAC	TCGAAGTCGT	CATCCATCCG
	451	CAATCTGTGA	TACACAGCAT	GGTGCGCTAC	CGCGACGGCT	CCGTGTTGGC
	501	GCAACTGGGC	AATCCCGATA	TGCGAACGCC	TATCGCTTAT	TGTTTGGGTT
	551	TGCCCGAGCG	CATCGATTTC	GGTGTGCGCG	ACCTGGATT	CGACGCATTG
	601	TCCGCGCTGA	CCTTCCAAAA	GCCCGACTTT	GACCGCTTCC	CCTGCCTGAA
	651	GCTCGCTTAT	GAAGCCATGA	ACGCAGGCGG	AGCCGCGCCC	TGCGTATTGA
	701	ACGCCGCCAA	CGAAGCCGCC	GTCGCCGCCT	TTTGGACGG	ACAGATTAAG
	751	TTTACCGACA	TTGCCAAAAC	CGTCGCCCAT	TGCTTTTCAC	AAGACTTTTC
	801	AGACGGCATA	GGCGACATAG	GGGGGCTCTT	GGCGCAAGAT	GCCCGGACAC
	851	GCGACAAGC	GCGGGCATT	ATCGGCACAC	TGCGCTGA	

This corresponds to the amino acid sequence <SEQ ID 1718; ORF 572.a>:

a572 . pep	1	MCAIVGAVGL	PSALAAQKG	KTIYLANKET	LTVSGALFME	TARANGAAVL
	51	PVDSEHNAVF	QVLPRDYG	RINEHGIASII	LTASGGPFLT	ADLNTFDSIT
	101	PDQAVKHPNW	RMGRKISVDS	ATMMNKGLEL	IEAHWLFNCP	PPDKLEVVIHP
	151	QSVIHSMVRY	RDGSLAQLG	NPDMRTPIAY	CLGLPERIDS	GVGDLDFDAL
	201	SALT	FTQKPDF	DRFPCLLAY	EAMNAGGAAP	CVLNAANEAA
	251	FTDI	AKTVAH	CLSQDFSDGI	GDIGLLAQD	ARTRAQARAF
						IGTLR*

m572/a572 98.3% identity in 295 aa overlap

	10	20	30	40	50	60
m572 . pep	MCAIVGAVGLPSALAAQKG	KTIYLANKETLTVSGALFME	TARANGAAVL	PVDSEHNAVF		
a572	MCAIVGAVGLPSALAAQKG	KTIYLANKETLTVSGALFME	TARANGAAVL	PVDSEHNAVF		
	10	20	30	40	50	60
m572 . pep	QVLPRDYAGRLNEHGIASII	LTASGGPFLTADLNTFDRIT	PAQAVKHPNWRMGRKISVDS			
a572	QVLPRDYTGRLNEHGIASII	LTASGGPFLTADLNTFDSIT	PDQAVKHPNWRMGRKISVDS			
	70	80	90	100	110	120
m572 . pep	QVLPRDYAGRLNEHGIASII	LTASGGPFLTADLNTFDRIT	PAQAVKHPNWRMGRKISVDS			
a572	QVLPRDYTGRLNEHGIASII	LTASGGPFLTADLNTFDSIT	PDQAVKHPNWRMGRKISVDS			
	70	80	90	100	110	120

881

	130	140	150	160	170	180
m572.pep	ATMMNKGLELIEAHWLFNCPDPKLEVVVHPQSVIHSMVRYRDSVLAQLGNPDMRTPIAY					
a572	ATMMNKGLELIEAHWLFNCPDPKLEVVVHPQSVIHSMVRYRDSVLAQLGNPDMRTPIAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m572.pep	CLGLPERIDSGVGDLDLFDALSALTFQKPDFDRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
a572	CLGLPERIDSGVGDLDLFDALSALTFQKPDFDRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
	190	200	210	220	230	240
	250	260	270	280	290	
m572.pep	VAAFLDGQIKFTDIAKTVAHCLAQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
a572	VAAFLDGQIKFTDIAKTVAHCLSQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1719>:

g573.seq..

```

1  atgcctgtt  tgtgccgct  taatcgcaat  atcggcagtt  tccaaatcac
51  gaatctcacc  gaccataatg  atgtccgggt  cctgacgcag  gaaagacttc
101 aaagcagcgg  caaaagtcag  accctgctta  tcattgacgt  taacctgatt
151 gatgcccgcc  aggttaatct  cggcagggtc  ttccgccggt  gcaatattta
201 ccgactccgt  attcaaaata  ttcaaacagg  tatagagcga  caccgtctta
251 ccgaaacccg  tcggaccggt  taccagcacc  atcccgtaat  gacgggtgaat
301 cgcttccaac  aacaattttt  tctggaacgg  ctcaaaaccc  agctggtcga
351 tgttcaaaag  cgccgcatcg  gaattcaaaa  tccgcatcac  gaccttttcg
401 ccaaacagcg  tcggcaatgt  gctgacacgg  aaatcgacag  gcttgccgcc
451 cttttgaaag  gtcagctgca  tcctaccgtc  ctgcggtatc  cgtttttcgg
501 aaatgtccaa  acgcgacatt  accttaatcc  gggaagcaag  ctgccccctt
551 accgcaatgg  cgccgtgaac  cacctcgccg  agctgcccgt  ccacacggaa
601 acggatacgc  gcatttgtgt  cgtaaaactc  gaaatggatg  tcggatgccc
651 cgctacgcaa  ggcacccgac  aaagttttat  ggataaacct  cggaacaggg
701 ccgtctctcg  cctcctcgtc  gtcgatatac  aggggtgtgc  ttctctcttc
751 ctcttgcccc  tccccaaagt  cctgaagcag  cgatgtcgaa  cgcgaaacca
801 cccaatcgag  caaacccgcc  aactgggtcat  cctcgacaat  gaccaactca
851 accgcaatcc  ctgcccgcga  aaccgttttc  tgaatttgcg  gcatctgggt
901 cggatcggaa  accgcaaaaa  atactttgtc  gccccacgg  aaaaccggca
951 cacagtggaa  ctccaccatc  tgctcctccg  tcaacacccc  catcagcacc
1001 ctgtggcgcg  gataatgacg  caaatcaaga  atcgaataac  tgaacaccct
1051 cgcaatcaat  gccgcaagcg  acttgggcga  aatgacacgg  tctga

```

This corresponds to the amino acid sequence <SEQ ID 1720; ORF 573.ng>:

g573.pep..

```

1  MPCLCRINRN  IGSFQITNLT  DHNDVRVLTQ  ERLQSSGKSO  TLLIIDVNLI
51  DARQVNLGRV  FRCNIYRLR  IQNIQTGIER  HRLTRTRRTG  YQHPVVRTVN
101 RFQQQFFLER  LKTELVDVQR  RGIGIQNPBH  DLFAKQRRQC  ADTEIDRLAA
151 LLKGQLHPTV  LRPFFFGNVQ  TRHYLNPGSK  LPPYRNGRLN  HLAELPVHTE
201 TDTRIVFVKL  EMDVGCPATQ  GIRQSFMDKP  RNRAVFCLLV  VDIQGVAFLE
251 LLPLPKLLKQ  RCRTTRTHPI  E  QTRQLVILDN  DQLNRNPCGR  NRFLNLRHLG
301 RIGNRKKYFV  APTENRHTVE  LHHLLLRQHP  HQHPVARIMT  QIKNRITEHP
351 RNQCRKRLGR  NDTV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1721>:

m573.seq..

```

1  ATGCCCTGTT  TGTGCCGCTT  TAATCGCAAT  ATCGGCAGTT  TCCAAATCAC
51  GAATCTCACC  GACCATAATG  ATGTCCGGGT  CCTGACGCAG  GAAAGACTTC
101 AAAGCAGCGG  CAAAAGTCAG  GCCCTGCTTA  TCATTGACGT  TAACCTGATT
151 GATGCCCGGC  AGGTTAATCT  CGGCAGGGTC  TTCCGCCGTT  GCAATATTTA
201 CCGACTCCGT  ATTCAAAATA  TTCAAACAGG  TATAGAGCGA  CACCGTCTTA
251 CCCGAACCCG  TCGGACCGGT  TACCAGCACC  ATCCCCGTAG  GACGGTGAAT
301 CGTTACCAAC  aCaw.TTTT  TCTGAAACGG  CTCAAACCCG  AGCTGGTCGA
351 TGTTCAAAGA  CGCGGCATCG  GAATTCAAAA  TCCGCATCAC  GACCTTTTCG
401 CCAAACAGCG  TCGGCAATGT  GCTGACACGG  AAATCGACAG  GCTTGCCGCC
451 CTTTGTAAAG  GTCAGCTGCA  TCCTGCCGTC  CTGCGGTATC  CGTTTTTCGG
501 AAATGTCCAA  ACGCGACATT  ACCTTAATCC  GTGAAGCAAG  CTGCCCCCTT

```

882

```

551 ACCGCAATGG GCGGCTGAAC CACCTCGCGG AGCTGCCCCG CCACACGGAA
601 ACGGATACGG GCATTGTGTT CGTAAACTC GAAATGGATG TCCGATGCCC
651 CGCTGCGCAA GGCATCCGAC AAAGTCTTAT GGATAAACCT CGGAACAGGG
701 CCGTCTTCTG CCTCCTCGTT GTCGATATAC AGGGTGTGGC TTTCTCTTC
751 CTCTGCCCC TCCCCAAGCT CCTGAAGCAG CGATGTCGAA CGCGAACCCA
801 CCCAATCGAG CAAACCCGCC AACTGGTCAT CCTCGACAAT GACCAACTCA
851 ACCTCAATCC CTGCGGCAGA AACGGTTTTC TGAATTGCG GCATCTGTGT
901 CGGATCGGAA ACCGCAAAAA ATACTTGTG GCCCGACGG AAAACCGGCA
951 CACAGTGGAA CTCCACCATC TGCTCCTCG TCAACACCCC CATCAGCACC
1001 CTGTGGCGCG GATAATGACG CAAATCAAGA ATCGAATAAC TGAACACCCT
1051 CGCAATCAAT GCCGCAAGCG ACTTGGGCGA AATGACACCG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1722; ORF 573>:

m573.pep..

```

1  MPCLCRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ ALLIIDVNLI
51  DARQVNLGRV FRRNCIYRLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVN
101 RYQHXXFFLKR LKTELVDVQR RGIGIQNPBH DFLAKQRRQC ADTEIDRLAA
151 LLKQQLHPAV LRYPPFGNVQ TRHYLNP*SK LPPYRNGRLN HLAELPVHTE
201 TDTGIVFVKL EMDVRCPAAG GIRQSLMDKP RNRAVFCLLV VDIQGVAFLF
251 LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNLNPGCR NGFLNLRHLC
301 RIGNRKKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

m573/g573 95.9% identity in 364 aa overlap

m573.pep	10	20	30	40	50	60
	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQERLQSSGKSQALLIIDVNLI DARQVNLGRV					
g573	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQERLQSSGKSQTLIIIDVNLI DARQVNLGRV					
	10	20	30	40	50	60
m573.pep	70	80	90	100	110	120
	FRRNCIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVNRYQHXXFFLKR LKTELVDVQR					
g573	FRRNCIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVRTVNRFQQQFFLER LKTELVDVQR					
	70	80	90	100	110	120
m573.pep	130	140	150	160	170	180
	RGIGIQNPBHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFGNVQTRHYLNPXSK					
g573	RGIGIQNPBHDLFAKQRRQCADTEIDRLAALLKGQLHPTVLRYPPFGNVQTRHYLNPGSK					
	130	140	150	160	170	180
m573.pep	190	200	210	220	230	240
	LPPYRNGRLNHLAELPVHTETDTRIVFVKLEMDVRCPAAGGIRQSLMDKPRNRAVFCLLV					
g573	LPPYRNGRLNHLAELPVHTETDTRIVFVKLEMDVGCPTAQGIRQSFMDKPRNRAVFCLLV					
	190	200	210	220	230	240
m573.pep	250	260	270	280	290	300
	VDIQGVAFLFLLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
g573	VDIQGVAFLFLLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNRNPGCRNRFNLRHLG					
	250	260	270	280	290	300
m573.pep	310	320	330	340	350	360
	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
g573	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
	310	320	330	340	350	360
m573.pep	NDTVX					
g573	NDTVX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1723>:

883

a573.seq

```

1 ATGCCCTGTT TGTGCCGCCT TAATCGCAAT ATCGGCAGTT TCCAAATCAC
51 GAATCTCACC GACCATAATG ATGTCCGGGT CCTGACGCAG GAAAGACTTC
101 AAAGCAGCGG CAAAAGTCAG ACCCTGCTTA TCATTGACGT TAACCTGATT
151 GATGCCCGGC AGGTTAATCT CGGCAGGGTC TTCCGCCGTT GCAATATTTA
201 CCGACTCCGT ATTCAAAATA TTCAAACAGG TATAGAGCGA CACCGTCTTA
251 CCCGAACCCG TCGGACCGGT TACCAGCACC ATCCCGTAGG GACGGTGAAT
301 CGCTTCCAAC AACAATTTTT TCTGAAACGG CTCAAACCG AGCTGGTCGA
351 TGTTCAAAGA CGCGGCATCG GAATTCAAAA TCCGCATCAC GACCTTTTCG
401 CCAAACAGCG TCGGCAATGT GCTGACACGG AAATCGACAG GCTTGCCGCC
451 CTTTTGAAAG GTCAGCTGCA TCCTGCCGTC CTGCGGTATC CGTTTTTCGG
501 AAATGTCCAA ACGCGACATT ACCTTAATCC GGAAGCAAG CTGCCCCCTT
551 ACCGCAATGG GCGGCTGAAC CACCTCGCGG AGCTGCCCGT CCACACGGAA
601 ACGGATACGG GCATTGTGTT CGTAAACTC GAAATGGATG TCCGATGCCC
651 CGCTGCGCAA GGCATCCGAC AAAGTCTTAT GGATAAACCT CGGAACAGGG
701 CCGTCTTCTG CCTCCTCGTT GTCGATATAC AGGGTGTTGGC TTTCCTCTTC
751 CTCCTGCCCC TCCCCAAGCT CCTGAAGCAG CGATGTGCGA CGCGAACCCA
801 CCCAATCGAG CAAACCCGCC AACTGGTCAT CCTCGACAAT GACCAACTCA
851 ACCTCAATCC CTGCGGCAGA AACGGTTTTT TGAATTTGCG GCATCTGTGT
901 CGGATCGGAA ACCGCAAAAA ATACTTTGTC GCCCGACGG AAAACCGGCA
951 CACAGTGGAA CTCCACCATC TGCTCCTCCG TCAACACCCC CATCAGACCC
1001 CTGTGGCGCG GATAATGACG CAAATCAAGA ATCGAATAAC TGAACACCCT
1051 CGCAATCAAT GCCGCAAGCG ACTTGGGCGA AATGACACCG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1724; ORF 573.a>:

a573.pep

```

1 MPCLCRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ TLLIIDVNLI
51 DARQVNLGRV FRRCNLYRLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVN
101 RFQQQFFLKR LKTELVDVQR RGIGIQNPBH DLFAKQRRQC ADTEIDRLAA
151 LLKGQLHPAV LRYPPFGNVQ TRHYLNPGSK LPPYRNGRLN HLAELPVHTE
201 TDTGIVFVKL EMDVRCPAAG GIRQSLMDKP RNRAVFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNLNPGCR NGFLNLRHLC
301 RIGNRKKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

m573/a573 98.6% identity in 364 aa overlap

	10	20	30	40	50	60
m573.pep	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ ALLIIDVNLI DARQVNLGRV					
a573	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ TLLIIDVNLI DARQVNLGRV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m573.pep	FRRCNLYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTNVRYQHFFLKR LKTELVDVQR					
a573	FRRCNLYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTNVRFQQQFFLKR LKTELVDVQR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m573.pep	RGIGIQNPBHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFGNVQTRHYLNPGSK					
a573	RGIGIQNPBHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFGNVQTRHYLNPGSK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m573.pep	LPPYRNGRLNHLAELPVHTE TDTGIVFVKLEMDVRCPAAGGIRQSLMDKPRNRAVFCLLV					
a573	LPPYRNGRLNHLAELPVHTE TDTGIVFVKLEMDVRCPAAGGIRQSLMDKPRNRAVFCLLV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m573.pep	VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
a573	VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
	250	260	270	280	290	300

884

	310	320	330	340	350	360
m573.pep	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
a573	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
	310	320	330	340	350	360
m573.pep	NDTVX					
a573	NDTVX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1725>:

g574.seq

```

1   atgctgccga atctgccaaa cagccttaag aaagccgata tggacaacga
51  attgtggatt atcctgctgc cgattatcct ttgcccgtc ttcttcacga
101 tgggctgggt tgccgcccgc gtggatatga aaaccgtatt gaagcaggca
151 aaaagcatcc ctctgggatt ttataaaagc ctggacgctt tggctgaccg
201 caacagcggg cgcgcggcaa gggagttggc ggaagtcgtc gacggccggc
251 cgcaatcgta tgatttgaac cttaccctcg gcaaaacttta ccgtcagcgc
301 ggcgaaaacg acaaagccat caacatacac cggacaatgc tcgattctcc
351 cgatacggtc ggcgaaaagc gcgcgcgcgt cctgtttgaa ttggcgcaaa
401 actaccaaa ggcgggtttg gtcgatcgtg ccgaacagat tttttgggg
451 ctgcaagacg gtgaaatggc gcgtagaagg agacagcacc tgctcaatat
501 ctaccagcag gacagggatt gggaaaaagc ggttgaaacc gcccaacttc
551 ttagtcacga cgaacagaca tatcagtttg agattgcaca gttttattgc
601 gaacttgccc aagccgcgct gttcaagtcc aatttcgatg ccgcgcgctt
651 caatgtcggc aaggcactcg aagccaacaa aaaatgcacc cgcgccaaca
701 tgattttggg cgacattgaa caccgacaag gcaatttccc tgccgcgctc
751 gaagcctatg ccgccatcga gcagcaaac catgcatact tgagcatggt
801 cggcgagaag ctttacgaag cctatgccgc gcagggaaaa cctgaagaag
851 gcttgaaccg tctgacagga tatatgcaga cgtttcccga acttgacctg
901 atcaatgtcg tgtacgagaa atccctgctg cttaaggcgc agaaaagaagc
951 cgcgcaaac gcgcgcgagc ttgtccgcgc caagcccgcac cttaacggcg
1001 tgtaccgcct gctcggtttg aaactcagcg atttggatcc ggcttggaag
1051 gccgatgcgg acatgatgcg ttcggttatc ggacggcagc tccagcgagc
1101 cgtgatgtac cgttgccgca actgccactt caaatcccaa gtctttttct
1151 ggcactgtcc cgctgcaac aaatggcaga cgtttacgcc gaataaaatc
1201 gaagtttaa

```

This corresponds to the amino acid sequence <SEQ ID 1726; ORF 574.ng>:

g574.pep..

```

1   MLPNLPNSLK KADMDNELWI ILLPIILLPV FFTMGWFAAR VDMKTVLKQA
51  KSIPSGFYKS LDALVDRNSG RAARELAEVV DGRPQSYDLN LTGLKLYRQR
101 GENDKAINIH RTMLDSPDTV GEKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LQDGEAREHA RQHLLNIYQQ DRDWEKAVET AQLLSHDEQT YQFEIAQFYC
201 ELAQAALEFKS NFDAARFNVG KALEANKKCT RANMILGDIE HRQGNFPAAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQK PEEGLNRLTG YMQTFPELDL
301 INVVEKSLK LKGEKEAAQT AVELVRRKPD LNGVYRLLGL KLSLDLPAWK
351 ADADMMRSVI GRQLQRSVMY RCRNCHFSQ VFFWHCPACN KWQTFTPNKI
401 EV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1727>:

m574.seq..

```

1   ATGCGCCCGA ATCTACCAAA CAGCCTTAAG AAAGCCGATA TGGACAACGA
51  ATTGTGGATT ATCCTGCTGC CGATTATCCT TTTGCCCGTC TTCTTCGCGA
101 TGGGCTGGTT TGCCGCCCGC GTGGATATGA AAACCGTATT GAAGCAGGCA
151 AAAAGCATCC CTTCGGGATT TTATAAAAGC TTGGACGCTT TGGTCGACCG
201 CAACAGCGGG CGCGCGGCAA GGGAGTTGGC GGAAGTCGTC GACGGCCGGC
251 CGCAATCGTA TGATTTGAAC CTCACCCTCG GCAAACTTTA CCGCCAGCGT
301 GGCGAAAACG ACAAAGCCAT CAACATACAC CCGACAATGC TCATTCTCC
351 CGATACGGTC GGCgAAAAGC GCGCGCGCGT CCTGTTTGAA TTGGCGCAAA
401 ACTACCAAG TGCGGGGTTG GTCGATCGTG CCGAACAGAT TTTTGTGGG
451 CTGCAAGACG GTAAAATGGC GCGTGAAGCC AGACAGCACC TGCTCAATAT
501 CTACCAACAG GACAGGGATT GGGAAAAAGC GGTTGAAACC GCCCGGCTGC
551 TCAGCCATGA CGATCAGACC TATCAGTTTG AAATCGCCCA GTTTTATGTC
601 GAACTTGCCC AAGCCGCGCT GTTCAAGTCC AATTTCGATG TCGCGCGTTT

```

885

```
651 CAATGTCGGC AAGGCACTCG AAGCCAACAA AAAATGCACC CGCGCCAACA
701 TGATTTTGGG CGACATCGAA CACCGACAAG GCAATTTCCC TGCCGCCGTC
751 GAAGCCTATG CCGCCATCGA GCAGCAAAAC CATGCATACT TGAGCATGGT
801 CGGCGAGAAG CTTTACGAAG CCTATGCCGC GCAGGGAAAA CCTGAAGAAG
851 GCTTGAACCG TCTGACAGGA TATATGCAGA CGTTTCCCGA ACTTGACCTG
901 ATCAATGTCG TGTACGAGAA ATCCCTGCTG CTTAAGTGCG AGAAAGAAGC
951 CGCGCAAACC GCCGTCGAGC TTGTCCGCCG CAAGCCCCGAC CTTAACGGCG
1001 TGTACCGCCT GCTCGGTTTG AACTCAGCG ATATGAATCC GGCTTGGAAG
1051 GCCGATGCCG ACATGATGCG TTCGGTTATC GGACGGCAGC TACAGCGCAG
1101 CGTGATGTAC CGTTGCCGCA ACTGCCACTT CAAATCCCAA GTCTTTTCTT
1151 GGCCTGCCC CGCCTGCAAC AAATGGCAGA CGTTTACCCC GAATAAAATC
1201 GAAGTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1728; ORF 574>:

m574.pep..

```
1 MRPNLPNSLK KADMDNELWI ILLPIILLPV FFAMGWFAAR VDMKTVLKQA
51 KSIPSGFYKS LDALVDRNSG RAARELAEVV DGRPQSYDLN LTLGKLYRQR
101 GENDKAINIH RTMLDSPDTV GEKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LQDGKMAREA RQHLLNIYQQ DRDWEKAVET ARLLSHDDQT YQFEIAQFYC
201 ELAQALFKS NFDVARFNVG KALEANKKCT RANMILGDIE HRQGNFPAAV
251 EAYAAIEQQN HAYLSMVGEK LYEAAYAAQGK PEEGLNRLTG YMQTFPELDL
301 INVVEKSL LKCEKEAAQT AVELVRRKPD LNGVYRLGL KLSDMNPAWK
351 ADADMRSVI GRQLQRSVMY RCRNCHFKSQ VFWHCPACN KWQTFTPNKI
401 EV*
```

m573/g573 97.8% identity in 402 aa overlap

	10	20	30	40	50	60
m574.pep	MRPNLPNSLK	KADMDNELWI	ILLPIILLPV	FFAMGWFAAR	VDMKTVLKQA	KSIPSGFYKS
g574	MLPNLPNSLK	KADMDNELWI	ILLPIILLPV	FFAMGWFAAR	VDMKTVLKQA	KSIPSGFYKS
	10	20	30	40	50	60
	70	80	90	100	110	120
m574.pep	LDALVDRNSG	RAARELAEVV	DGRPQSYDLN	LTLGKLYRQR	GENDKAINIH	RTMLDSPDTV
g574	LDALVDRNSG	RAARELAEVV	DGRPQSYDLN	LTLGKLYRQR	GENDKAINIH	RTMLDSPDTV
	70	80	90	100	110	120
	130	140	150	160	170	180
m574.pep	GEKRARVLFE	LAQNYQSAGL	VDRAEQIFLG	LQDGKMAREA	RQHLLNIYQQ	DRDWEKAVET
g574	GEKRARVLFE	LAQNYQSAGL	VDRAEQIFLG	LQDGKMAREA	RQHLLNIYQQ	DRDWEKAVET
	130	140	150	160	170	180
	190	200	210	220	230	240
m574.pep	ARLLSHDDQT	YQFEIAQFYC	ELAQALFKS	NFDVARFNVG	KALEANKKCT	RANMILGDIE
g574	AQLSHDEQTY	QFEIAQFYC	ELAQALFKS	NFDVARFNVG	KALEANKKCT	RANMILGDIE
	190	200	210	220	230	240
	250	260	270	280	290	300
m574.pep	HRQGNFPAAV	EAYAAIEQQN	HAYLSMVGEK	LYEAAYAAQGK	PEEGLNRLTG	YMQTFPELDL
g574	HRQGNFPAAV	EAYAAIEQQN	HAYLSMVGEK	LYEAAYAAQGK	PEEGLNRLTG	YMQTFPELDL
	250	260	270	280	290	300
	310	320	330	340	350	360
m574.pep	INVVEKSL	LKCEKEAAQT	AVELVRRKPD	LNGVYRLGL	KLSDMNPAWK	ADADMRSVI
g574	INVVEKSL	LKCEKEAAQT	AVELVRRKPD	LNGVYRLGL	KLSDMNPAWK	ADADMRSVI
	310	320	330	340	350	360
	370	380	390	400		
m574.pep	GRQLQRSVMY	RCRNCHFKSQ	VFWHCPACN	KWQTFTPNKI	EVX	
g574	GRQLQRSVMY	RCRNCHFKSQ	VFWHCPACN	KWQTFTPNKI	EVX	
	370	380	390	400		

```
a574.seq
1 ATGCGCCCGA ATCTGCCAAA CAGCCTTGAG AAAGCCGATA TGGACAATGA
51 ATTGTGGATT ATCCTGCTGC CGATTATCCT TTTGCCCGTT TTCTTCGCGA
101 TGGGCTGGTT TGCCGCCCGC GTGGATATGA AGACTGTATT AAAGCAGGCA
151 AAAAGCATAC CTGCGGGATT TTATAAAAGT CTGGATGCCT TGTTTGACCG
201 CAACACGCGG CGCGCGGCAA GGGAGTTGGC GGAAGTCGTC GACGGCCCGC
251 CGCAATCGTA TGATTTGAAC CTCACCCTCG GCAAACTTTA CCGCCAGCGT
301 GGCGAAAACG ACAAAGCCAT CAATATGCAC CAAACATTGC TTGACTCTCC
351 CGATAACAAC GGAGCCAAGC GCGCGCGCGT CCTGTTTGAA TTGGCGCAAA
401 ACTACCAAAG TCGCGGGTTG GTCGATCGTG CGCAACAGAT TTTTGTGGG
451 CTGCAAGACG GTGAAATGGC GCGTGAAGCC AGACAGCACC TGCTCAATAT
501 CTACCAACAG GACAGGGATT GGGAAAAAGC GGTTGAAACC GCCCGGCTGC
551 TCAGCCATGA CGATCAGACC TATCAGTTTG AAATCGCCCA GTTTTATTGC
601 GAACTTGCCC AAGCCGCGCT GTTCAAGTCC AATTTCGATG CCGCGCGCTT
651 CAATGTCGGC AAGGCACTCG AAGCCAACAA AAAATGCACC CGCGCCAATA
701 TGATTTTGGG GCACATCGAA CACCGACAAG GCAAATTTCC CCGCGCCGTC
751 GAAGCCTATG CCGCCATCGA GCAGCAAAAC CATGCATACT TGAGTATGGT
801 CGGCGAGAAG CTTTACGAAG CCTATGCCGC GCAGGGAAAA CCTGAAGAAG
851 GCTTGAACCG TCTGACAGGA TATATGCAGA CGTTTCCCGA ACTTGACCTG
901 ATCAATGTCG TGTACAGAA ATCCCTCGTG CTTAAGTCGC AGAAAGAAGC
951 CGGCGAAACC CGCGTCGAGC TTGTCGCGCG CAAGCCCGAC CTC AACGCGC
1001 TGTACCGCCT GCTTGGTTTG AAATCAGCG ATTTGGATCC GGCTTGAAA
1051 GCCGATGCCG ATATGATGCG TTCGTTATC GGACGGCAGC TACAGCGCAG
1101 CGTGATGTAC CGGTGCCGAA ACTGCCACTT CAAATCACAA GTCTTTTTCT
1151 GGCATTGTCC TGCCTGCAAC AAATGGCAGA CGTTTACGCC AAACAAAATC
1201 GAAGTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1730; ORF 574.a>:

a574.pep

1	<u>MRPNLPNSLE</u>	<u>KADMDNELWI</u>	<u>ILLPIILLPV</u>	<u>FFAMGWFAAR</u>	<u>VDMKTVLKQA</u>
51	KSIPSGFYKS	LDALVDNRNSG	RAARELAEV	DGRPQSYDLN	LTIGKLYRQR
101	GENDKAINMH	QTLLEDSPDT	GAKRARVLFE	LAQNYQSAGL	VDRAEQIFGL
151	LQDGMAREA	RQHLLNLYQQ	DRDWEKAVET	ARLLSHDDQT	YQFEIAQFYC
201	ELAQAALFKS	NFDAARFNVG	KALEANKKCT	RANMILGDIE	QRQGNFPAAV
251	EAYAAIEQQN	HAYLSMVGEK	LYEAYAAQGK	PEEGLNRLTG	YMQTFPELDL
301	INVVEKSL	LKCEKEAAQT	AVELVRRKPD	LNGVYRLLGL	KLSDLDPAWK
351	ADADMMSVI	GRQLQRSVMY	RCRNCHFKSQ	VFFWHCPACN	KWQTFTPNKI
401	EV*				

m574/a574 97.5% identity in 402 aa overlap

	10	20	30	40	50	60
m574.pep	MRPNLPNSLKKADMDELWIIILLPIILLPVFFAMGWFAARVDMKTVLKQAKSIPSGFYKS					
a574	MRPNLPNSLEKADMDELWIIILLPIILLPVFFAMGWFAARVDMKTVLKQAKSIPSGFYKS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m574.pep	LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGLKLYRQRGENDKAINIHRTMLDSPDTV					
a574	LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGLKLYRQRGENDKAINMHQTLLDSPDTT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m574.pep	GEKRARVLFELAQNYQSAGLVDRAEQIFLGLQDGKMAREARQHLLNIYQQDRDWEKAVET					
a574	GAKRARVLFELAQNYQSAGLVDRAEQIFLGLQDGEMAREARQHLLNIYQQDRDWEKAVET					
	130	140	150	160	170	180
	190	200	210	220	230	240
m574.pep	ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFDFVARFNVGKALEANKKCTRANMILGDIE					
a574	ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFDAARFNVGKALEANKKCTRANMILGDI					

887

	190	200	210	220	230	240
	250	260	270	280	290	300
m574.pep	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQ GKPEEGLNRLTG YMQTFPELDL					
a574	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQ GKPEEGLNRLTG YMQTFPELDL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m574.pep	INVVYEKSLLLKCEKEAAQTAVELVRRKPD LNGVYRLLGLKLSDMNPAWKADADMMRSVI					
a574	INVVYEKSLLLKCEKEAAQTAVELVRRKPD LNGVYRLLGLKLSDLPAWKADADMMRSVI					
	310	320	330	340	350	360
	370	380	390	400		
m574.pep	GRQLQRSVMYRCRNCHFKSQVFFWHCPACNKWQTFTPNKIEVX					
a574	GRQLQRSVMYRCRNCHFKSQVFFWHCPACNKWQTFTPNKIEVX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1731>:

g575.seq (partial)

```

1  ..atgccgtgcc tccgccggca agcagcaagg tgtacgaacc gccgaacaga
51  ccgtcaaaca gtccgctttc ggtttcttct tcggcagaaa cctgttcgac
101 aggttcggca acgggttcgg cggcaacttc actggctgtt tccgcaacag
151 gttcggaaac ggtgttaccg gtttcgtcgg tcggcgtgtc gatggcagaa
201 gcggcggctt cttggggggg cggattcggc agcggtttcc gatgcggcag
251 tatttgcagc ggggtacagg cggggttggc gttctgtcgc cgaagccgga
301 gtttcggaca ctgcgggttt ggggttcggg cgaacggccg gtttttccgc
351 ttttgettcg ggccgggcaa cttttgcttc aggtttttca accggttttt
401 cgacagggtt ctctatcggc ttctccacag ttgcctgtt ggacgggtca
451 gacggcatgg atgcagtttc ggttttgggt ttccgcgttt gcggtttggg
501 ttgttcgcgt ttgatttttt tgggtgtcgc cgctttgate ctgttcagat
551 tcggaatgtg a*
```

This corresponds to the amino acid sequence <SEQ ID 1732; ORF 575.ng>:

g575.pep (partial)

```

1  ..MPCLRRQAAR CTNRRTRDQT VRFRLLRQK PVRQVRQVR RQLHWLFPQQ
51  VRKRCYRFRR SACRWQKRRL LGGADSAVS DAAVFAAGTG PGWRSVAEAG
101 VSDTAGLGSG RTAGFSAFAS GAATFASGFS TGFSTGFSIG FSTVACLDGS
151 DGMDAVSALG FAVCGLGCSA LIFLGAAALI LFRFGM*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1733>:

m575.seq..

```

1  ATGGTTTCGG GCGAGGAAGC CTTCAGGAAG CCTGCCAGTC CGGAGGGTGA
51  GGCAGGTTTT GCGGAAGCTG TTTCTTCTGT GCCGATATGG TTGTTTGAGG
101 GCAGGTGTGC GGAGAAATCG GTATCGACGG TTTCCGGTTT GTTTTCGGCA
151 GTTTGGGCGA CAGATTCCGG TTCGGGCGTG TCGATGACGA TTTCGACAGG
201 GTTGTACGGG TTGAAGGTCT CGGGCTCGTA CACGCTGTCT GTGGATTCTGA
251 TGGCGTTCCA ATCGGCATCC GCGCGTTTTT GGGTTTCTTC ATCCTGCGTA
301 AGTGCGCCGG ATAAATGCC GTTTTGCGCG GCTGCCAGGC TGTCGAAATC
351 CAAGTCGATG CGGTTGGAAG GCGTATCGGT TTCGACATCG AACGTTTGTT
401 TTGCCGATAA CTCTTCTTCA GATTCCCAT CTAAGGCAAG TGTGTCGTTT
451 ACATCGTTTT TCGGAGCGGG TTCGGGCGTT GCCGGAGTTT CCACTTCGGC
501 AAAGGTGATT TCTATGCCGT CGTCTGCCGC GTCGTCAAGG TCAGGCTCTT
551 CCTCAGGGAC GGATTCTTCG GTACGGCGCG CGCGTTTGGG TTGGGCAAGG
601 CGCAAAGACA GCAGCAGGGC GATTAATGCC GCGCCTCCGC CGGCAAGCAG
651 CAAGGTGTAC GAACCGCCGA ACAGACCGTC AAACAGTCCG CTTTCGGTTT
701 CTTCTTCGGC AGAAACCTGT TCGACAGGTT CGGAAACGGC GTTACCGGTT
751 TCGTCGGTCG GCGTGTGAT GGCAGAAGCG GCGGCTTCTT GGGGGCGCGA
801 TTCGGCAGCG GTTTCCGATG CGGCAGTATT TGCAGCGGGT ACAGGTTCCG
851 GTCGAACGGC CGGTTTTTCC GCTTTTGCTT CGGGCGCGGC AACTTTGCT
901 TCAGGTTTTT CAACCGGTTT CTCTACCGTT GCCTGTTTGG ACGGTTCCGA
951 CGGCATGGAT GCGGTTTCGG CTTTGGGTTT CGCCGTTTGC GGTTTGGGTT
1001 GTTCCGCTTT GATCCTGTTC AGATTCCGAA TGTGA
```

888

This corresponds to the amino acid sequence <SEQ ID 1734; ORF 575>:

m575.pep

```

1  MVSGEAEFRK PASPEGEAGF AEAUVSSVPIW LFEGRLSEKS VSTVSGLFSA
51  VWATDSGSGV SMTISTGLYG LKVSYSYTLS VDSMAFQSAS ARFWVSSSCV
101 SAPDKMPFCA AARLSKSKSM RLEGVSVSTS NVCFADNSSS DSPSKASVSF
151 TSFFGAGSGV AGVSTSAKVI SMPSSAASSR SGSSSGTDSS VRRARLDWAR
201 RKSSSRAINA APPPASSKVY EPPNRPSNSP LSVSSSAETC STGSETALPV
251 SSVGVSMAEA AASWGADSAA VSDAAVFAAG TSGSRTAGFS AFASGAATFA
301 SGFSTGFSV ACLDGS DGM DAVSALGF A VCGLGCSALI LFRFGM*

```

m575/g575 70.2% identity in 114 aa overlap

```

                240      250      260      270      280
m575.pep      SSAETCSTGSETALPVSSVGVSMAEAAASWGADSAVSDAAVFAAGTG-----
                |||||
g575          LHWLFPPQVRKRCYRFRRSACRWQKRLLGGADSAVSDAAVFAAGTGPWRSVAEAGVS
                50      60      70      80      90      100

                290      300      309      310      320
m575.pep      -----SGRTAGFSAFASGAATFASGFSTGFST-----VACLDGSDGMDAVSALGFA
                |||||
g575          DTAGLGSGRTAGFSAFASGAATFASGFSTGFSTGFSIGFSTVACLDGSDGMDAVSALGFA
                110     120     130     140     150     160

                330      340
m575.pep      VCGLGCSALI-----LFRFGMX
                |||||
g575          VCGLGCSALIFLGAAALILFRFGMX
                170     180

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1735>:

a575.seq

```

1  ATGGTTTCGG GCGAGGAAGC CTTCAGGAAG CCTGCCAGTC CGGAGGGTGA
51  GGCAGGTTTT GCGGAAGCTG TTTCTTCTGT GCCGATATGG TTGTTTGAGG
101 GCAGGTGTGC GGAGAAATCG GTATCGACGG TTTCGGGTTT GTTTTCGGCA
151 GTTTGGGCGA CAGATTCGGG TTCGGGCGTG TCATGACGA TTTCGACAGG
201 GTTGTACGGG TTGAAGGTCT CGGGCTCGTA CACGCTGTCT GTGGATTCTGA
251 TGGCGTTCCA ATCGGCATCC GCGCGTTTTT GGGTTTCTTC ATCCTGCGTA
301 AGTGCGCCGG ATAAATGCC GTTTTGC GCTGCCAGGC TGTCGAAATC
351 CAAGTCGATG CGGTTGGAAG GCGTATCGGT TTCGACATCG AACGTTTGTT
401 TTGCCGACAA CTCTTCTTCA GATCCCCAT CTAAGGCAAG TGTGTCGTTT
451 ACATCGTTTT TCGGAGCGGG TTCGGGCGTT GCCCGAGTTT CGACTTCGGC
501 AAAGGTGATT TCTATGCCGT CGTCTGCCGC GTCGTCAAGG TCAGGCTCTT
551 CCTCAGGGAC GGATTCTTCG GTACGGCGCG CGCGTTTGA TTGGGCAAGG
601 CGCAAAAGCA GCAGCAGGGC GATCAATGCC GCGCTCCGC CGGCAAGCAG
651 CAAGGTGTAC GAACCGCCGA ACAGTCCGCT TTCGGTTTCT TCTTCGGCAG
701 AAACCTGTTT GACAGGTTTC GAAACGGCGT TACCGGTTTC TCGGTTCGGC
751 GTGTCGATGG CAGAAGCGGC GGCTTCTTGG GGGCGGGATT CGGCAGCGGT
801 TTCCGATGCG GCAGTATTTG CAGCGGTAC AGGTTCCGGT CGAACGGCCG
851 GTTTTTCGGC TTTTGCTTCG GCGCGGCAA CTTTGCTTC AGGTTTTCFA
901 ACCGGTTTCT CTACCGTTGC CTGTTTGGAC GGTTCGGACG GCATGGATGC
951 GGTTTCGGCT TTGGGTTTCG CCGTTTGGC TTTGGGTTGT TCCGCTTTGA
1001 TCCTGTTTCA ATTCCGAATG TGA

```

This corresponds to the amino acid sequence <SEQ ID 1736; ORF 575.a>:

a575.pep

```

1  MVSGEAEFRK PASPEGEAGF AEAUVSSVPIW LFEGRLSEKS VSTVSGLFSA
51  VWATDSGSGV SMTISTGLYG LKVSYSYTLS VDSMAFQSAS ARFWVSSSCV
101 SAPDKMPFCA AARLSKSKSM RLEGVSVSTS NVCFADNSSS DSPSKASVSF
151 TSFFGAGSGV AGVSTSAKVI SMPSSAASSR SGSSSGTDSS VRRARLDWAR
201 RKSSSRAINA APPPASSKVY EPPNSPLSVS SSAETCSTGS ETALPVSSVG
251 VSMAEAAASW GADSAAVSDA AVFAAGTGS RTAGFSAFAS GAATFASGFS
301 TGFSTVACLD GSDGMDAVSA LGFAVCGLGC SALILFRFGM *

```


889

m575/a575 98.8% identity in 344 aa overlap

	10	20	30	40	50	60
m575.pep	MVSGEEAFRK	PASPEGEAGFAE	AVSSVPIWLF	EGRLSEKSVST	VSGLFSAVWAT	DSGSGV
a575	MVSGEEAFRK	PASPEGEAGFAE	AVSSVPIWLF	EGRLSEKSVST	VSGLFSAVWAT	DSGSGV
	70	80	90	100	110	120
m575.pep	SMTISTGLYGL	KVSGSYTSLV	SDSMFQSA	SARFWVSS	SCVSAPDK	MPFCAAARLSKSKSM
a575	SMTISTGLYGL	KVSGSYTSLV	SDSMFQSA	SARFWVSS	SCVSAPDK	MPFCAAARLSKSKSM
	130	140	150	160	170	180
m575.pep	RLEGVSVST	SNVCFADNSS	SDSPSKASV	SFTSFFGAG	SGVAGVST	SAKVISMPSSAASSR
a575	RLEGVSVST	SNVCFADNSS	SDSPSKASV	SFTSFFGAG	SGVAGVST	SAKVISMPSSAASSR
	190	200	210	220	230	240
m575.pep	SGSSSGTD	SSVRRARLD	WARRKSSSR	AINAAPPP	PASSKVYEP	PNRPSNSPLSVSSSAETC
a575	SGSSSGTD	SSVRRARLD	WARRKSSSR	AINAAPPP	PASSKVYEP	PNRPSNSPLSVSSSAETC
	250	260	270	280	290	300
m575.pep	STGSETALP	VSSVGVSMAE	AAASWGAD	SAAVSDAA	VFAAGTGS	GRTAGFSAFASGAATFA
a575	STGSETALP	VSSVGVSMAE	AAASWGAD	SAAVSDAA	VFAAGTGS	GRTAGFSAFASGAATFA
	310	320	330	340		
m575.pep	SGFSTGFST	VACLDGSDG	MDAVSALG	FAVCGLGCS	ALILFRFGMX	
a575	SGFSTGFST	VACLDGSDG	MDAVSALG	FAVCGLGCS	ALILFRFGMX	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1737>:

g576.seq.. (partial)

```

1  ..atgggcgtgg acatcggacg ctccctgaaa caaatgaagg aacagggcgc
51  ggaaatcgat ttgaaagtct ttaccgatgc catgcaggca gtgtatgacg
101 gcaaagaaat caaaatgacc gaagagcagg cccaggaagt gatgatgaaa
151 ttccctgcagg agcagcaggc taaagccgta gaaaaacaca aggcggatgc
201 gaaggccaac aaagaaaaag gcgaagcctt cctgaaggaa aatgccgccg
251 aagacggcgt gaagaccact gcttccggtc tgcagtacaa aatcaccaaa
301 caggggtgaag gcaaacagcc gacaaaagac gacatcgtaa ccgtggaata
351 cgaaggccgc ctgattgacg gtaccgtatt cgacagcagc aaagccaacg
401 gcggcccggc caccttcctt ttgagccaag tgattccggg ttggaccgaa
451 ggcgtacggc ttctgaaaga aggcggcgaa gccacgttct acatcccgtc
501 caaccttgcc taccgcgaac aggtgcgagg cgaaaaaatc ggtccgaacg
551 ccactttggt atttgacgtg aaactgggtc aaatcggcgc acccgaaaac
601 gcgcccgcga agcagccgga tcaagtcgac atcaaaaaag taaattaa

```

This corresponds to the amino acid sequence <SEQ ID 1738; ORF 576.ng>:

g576.pep.. (partial)

```

1  ..MGVDIGRSLK QMKEQGAIEID LKVFTDAMQA VYDGKEIKMT EEQAQEVMMK
51  FLQEQQAKAV EKHKADAKAN KEKGEAFLKE NAAEDGVKTT ASGLQYKITK
101 QGEGKQPTKD DIVTVEYEGR LIDGTVFDSS KANGGPATFP LSQVIPGWTE
151 GVRLLKEGGE ATFYIPSNLA YREQGAGEKI GPNATLVFDV KLVKIGAPEN
201 APAKQPDQVD IKKVN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1739>:

m576.seq.. (partial)

```

1  ..ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA

```

890

```

51   GCAAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
101  CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
151  GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAGGCCGT
201  AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
251  TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
301  CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
351  CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
401  TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
451  GTGATTCCGG GTTGGACCGA AGCGGTACAG CTTCTGAAAG AAGGCGGCGA
501  AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
551  GCGACAAAAT CGGTCCGAAC GCCACTTGG TATTTGATGT GAAACTGGTC
601  AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
651  CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1740; ORF 576>:

m576.pep.. (partial)

```

1   .MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
51  AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
101 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
151 VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFVDVKLV
201 KIGAPENAPA KQPAQVDIKK VN*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m576/g576 97.2% identity in 215 aa overlap

```

              10      20      30      40      50      60
m576.pep      MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQAQEVMMKFLQ
              |||:|||||
g576           MGVDIGRSLKQMK EQGAEIDLKV FTDAMQAVYD GKEIKMTEEQAQEVMMKFLQ
              10      20      30      40      50

              70      80      90      100     110     120
m576.pep      EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASGLQYKITKQEGGKQPTKDDIV
              |||:|||||
g576           EQQAKAVEKH KADAKANKEK GEAFLENAA EDGVKTTASGLQYKITKQEGGKQPTKDDIV
              60      70      80      90      100     110

              130     140     150     160     170     180
m576.pep      TVEYEGRLID GTVFDSSKAN GGPVTFPLSQVIPGWTEGVQLLKEGGEATFYIPSNLAYRE
              |||:|||||
g576           TVEYEGRLID GTVFDSSKAN GPATFPLSQVIPGWTEGVRLLEKGEATFYIPSNLAYRE
              120     130     140     150     160     170

              190     200     210     220
m576.pep      QGAGDKIGPNATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN
              |||:|||||
g576           QGAGEKIGPNATLVFDVKLVKIGAPENAPAKQPDQVDIKKVN
              180     190     200     210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1741>:

a576.seq

```

1   ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCCGCC TGCGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAGGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA

```

891

```

601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAAT CGGCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1742; ORF 576.a>:

```

a576.pep
  1 MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
 51 MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

m576/a576 99.5% identity in 222 aa overlap

m576.pep
                                     10      20      30
                                     MQQASYAMGV DIGRSLKQMK EQGAEIDLKV
                                     |||
a576      CGKKEAAPAS ASEPAASSA QGDTSSIGSTM MQQASYAMGV DIGRSLKQMK EQGAEIDLKV
                                     30      40      50      60      70      80

m576.pep
                                     40      50      60      70      80      90
                                     FTEAMQAVYD GKEIKMTEEQ AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA
                                     |||
a576      FTEAMQAVYD GKEIKMTEEQ AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA
                                     90     100     110     120     130     140

m576.pep
                                     100     110     120     130     140     150
                                     KDGVKTTAS GLQYKITQ GEGKQPTK DDIVTVEY EGRLIDGT VFDSSKAN GGPVTFPL SQ
                                     |||
a576      KDGVKTTAS GLQYKITQ GEGKQPTK DDIVTVEY EGRLIDGT VFDSSKAN GGPVTFPL SQ
                                     150     160     170     180     190     200

m576.pep
                                     160     170     180     190     200     210
                                     VIPGWTEGV QLLKEGGE ATFYIPSN LAYREQGAG DKIGPNATL VFDVKLVK IGAPENAPA
                                     |||
a576      VILGWTEGV QLLKEGGE ATFYIPSN LAYREQGAG DKIGPNATL VFDVKLVK IGAPENAPA
                                     210     220     230     240     250     260

m576.pep
                                     220
                                     KQPAQVDIKK VN
                                     |||
a576      KQPAQVDIKK VN
                                     270

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1743>:

g576-1.seq

```

  1 ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
 51 ACTTTCCGCC TCGGCGAAAA AAGAAGCCGC CCCCAGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTGCCGCG CAGGGCGACA CCTCTTCAAT CGGCAGCAG
151 ATGCAGCAGG CAAGCTATGC AATGGGCGTG GACATCGGAC GCTCCCTGAA
201 ACAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGATG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCCCAGGAAG TGATGATGAA ATTCTTGCA GAGCAGCAGG CTAAAGCCGT
351 AGAAAAACAC AAGCGGATG CGAAGGCCAA CAAAGAAAAA GGCGAAGCCT
401 TCCTGAAGGA AATGCGCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGT
451 CTGCAGTACA AAATCACCAA ACAGGGTGAA GGCAAACAGC CGACAAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACCGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG CCACCTTCCC TTTGAGCCAA
601 GTGATTCCGG GTTGGACCGA AGGCGTACGG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGAAAAAAT CGGTCCGAAC GCCACTTTGG TATTTGACGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG ATCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1744; ORF 576-1.ng>:

g576-1.pep

```

1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASAA QGDTSSIGST
51  MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTDAMQAVYD GKEIKMTEEQ
101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPATFPLSQ
201 VIPGWTEGVR LLKEGGEATF YIPSNLAYRE QGAGEKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPDQVDIKK VN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1745>:

m576-1.seq

```

1  ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTTCGG CCGCTTTGGC
51  ACTTTCCGCC TGCGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCGCG TTCTTCCGCG CAGGGCGACA CCTTTCGAT CGGCAGCAGC
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
601 GTGATTCCGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAAT CGGTCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1746; ORF 576-1>:

m576-1.pep

```

1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

g576-1/m576-1 97.8% identity in 272 aa overlap

	10	20	30	40	50	60
g576-1.pep	MNTIFKISAL	TLSAALALS	ACGKKEAPAS	ASEPAASAA	QGDTSSIGST	MQQASYAMGV
m576-1	MNTIFKISAL	TLSAALALS	ACGKKEAPAS	ASEPAASSA	QGDTSSIGST	MQQASYAMGV
	10	20	30	40	50	60
g576-1.pep	DIGRSLKQMK	EQGAEIDLKV	FTDAMQAVYD	GKEIKMTEE	QAQEVMMKFLQ	EQQAKAVEKH
m576-1	DIGRSLKQMK	EQGAEIDLKV	FTDAMQAVYD	GKEIKMTEE	QAQEVMMKFLQ	EQQAKAVEKH
	70	80	90	100	110	120
g576-1.pep	KADAKANKEK	GEAFLENAA	KDGVKTTASG	LQYKITKQGE	GKQPTKDDIV	TVEYEGRLID
m576-1	KADAKANKEK	GEAFLENAA	KDGVKTTASG	LQYKITKQGE	GKQPTKDDIV	TVEYEGRLID
	130	140	150	160	170	180
g576-1.pep	GTVFDSSKAN	GGPATFPLSQ	VIPGWTEGV	RLLEKGEATF	YIPSNLAYRE	QGAGEKIGPN
m576-1	GTVFDSSKAN	GGPATFPLSQ	VIPGWTEGV	RLLEKGEATF	YIPSNLAYRE	QGAGEKIGPN
	190	200	210	220	230	240
g576-1.pep	ATLVFDVKLV	KIGAPENAP	AKQPDQVDIKK	VN		
m576-1	ATLVFDVKLV	KIGAPENAP	AKQPAQVDIKK	VN		
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1747>:

a576-1.seq

893

```

1  ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTTCCG CCGCTTGGC
51  ACTTTCCGCC TGCGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTTCGCGC CAGGGCGACA CCTCTTCGAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC GATGGCGGTG GACATCGGAC GCTCCCTGAA
201 GCAATGAAG GAACAGGGCG CGGAAATCGA TTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATACCCAA ACAGGGCGAA GGCAAACAGC CGACCAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAAC GGCGGCCCGG TCACCTTCCC TTTAGCCAA
601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAAT CGGCCCGAAC GCCACTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAGTCTGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1748; ORF 576-1.a>:

a576-1.pep

```

1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLKQMK EQGAEIDLK FTEAMQAVYD GKEIKMTEEQ
101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLEKNA KDVKTASG
151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

a576-1/m576-1 99.6% identity in 272 aa overlap

	10	20	30	40	50	60
a576-1.pep	MNTIFKISALTLSAALALSACGKKEAAPASASEPAAASSAQGDTSSIGSTMQQASYAMGV					
m576-1	MNTIFKISALTLSAALALSACGKKEAAPASASEPAAASSAQGDTSSIGSTMQQASYAMGV					
	10	20	30	40	50	60
a576-1.pep	DIGRSLKQMKEQGAEIDLKVFTEAMQAVYDGKEIKMTEEQAQEVMKFLQEQQAKAVEKH					
m576-1	DIGRSLKQMKEQGAEIDLKVFTEAMQAVYDGKEIKMTEEQAQEVMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
a576-1.pep	DIGRSLKQMKEQGAEIDLKVFTEAMQAVYDGKEIKMTEEQAQEVMKFLQEQQAKAVEKH					
m576-1	DIGRSLKQMKEQGAEIDLKVFTEAMQAVYDGKEIKMTEEQAQEVMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
a576-1.pep	KADAKANKEKGEAFLEKNAAKDGVKTASGLQYKITKQEGGKQPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLEKNAAKDGVKTASGLQYKITKQEGGKQPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
a576-1.pep	KADAKANKEKGEAFLEKNAAKDGVKTASGLQYKITKQEGGKQPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLEKNAAKDGVKTASGLQYKITKQEGGKQPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
a576-1.pep	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
m576-1	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
a576-1.pep	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
m576-1	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
a576-1.pep	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
m576-1	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
	250	260	270			
a576-1.pep	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
m576-1	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
	250	260	270			

Expression of ORF 576

The primer described in Table 1 for ORF 576 was used to locate and clone ORF 576. ORF 576 was cloned in pET and pGex vectors and expressed in E.coli as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 3A shows the results of affinity purification and Figure 3B shows the expression in E.coli. Purified His-fusion protein was used to immunize mice, whose sera were used for ELISA (positive result), FACS analysis (Figure 3C), western blot (Figure 3D). These experiments confirm that ORF 576 is a surface-exposed protein and that it is a useful immunogen. The

hydrophilicity plots, antigenic index, and amphipathic regions of ORF 576 are provided in Figure 7. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 576 and the amino acid sequence encoded thereby is provided in Example 1.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1749>:

```
g577.seq..
1  atggaaagga gcggtgtatt tggtaaaatt gtcggcaatc gcatactccg
51  tatgccgtcc gaacacgctg ccgcattcta tccgaaaccg tgcaaatcgt
101 ttaactaac gcaatcttgg ttcagagtgc gaagctgtcc gtgcggcgtt
151 tttatttacg gagcaaacat gaaacttatc tataccgtca tcaaaatcat
201 tatectgctg ctcttctctg tgcttgccgt cattaatatg gatgccgtta
251 ccttttccta tcttcgggg cagagtgtca atctgccgct gattgtcgta
301 ttgttcggcg cgtttctcgt cggcatcgtg ttcggaatgt ttgccctggt
351 cgggcggctg ctgtccttgc gcggcgaaaa cagccgcctg cgtgcggaag
401 tgaagaaaag tgcgcgcttg agcggacaga aattgactgc accgccgata
451 caaatgctg ccgaatctgc caaacgcct taa
```

This corresponds to the amino acid sequence <SEQ ID 1750; ORF 577.ng>:

```
g577.pep
1  MERSGVFGKI VGNRILRMPS EHAAAFYPKP CKSFKLTQSW FRVRSPCGIV
51  FIYGANMKLI YTVIKIILL LFLLLAVINM DAVTFSYLPQ QSVNPLIVV
101 LFGAFVVGIV FGMFALFGRL LSLRGENSRL RAEVKKSARL SGQKLTAPPI
151 QNAESAQKP *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1751>:

```
m577.seq..
1  ATGGAAAGGA ACGGTGTATT TGGTAAAATT GTCGGCAATC GCATACTCCG
51  TATGTCGTCC GAACACGCTG CCGCATCCTA TCCGAAACCG TGCAAAATCGT
101 TTAAGTAGC GCAATCTTGG TTCAGAGTGC GAAGCTGTCT GGGCGGCGTT
151 TTTATTACG GAGCAAACAT GAAACTTATC TATACCGTCA TCAAAATCAT
201 TATCCTGCTG CTCTTCCTGC TGCTTGCCGT CATTAATACG GATGCCGTGA
251 CCTTTTCCTA CCTGCCGGGG CAAAATTTCG ATTTGCCGCT GATTGTCGTA
301 TTGTTCCGCG CATTGTAGT CCGTATTATT TTTGGAATGT TTGCCTTGTT
351 CGGACGGTTG TTGTCGTTAC GTGGCGAGAA CGGCAGGTTG CGTGCCGAAG
401 TAAAGAAAAA TGCGCGTTTG ACGGGGAAGG AGCTGACCGC ACCACCGGCG
451 CAAAATGCGC CCGAATCTAC CAAACAGCCT TAA
```

This corresponds to the amino acid sequence <SEQ ID 1752; ORF 577>:

```
m577.pep..
1  MERNGVFGKI VGNRILRMSS EHAAASYPKP CKSFKLAQSW FRVRSCLGGV
51  FIYGANMKLI YTVIKIILL LFLLLAVINT DAVTFSYLPQ QKFDLPLIVV
101 LFGAFVVGII FGMFALFGRL LSLRGENGRL RAEVKKNARL TGKELTAPPA
151 QNAPESTKQP *
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

```
m577/g577  88.1% identity in 160 aa overlap

              10      20      30      40      50      60
m577.pep    MERNGVFGKIVGNRILRMSSEHAAASYPKPCKSFKLAQSWFRVRSCLGGVFIYGANMKLI
              |||:||||||| ||||| |||||:||||||| |||||
g577         MERSGVFGKIVGNRILRMPSEHAAAFYPKPCKSFKLTQSWFRVRSPCGIVFIYGANMKLI
              10      20      30      40      50      60
              70      80      90     100     110     120
m577.pep    YTVIKIILLFLLLAVINTDAVTFSYLPQKFDLPLIVVLFGAFVVGIIFGMFALFGRL
```

895

```

|||||
g577 YTVIKIIILLFLLLAVINMDAVTFSYLPQSVNLPLIVVLFGAFVVGIVFGMFALFGRL
      70      80      90      100      110      120

      130      140      150      160
m577.ppep LSLRGENGRRLRAEVKKNARLTGKELTAPPAQNAPESTKQPX
          |||||:|||||:||||:|:||||| ||| ||:||||
g577 LSLRGENSRLRAEVKK SARLSGQKLTAPPIQNAESAQKQPX
          130      140      150      160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1753>:

```

a577.seq
1 ATGGAAAGGA ACGGTGTATT TGGTAAAATT GTCGGCAATC GCATACTCCG
51 TATGTCGTCC GAACACGCTG CCGCATCCTA TCCGAAACCG TGCAAATCGT
101 TTAAACTAGC GCAATCTTGG TTCAGAGTGC GAAGCTGTCC GGGCGGCGTT
151 TTTATTTACG GAGCAAACAT GAAACTTATC TATACCGTCA TCAAATCAT
201 TATCCTGCTG CTCTTCCTGC TGCTTGCTGT CATTAAATACG GATGCCGTTA
251 CCTTTTCCTA CCTGCCGGGG CAAAAATTCG ATTTGCCGCT GATTGTCGTA
301 TTGTTCCGCG CGTTTGTCTG CGGCATCGTG TTCGGAATGT TTGCCTTGTT
351 CGGACGGTTG TTGTCGTTAC GTGGCGAGAA CGGCAGGTG CGTGCCGAAG
401 TAAAGAAAAA TGC GCGTTTG ACGGGGAAGG AGCTGACCGC ACCACCGGCG
451 CAAATGCGC CCGAATCTGC CAAACAGCCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1754; ORF 577.a>:

```

a577.ppep
1 MERNGVFGKI VGNRILRMSS EHAAASYPKP CKSEKLAQSW FRVRSPPGGV
51 FIYGANMKLI YTVIKIIILL LFLLLAVINT DAVTFSYLPQ QKFDLPLIVV
101 LFGAFVVGIV FGMFALFGRL LSLRGENGRRL RAEVKKNARL TGKELTAPPA
151 QNAPESAKQP *

```

m577/a577 98.1% identity in 160 aa overlap

```

      10      20      30      40      50      60
m577.ppep MERNGVFGKIVGNRILRMSSSEHAAASYPKPCKSEKLAQSWFRVRSCLGGVFIYGANMKLI
          |||||
a577 MERNGVFGKIVGNRILRMSSSEHAAASYPKPCKSEKLAQSWFRVRSPPGGVFIYGANMKLI
      10      20      30      40      50      60

      70      80      90      100      110      120
m577.ppep YTVIKIIILLFLLLAVINTDAVTFSYLPQKFDLPLIVVLFGAFVVGIIFGMFALFGRL
          |||||
a577 YTVIKIIILLFLLLAVINTDAVTFSYLPQKFDLPLIVVLFGAFVVGIVFGMFALFGRL
      70      80      90      100      110      120

      130      140      150      160
m577.ppep LSLRGENGRRLRAEVKKNARLTGKELTAPPAQNAPESTKQPX
          |||||
a577 LSLRGENGRRLRAEVKKNARLTGKELTAPPAQNAPESTKQPX
      130      140      150      160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1755>:

```

g578.seq..
1 atgggaaagc tcgacatcgg gatattgttt gccgatttct tcaaagattt
51 cgcgccacag ttcggtggtt tccaaaacgt tggctttgcc tacggagcag
101 acttttttgc tgcgtttttg ggcgatttgc aaggccacgt gggcgatgag
151 gcggatttgc ctttcgctgt atttcattgt gttgtagcct tcgtgttcgc
201 cgttttccaa aacacggatg ccgcgcggtt cgccgaaata aatatcgccg
251 gtaagtctgc gcacaatcaa aatatccaaa ccggcaacga tttcaggctt
301 gagcgtggag gcgttggtta a

```

This corresponds to the amino acid sequence <SEQ ID 1756; ORF 578.ng>:

```

g578.ppep
1 MGKLDIGILF ADFFKDFAPQ FGGFQNVGFA YGADFFAAFL GGLEGHVGD
51 ADFAFAVFIG VVAFVFAVFQ NTDAARFAEI NIAGKFAHNQ NIQTGNDFRL

```

101 ERGGVG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1757>:

m578.seq..

```

1  ATGGGAAAGC TCGACATCAG GGTACTCTTT GCCGATTCTT TCAAAGATTT
51  CGCGCCACAA TTCGGTGGTT TCCAAAACGT TGGCTTTGCC TACGGAACAG
101 ACTTTTTTGC TCGTTTTTGC GCGGATTGG AAGGCAACAT GGGCAATACG
151 GCGGATTTCG CTTTCGCTGT ATTTTCATGGT GTTGTAGCCT TCGCGTTCGC
201 CGTTTTCCAG AACGCGGATG CCGCGCGGTT CGCCGAAATA GATGTCGCCG
251 GTGAGTTCGC GCACAATCAA AATATCCAAA CCGCAACGA TTCAGGCTT

```

This corresponds to the amino acid sequence <SEQ ID 1758; ORF 578>:

m578.pep..

```

1  MGKLDIRVLF ADFFKDFAPQ FGGFQNVGFA YGTDFFAAFL GGLEGNMNGT
51  ADFAFAVFHG VVAFAFAVFQ NADAARFAEI DVAGEFAHNQ NIQTGNDFRL
101 QRGGVG*

```

m578/g578 87.7% identity in 106 aa overlap

	10	20	30	40	50	60
m578.pep	MGKLDIRVLFADFFKDFAPQFGGFQNVGFAYGTDFFAAFLGGLEGNMNGNTADFAFAVFHG					
	: : :					
g578	MGKLDIGILFADFFKDFAPQFGGFQNVGFAYGADFFAFLGGLEGHVGDADFAFAVFHG					
	10	20	30	40	50	60
	70	80	90	100		
m578.pep	VVAFAFAVFQNAARFAEIDVAGEFAHNQNIQTGNDFRLQRGGVGX					
	: : : : : :					
g578	VVAFVFAVFQNTDAARFAEINIAGKFAHNQNIQTGNDFRLRGGGVGX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1759>:

a578.seq

```

1  ATGGGAAAGC TCGACATCAG GGTATTCTTT GCCGATTCTT TCAAAGATTT
51  CGCGCCACAA TTCGGTGGTT TCCAAAACGT TGGCTTTGCC TACGGAGCAG
101 ACTTTTTTGC TCGTTTTTGC GCGGATTGG AAGGCGACGT GGGCAATACG
151 GCGGATTTCG CTTTCGCTGT ATTTTCATGGT GTTGTAGCCT TCGCGTTCGC
201 CGTTTTCCAG AACACGGATG CCGCGCGGTT CGCCGAAATA AATATCGCCG
251 GTGAGTTCGC GCACAATCAA AATATCCAAA CCCGCAACGA TTCAGACTT
301 GAGCGTGGAG GCGTTGGCTA G

```

This corresponds to the amino acid sequence <SEQ ID 1760; ORF 578.a>:

a578.pep

```

1  MGKLDIRVFF ADFFKDFAPQ FGGFQNVGFA YGADFFAFL GGLEGDVGNT
51  ADFAFAVFHG VVAFAFAVFQ NTDAARFAEI NIAGEFAHNQ NIQTRNDFRL
101 ERGGVG*

```

m578/a578 91.5% identity in 106 aa overlap

	10	20	30	40	50	60
m578.pep	MGKLDIRVLFADFFKDFAPQFGGFQNVGFAYGTDFFAAFLGGLEGNMNGNTADFAFAVFHG					
	: : :					
a578	MGKLDIRVFFADFFKDFAPQFGGFQNVGFAYGADFFAFLGGLEGDVGNTADFAFAVFHG					
	10	20	30	40	50	60
	70	80	90	100		
m578.pep	VVAFAFAVFQNAARFAEIDVAGEFAHNQNIQTGNDFRLQRGGVGX					
	: : : : : :					
a578	VVAFAFAVFQNTDAARFAEINIAGEFAHNQNIQTRNDFRLRGGGVGX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1761>:

g579.seq..

```

1  ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT

```


897

```

51  TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101 CATTGGGACG GTTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GCGCGGGGTT TGGCGGTGGC GTTGTCTTA AAAGACCAGC TGTCCAATTT
201 TGCCGCCGGC GCGCTGATTA TCCTGTCCG CCCGTTCAA GTCGGCGACT
251 TTATCCGTGT CGGCGGTTTT GAAGGATATG TCCGGGAAAT CAAAATGGTG
301 CAGACTTCTT TGCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCAGCCTG CCGCTTTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATTT GAAAGTGGCG
451 AAAGAGGCGG TGTTGAAAGC CGCCGCCGAA CACCCCTTGA GCGTTCAAAA
501 CGAAGAGCGG CAGCCCGCCG CCTACATCAC CGCCTTGGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1762; ORF 579.ng>:

```

g579.pep..
1  MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51 GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSLRRTDNE EVVLPNSVVM GNSIVNRSSL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAAE HPLSVQNEER QPAAYITALG DNAIEITLWA WANEADRWTL
201 QCDLNEQVVE NLRKVNINIP FPQORDIHIIN S*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1763>:

```

m579.seq..
1  ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT
51 TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101 CATTGGGCAG ATTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GCGCGGGGTT TGGCGGTGGC GTTGTCCCTG AAAGACCAGC TGTCCAATTT
201 TGCCGCCGGC GCACTGATTA TCCTGTCCG CCCGTTCAA GTCGGCGATT
251 TTATCCGCGT CGGCGGTTTT GAAGGATATG TCCGAGAGAT TAAATGGTG
301 CAGACTTCTT TGCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCACACTG CCGCTGTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATTT GAAAGTGGCG
451 AAAGAGGCGG TGTTGAAAGC CGCCGTCGAA CACCCCTTGA GCGTTCAAAA
501 CGAAGAGCGG CAGGCTGCCG CCTACATCAC CGCCTTGGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1764; ORF 579>:

```

m579.pep..
1  MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51 GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSLRRTDNE EVVLPNSVVM GNSIVNRSTL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAVE HPLSVQNEER QAAAYITALG DNAIEITLWA WANEADRWTL
201 QCDLNEQVVE NLRKVNINIP FPQORDIHIIN S*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m579/g579 98.7% identity in 231 aa overlap

```

              10      20      30      40      50      60
m579.pep  MRAAMTRAQVDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSL
            |||||
g579       MRAAMTRAQVDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSL
            |||||
              10      20      30      40      50      60

              70      80      90     100     110     120
m579.pep  KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSLRRTDNEEVVLPNSVVM
            |||||
g579       KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSLRRTDNEEVVLPNSVVM
            |||||
              70      80      90     100     110     120

```

898

	130	140	150	160	170	180
m579.pep	GNSIVNRSTLPLCRAQVIVGVNDYNDLKVAKAEAVLKAAVEHPLSVQNEERQAAAYITALG					
	: : : : : :					
g579	GNSIVNRSSLPLCRAQVIVGVNDYNDLKVAKAEAVLKAAAEHPLSVQNEERQPAAYITALG					
	130	140	150	160	170	180

	190	200	210	220	230
m579.pep	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQRDIHIINSX				
	: : : :				
g579	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQRDIHIINSX				
	190	200	210	220	230

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1765>:

```
a579.seq
1  ATGAGGGCGG  CGATGACGCG  CGCGCAGGTC  GATGCCACGC  TGATTAGTTT
51  TTTGTGTAAT  GTTGCCAATA  TCGGCTTATT  GATTTTGGTG  ATTATTGCCG
101 CATTGGGCAG  ATTGGGCGTT  TCCACAACAT  CCGTAACCGC  CTTAATCGGC
151 GGCGCGGGTT  TGGCGGTGGC  GTTGTCTTGG  AAAGACCAGC  TGTCCAATTT
201 TGCCGCCGGC  GCGCTGATTA  TCCTGTTCCG  CCCGTTCAAA  GTCGGCGATT
251 TTATCCGCGT  CGGCGGTTTT  GAAGGATATG  TCCGAGAGAT  TAAATGGTG
301 CAGACTTCTT  TGCGGACGAC  CGACAACGAA  GAAGTCGTGC  TGCCCAACAG
351 CGTGGTGATG  GGCAACAGCA  TCGTCAACCG  TTCCCACTG  CCGCTGTGCC
401 GCGCCCAAGT  GATAGTCGGC  GTCGATTACA  ACTGCGATTT  GAAAGTGGCG
451 AAAGAGGCGG  TGTTGAAAGC  CGCCGTCGAA  CACCCCTTGA  GCGTTCAAAA
501 CGAAGAGCGG  CAGGCCGCCG  CCTACATCAC  CGCCTGGGC  GACAATGCCA
551 TCGAAATCAC  ATTATGGGCT  TGGGCAAACG  AAGCAGACCG  CTGGACGCTG
601 CAATGCGACT  TGAACGAACA  AGTGGTCGAA  AACCTCCGCA  AAGTCAATAT
651 CAACATCCCG  TTCCCGCAAC  GCGACATACA  CATCATCAAT  TCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1766; ORF 579.a>:

```
a579.pep
1  MRAAMTRAQV  DATLISFLCN  VANIGLLILV  IIAALGRLGV  STTSVTALIG
51  GAGLAVALSL  KDQLSNFAAG  ALIILFRPFK  VGDFIRVGGF  EGYVREIKMV
101 QTSRLTTDNE  EVVLPNSVVM  GNSIVNRSTL  PLCRAQVIVG  VDYNCDLKVA
151 KEAVLKAAVE  HPLSVQNEER  QAAAYITALG  DNAIEITLWA  WANEADRWTL
201 QCDLNEQVVE  NLRKVNINIP  FPQRDIHIIN  S*
```

m579/a579 100.0% identity in 231 aa overlap

	10	20	30	40	50	60
m579.pep	MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSL					
	: : : : :					
a579	MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSL					
	10	20	30	40	50	60

	70	80	90	100	110	120
m579.pep	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLTTDNEEVLPNSVVM					
	: : : : :					
a579	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLTTDNEEVLPNSVVM					
	70	80	90	100	110	120

	130	140	150	160	170	180
m579.pep	GNSIVNRSTLPLCRAQVIVGVNDYNDLKVAKAEAVLKAAVEHPLSVQNEERQAAAYITALG					
	: : : : :					
a579	GNSIVNRSTLPLCRAQVIVGVNDYNDLKVAKAEAVLKAAVEHPLSVQNEERQAAAYITALG					
	130	140	150	160	170	180

	190	200	210	220	230
m579.pep	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQRDIHIINSX				
	: : : :				
a579	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQRDIHIINSX				
	190	200	210	220	230

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1767>:

g579-1.seq

```

1  ATGGACTTCA  AACAAATTGA  TTTTTCACAC  CTGATCAGTG  TTTCCGGTTG
51  GGGGCATCTG  GCTGAAAAGG  CGTGGGCGTT  CGGGCTGAAC  CTTGCCGCCG
101 CGCTGCTTAT  TTTCTTGTC  GGGAAATGGG  CGGCGAAACG  CATTGTCGCC
151 GTAATGAGGG  CGGCGATGAC  GCGCGCGCAG  GTCGATGCCA  CGCTGATTAG
201 TTTTGTGTGT  AATGTTGCCA  ATATCGGCTT  ATTGATTTTG  GTGATTATTG
251 CCGCATTGGG  ACGGTTGGGC  GTTCCACAA  CATCCGTAAC  CGCCTTAATC
301 GCGGCGCGG  GTTGGCGGT  GCGTGTGCC  TTTAAAGACC  AGCTGTCCAA
351 TTTTGGCGC  GCGCGCTGA  TTATCCTGTT  CCGCCCGTTC  AAAGTCGGCG
401 ACTTTATCCG  TGTCGGCGGT  TTTGAAGGAT  ATGTCCGGGA  AATCAAAATG
451 GTGCAGACTT  CTTGCGGAC  GACCGACAAC  GAAGAAGTCG  TGCTGCCCAA
501 CAGCGTGGTG  ATGGGCAACA  GCATCGTCAA  CCGTTCACAG  CTGCCGCTTT
551 GCCGCGCCCA  AGTGATAGTC  GCGTCGATT  ACAACTGCGA  TTTGAAAGTG
601 GCGAAAGAGG  CGGTGTTGAA  AGCCGCCGCT  GAACACCCCT  TGAGCGTTCA
651 AAACGAAGAG  CGGCAGCCCG  CCGCTACAT  CACCGCCTTG  GCGGACAATG
701 CCATCGAAAT  CACATTATGG  GCTTGGGCAA  ACGAAGCAGA  CCGCTGGACG
751 CTGCAATGCG  ACTTGAACGA  ACAAGTGGTC  GAAACCTCC  GCAAAGTCAA
801 TATCAACATC  CCGTTCCCGC  AACGCGACAT  ACACATCATC  AATTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1768; ORF 008.ng>:

g579-1.pep

```

1  MDFKQDFDLH  LISVSGWGH  AEKAWAFGLN  LAAALLIFLV  GKWAAKRIVA
51  VMRAAMTRAQ  VDATLISFLC  NVANIGLLIL  VIIAALGRLG  VSTTSVTALI
101 GGAGLAVALS  LKDQLSNFAA  GALIILFRPF  KVGDFIRVGG  FEGYVREIKM
151 VQTSRLRTDN  EEVLPNSVV  MGNSIVNRSS  LPLCRAQVIV  GVDYNCDLKV
201 AKEAVLKAAA  EHPLSVQNEE  RQPAAYITAL  GDNAIEITLW  AWANEADRW
251 LQCDLNEQVV  ENLRKVNINI  PFPQORDIHII  NS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1769>:

m579-1.seq

```

1  ATGGACTTCA  AACAAATTGA  TTTTTCACAC  CTGATCAGTG  TTTCCGGTTG
51  GGAGCATCTG  GCTGAAAAGG  CGTGGGCGTT  CGGGCTGAAC  CTTGCCGCCG
101 CGCTGCTTAT  TTTTTCGTC  GGAAATGGG  CGGCGAAACG  CATTGTCGCT
151 GTGATGAGGG  CGGCGATGAC  GCGCGCGCAG  GTCGATGCCA  CGCTGATTAG
201 TTTTGTGTGT  AATGTTGCCA  ATATCGGCTT  ATTGATTTTG  GTGATTATTG
251 CCGCATTGGG  CAGATTGGGC  GTTCCACAA  CATCCGTAAC  CGCCTTAATC
301 GCGGCGCGG  GTTGGCGGT  GCGTGTGCC  CTGAAAGACC  AGCTGTCCAA
351 TTTTGGCGC  GCGCGACTGA  TTATCCTGTT  CCGCCCGTTC  AAAGTCGGCG
401 ATTTTATCCG  CGTCGGCGGT  TTTGAAGGAT  ATGTCCGAGA  GATTAAGATG
451 GTGCAGACTT  CTTGCGGAC  GACCGACAAC  GAAGAAGTCG  TGCTGCCCAA
501 CAGCGTGGTG  ATGGGCAACA  GCATCGTCAA  CCGTTCACAG  CTGCCGCTGT
551 GCCGCGCCCA  AGTGATAGTC  GCGTCGATT  ACAACTGCGA  TTTGAAAGTG
601 GCGAAAGAGG  CGGTGTTGAA  AGCCGCCGTC  GAACACCCCT  TGAGCGTTCA
651 AAACGAAGAG  CGGCAGGCTG  CCGCTACAT  CACCGCCTTG  GCGGACAATG
701 CCATCGAAAT  CACATTATGG  GCTTGGGCAA  ACGAAGCAGA  CCGCTGGACG
751 CTGCAATGCG  ACTTGAACGA  ACAAGTGGTC  GAAACCTCC  GCAAAGTCAA
801 TATCAACATC  CCGTTCCCGC  AACGCGACAT  ACACATCATC  AATTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1770; ORF 579-1>:

m579-1.pep

```

1  MDFKQDFDLH  LISVSGWEHL  AEKAWAFGLN  LAAALLIFLV  GKWAAKRIVA
51  VMRAAMTRAQ  VDATLISFLC  NVANIGLLIL  VIIAALGRLG  VSTTSVTALI
101 GGAGLAVALS  LKDQLSNFAA  GALIILFRPF  KVGDFIRVGG  FEGYVREIKM
151 VQTSRLRTDN  EEVLPNSVV  MGNSIVNRST  LPLCRAQVIV  GVDYNCDLKV
201 AKEAVLKAAV  EHPLSVQNEE  RQAAAYITAL  GDNAIEITLW  AWANEADRW
251 LQCDLNEQVV  ENLRKVNINI  PFPQORDIHII  NS*

```

m579-1/g579-1 98.6% identity in 282 aa overlap

	10	20	30	40	50	60
m579-1.pep	MDFKQDFDLHLISVSGWEHLAEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ					
g579-1	MDFKQDFDLHLISVSGWGHAEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ					
	10	20	30	40	50	60
m579-1.pep	VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA					
g579-1	VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA					
	70	80	90	100	110	120
m579-1.pep	VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA					
g579-1	VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA					
	70	80	90	100	110	120
m579-1.pep	GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVLPNSVVMGNSIVNRST					
	130	140	150	160	170	180

900

```

|||||
g579-1  GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTTDNEEVLPNSVVMGNSIVNRSS
          130      140      150      160      170      180
          190      200      210      220      230      240
m579-1.pep LPLCRAQVIVGVVDYNDLKVAKAEVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
          |||||
g579-1  LPLCRAQVIVGVVDYNDLKVAKAEVLKAAAEHPLSVQNEERQPAAYITALGDNAIEITLW
          190      200      210      220      230      240
          250      260      270      280
m579-1.pep AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQORDIHIINSX
          |||||
g579-1  AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQORDIHIINSX
          250      260      270      280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1771>:

a579-1.seq

```

1  ATGGACTTCA AACAATTGA TTTTTCAC CTGATAAGTG CTTCCGGCTG
51  GGAGCATCTG GCTGAAAAGG CGTGGGCGTT CGGGCTGAAC CTTGCCGCCG
101 CGCTGCTTAT TTTTTCGTC GGAAATGGG CGGCGAAACG CATGTGCGCC
151 GTGATGAGGG CGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 TTTTTCGTC AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 CCGCATTGGG CAGATTGGGC GTTCCACAA CATCCGTAAC CGCCTTAATC
301 GGCGGCGCGG GTTGGCGGT GCGGTGTGCC TTGAAAGACC AGCTGTCCAA
351 TTTTGCCGCC GCGCGCGTGA TTATCCTGTT CCGCCCGTTC AAAGTCGGCG
401 ATTTTATCCG CGTCGGCGGT TTTGAAGGAT ATGTCCGAGA GATTAAAATG
451 GTGCAGACTT CTTTGGCGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 CAGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTCCACA CTGCCGCTGT
551 GCCGCGCCCA AGTGATAGTC GCGCTCGATT ACAACTGCGA TTTGAAAGTG
601 GCGAAAGAGG CGGTGTTGAA AGCCGCGGTC GAACACCCCT TGAGCGTTCA
651 AAACGAAGAG CGGCAGGCCG CCGCTACAT CACCGCCTTG GCGGACAATG
701 CCATCGAAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
751 CTGCAATGCG ACTTGAACGA ACAAGTGGTC GAAAACCTCC GCAAAGTCAA
801 TATCAACATC CCGTTCCCGC AACGCGACAT ACACATCATC AATTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1772; ORF 579-1.a>:

a579-1.pep

```

1  MDFKQDFDLH LISASGWEHL AEKAWAFGLN LAAALLIFLV GKWAAKRIVA
51  VMRAAMTRAQ VDATLISFLC NVANIGLLIL VIIAALGRLG VSTTSVTALI
101 GGAGLAVALS LKQDLSNFAA GALIILFRPF KVGDFIRVGG FEGYVREIKM
151 VQTSRLRTDN EEVVLPSVSV MGNSIVNRST LPLCRAQVIV GVDYNDLKV
201 AKEAVLKAAV EHPLSVQNEE RQAAAYITAL GDNAIEITLW AWANEADRWT
251 LQCDLNEQVV ENLRKVNINI PFPQORDIHI NS*

```

a579-1/m579-1 99.6% identity in 282 aa overlap

```

          10      20      30      40      50      60
a579-1.pep MDFKQDFDLHLISASGWEHLAEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ
          |||||
m579-1  MDFKQDFDLHLISVSGWEHLAEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ
          10      20      30      40      50      60
          70      80      90      100     110     120
a579-1.pep VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA
          |||||
m579-1  VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA
          70      80      90      100     110     120
          130     140     150     160     170     180
a579-1.pep GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTTDNEEVLPNSVVMGNSIVNRST
          |||||
m579-1  GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTTDNEEVLPNSVVMGNSIVNRST
          130     140     150     160     170     180
          190     200     210     220     230     240
a579-1.pep LPLCRAQVIVGVVDYNDLKVAKAEVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
          |||||
m579-1  LPLCRAQVIVGVVDYNDLKVAKAEVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
          190     200     210     220     230     240
          250     260     270     280
a579-1.pep AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQORDIHIINSX

```

901

|||||
m579-1 AWANEADRWTLCQDLNEQVVENLRKVNINIPFPQIDIHIINSX
 250 260 270 280

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1773>:

g580.seq
1 atggattcgc ccaaggtcgg gtgcgggtgg atggttttgc cgatgtctgc
51 cgcgtcgcag ccatttcga tggcaaggca gacttcgccg atcatgtcgc
101 caccgttcgg accgacaatg ccgccgccga tgatgcggcc ggtttcggca
151 tcgaaaatca gcttggtaaa gccgtgtcgc caaccgttgg caatcgcacg
201 accggaagcc gcccatggga agttggcttt ggtaattttg cggcctgatg
251 ctttggcaga caattcgggt tcaccgaccc atgccacttc gggggaagtg
301 tag

This corresponds to the amino acid sequence <SEQ ID 1774; ORF 580.ng>:

g580.pep..
1 MDSPKVGCGW MVLPMASASQ PISMARQTSP IMSPPFGPTM PPPMMRPVSA
51 SKISLVKPLS QPLAIARPEA AHGKLALVIL RPDALADNSV SPTHATSGEV
101 *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1775>:

m580.seq..
1 ATGGATTTCGC CCAAGGTCGG GTGCGGGTGG ATGGTTTTGC CGATGTCTGC
51 CGCGTCGCAG CCCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATATCGC
101 CACCGTTCGG ACCGACAATG CCGCCGCCGA TGATGCGGCC GGTTTCGGCA
151 TCAAAAATCA GCTTGGTAAA GCCGTGTGCG CAACCGTTGG CAATCGCACG
201 GCCGGAAGCC GCCCACGGGA AGTTGGCTTT GGTGATTTTG CGGCCGGAGG
251 CTTTGGCGGA CAGTTCGGTT TCGCCACCC ACGCCACTTC GGGGGAAGTG
301 TAG

This corresponds to the amino acid sequence <SEQ ID 1776; ORF 580>:

m580.pep..
1 MDSPKVGCGW MVLPMASASQ PISMARQTSP IISPPFGPTM PPPMMRPVSA
51 SKISLVKPLS QPLAIARPEA AHGKLALVIL RPEALADSSV SPTHATSGEV
101 *

m580/g580 97.0% identity in 100 aa overlap

	10	20	30	40	50	60
m580.pep	MDSPKVGCGWMVLPMASASQPISMARQTSP IISPPFGPTM PPPMMRPVSASKISLVKPLS					
g580	MDSPKVGCGWMVLPMASASQPISMARQTSP IMSPPFGPTM PPPMMRPVSASKISLVKPLS					
	10	20	30	40	50	60
	70	80	90	100		
m580.pep	QPLAIARPEAAHGKLALVILRPEALADSSV SPTHATSGEVX					
g580	QPLAIARPEAAHGKLALVILRPDALADNSV SPTHATSGEVX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1777>:

a580.seq
1 ATGGATTTCGC CCAAGGTCGG GTGCGGGTGG ATGGTTTTGC CGATGTCTGC
51 CGCGTCGCAG CCCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATGTCTGC
101 CACCGTTCGG ACCGACAATG CCGCCGCCGA TGATGCGGCC GGTTTCAGCA
151 TCAAAAATCA GCTTGGTGAA ACCATTGTGCG CAACCGTTGG CAATCGCACG
201 GCCGGAAGCA GCCCATGGGA AGTTGGCTTT GGTGATTTTG CGGCCGGAGG
251 CTTTGGCAGA CAATTCGGTT TCGCCACCC ATGCCACTTC AGGAGAAGTG
301 TAA

This corresponds to the amino acid sequence <SEQ ID 1778; ORF 580.a>:

a580.pep
1 MDSPKVGCGW MVLPMASASQ PISMARQTSP IMSPPFGPTM PPPMMRPVSA
51 SKISLVKPLS QPLAIARPEA AHGKLALVIL RPEALADNSV SPTHATSGEV

902

101 *

m580/a580 98.0% identity in 100 aa overlap

	10	20	30	40	50	60
m580.pep	MDSPKVGCGWMVLPMSAASQPISMARQTSPIISPPFGPTMPPPMRPVSASKISLVKPLS					
a580	MDSPKVGCGWMVLPMSAASQPISMARQTSPIISPPFGPTMPPPMRPVSASKISLVKPLS					
	10	20	30	40	50	60

	70	80	90	100
m580.pep	QPLAIARPEAAHGKLALVILRPEALADSSVSPHATSGEVX			
a580	QPLAIARPEAAHGKLALVILRPEALADNSVSPHATSGEVX			
	70	80	90	100

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1779>:

g581.seq..

```

1  atgcacttcg cccagcttgt gggcacaacc ggtatagaac aaaatacgtt
51  ctgtcgtcgt ggttttaccg gcatcgatat gggcggaaat accgatgttg
101 cggtagacggc tgatcggggg cttacgagcc attttattag cctttcaaaa
151 ttagaaacgg aagttagaga atgctttgtt ggcttcagcc atacggtgta
201 cttcttcacg ttttttcaac gcaccgccac ggcttcgga cgcataatc
251 aactcgctcg ccaaacgcag atccatggat ttctcaccac gtttcggggc
301 cgcgtcgcga acccaacgca ttgccaaagc cagacggcgt ga

```

This corresponds to the amino acid sequence <SEQ ID 1780; ORF 581.ng>:

g581.pep..

```

1  MHFAQLVGQT GIEQNTFCRR GFTRIDMGGN TDVAVQADRG LTSHFISLSK
51  LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQLACQTQ IHGFLTTFAG
101 RVANPTHCS QTA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1781>:

m581.seq..

```

1  ATGCACTTCG CCCAGCTTGT GGGTCAAACC GGTATAGAAC AAAATACGTT
51  CTGTCGTCGT GGTTTTACCC GCGTCAATAT GGGCGGAAAT ACCGATGTTA
101 CGGTACAGGC TGATCGGGGT CTTACGAGCC ATTTTATTAG CCTTTCAAAA
151 TTAGAAACGG AAGTGAGAGA ATGCTTGTGTT GGCTTCAGCC ATACGGTGTA
201 CTTCTTCACG TTTTTCACG GCACCGCCAC GGCCTTCGGA CGCATCAATC
251 AATTCGCCTG CCAAACGCAG GTCCATGGAT TTCTCACCAC GTTTGCGGGC
301 CGCATCGCGA ACCCAGCGCA TTGCCAAAGC CAAACGGCGT GA

```

This corresponds to the amino acid sequence <SEQ ID 1782; ORF 581>:

m581.pep..

```

1  MHFAQLVGQT GIEQNTFCRR GFTRVNMGGN TDVTQADRG LTSHFISLSK
51  LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQFACQTQ VHGFLLTFAG
101 RIANPAHCQS QTA*

```

m581 / g581 93.8% identity in 113 aa overlap

	10	20	30	40	50	60
m581.pep	MHFAQLVGQTGIEQNTFCRRGFTRVNMGGNTDVTQADRGRLTSHFISLSKLETEVRECFV					
g581	MHFAQLVGQTGIEQNTFCRRGFTRIDMGGNTDVAVQADRGRLTSHFISLSKLETEVRECFV					
	10	20	30	40	50	60

	70	80	90	100	110
m581.pep	GFSHTVYFFTFFQRTATAFGRINQFACQTQVHGFLLTFAGRIANPAHCQSQTAX				
g581	GFSHTVYFFTFFQRTATAFGRINQLACQTQIHGFLTTFAGRVANPTHCSQTAX				
	70	80	90	100	110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1783>:

903

```

a581.seq
  1 ATGCACTTCG CCCAGCTTGT GGGTCAAACC GGTATAGAAC AAAATACGTT
 51 CTGTCGTCGT GGTTTTACCC GCATCGATAT GGGCGGAAAT ACCGATGTTA
101 CGGTACAGGC TGATCGGGGT CTTACGAGCC ATTTTATTAG CCTTCAAAA
151 TTAGAAACGG AAGTGAGAGA ATGCTTTGTT GGCTTCAGCC ATACGGTGTG
201 CTTCTTCACG TTTTTC AAC GCACCGCCAC GGCCTTCGGA CGCATCAATC
251 AATTGCGCTG CCAAACGCAG GTCCATGGAT TTCTCACCAC GTTTGCGGGC
301 CGCATCGCGA ACCCAGCGCA TTGCCAAAGC CAAACGGCGT GA

```

This corresponds to the amino acid sequence <SEQ ID 1784; ORF 581.a>:

```

a581.pep
  1 MHFAQLVGQT GIEQNTFCRR GFTRIDMGGN TDVTVQADRG LTSHFISLSK
 51 LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQFACQTQ VHGFLLTFAG
101 RINPAHCQS QTA*

```

m581/a581 98.2% identity in 113 aa overlap

	10	20	30	40	50	60
m581.pep	MHFAQLVGQTGIEQNTFCRRGFTRVNMGGNTDVTVQADRGLTSHFISLSKLETEVRECFV					
a581	MHFAQLVGQTGIEQNTFCRRGFTRIDMGGNTDVTVQADRGLTSHFISLSKLETEVRECFV					
	10	20	30	40	50	60
	70	80	90	100	110	
m581.pep	GFSHTVYFFTFFQRTATAFGRINQFACQTQVHGFLTTFAGRIANPAHCQSQTAX					
a581	GFSHTVYFFTFFQRTATAFGRINQFACQTQVHGFLTTFAGRIANPAHCQSQTAX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1785>:

```

g582.seq..
  1 atgcgctata ttcttttgac aggactgttg ccgacggcat ccgcttttgg
 51 agagaccgcg ctgcaatgcg ccgctttgac ggacaatggt acgcgtttgg
101 cgtgttacga caggattttt gcggcacagc ttccgtcttc ggcagggcag
151 gaagggcagg agtcgaaagc cgtactcaat ctgacggaaa ccgtccgcag
201 cagcttggat aagggcgagg cggtcattgt tgttgaaaaa ggcggggatg
251 cgcttcctgc cgacagtgcg ggcgaaaccg ccgatatact tacgcctttg
301 agcctgatgt acgacttggg caaaaacgat ttgcgcgggc tgttgggcgt
351 acgcgaacac aatccgatgt accttatgcc gttttggat aacaattcgc
401 ccaactatgc cccgagttcg ccgacgcgcg gtacgactgt acaggaaaaa
451 ttccggacagc agaaacgtgc ggaaacaaaa ttgcaggttt cgttcaaaag
501 caaaattgcc gaaaatttgt ttaaaacccg ccgagatctg tgggtcggct
551 acacccaaag atccgattgg cagatttaca accaaggcag gaaatccgcg
601 ccgttcgcga atacggatta caaacctgaa attttcctga cccagcctgt
651 gaagggcggat ttgccgttcg gcggcaggct gcgtatgctc ggtgcgggtt
701 ttgtccacca gtccaacgga cagagccgtc ccgaatcgcg ttcgtggaac
751 aggatttatg ccatggcagg catggaatgg ggcaaatgga cggtgattcc
801 gcgcgtgtgg gtgcgtgcgt tcgatcagag cggcgataaa aacgacaatc
851 ccgatattgc cgactatatg gggatggcg acgtgaagct gcagtaccgc
901 ctgaacgaca ggcagaatgt gtattccgta ttgcgctaca accccaaaac
951 gggctacggc gcgattgaag ccgcctacac gtttccgatt aagggcaaac
1001 tcaaaggcgt ggtacgcgga ttccacggtt acggcgagag cctgatcgac
1051 tacaaccaca agcagaacgg tatcggtatc gggttgatgt tcaacgactg
1101 ggacggcatc tga

```

This corresponds to the amino acid sequence <SEQ ID 1786; ORF 582.ng>:

```

g582.pep ..
  1 MRYILLTGLL PTASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGO
 51 EQQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRLLGVREH NPMYLMPPFY NNSPNYAPSS PTRGTTVQEK
151 FGQKRAETK LQVSFKSKIA ENLFKTRADL WFGYTQRSDW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW GKLTVI PRVW VRAFDQSGDK NDNPDADYM GYGVDVQLQYR
301 LNDQRNVYSV LRYNPKTGYG AIEAAYTFPI KGKLGKGVVRG FHGYGESLID
351 YNHKQNGIGI GLMPNDWDGI *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1787>:

```
m582.seq ..
1  ATGCGCTATA TTCTTTTGAC AGGACTGTTG CCGATGGCAT CCGCTTTTGG
51  AGAGACCGCG CTGCAATGCG CCGCTTTGAC GGACAATGTT ACGCGTTTGG
101 CGTGTTACGA CAGGATTTT GCGGCACAGC TTCCGTCTTC GGCAGGGCAG
151 GAAGGGCAGG AGTCGAAAGC CGTACTCAAT CTGACGGAAA CCGTCCGCAG
201 CAGCCTGGAT AAGGGCGAGG CGGTCATTGT TGTTGAAAAA GGCAGGGGATG
251 CGCTTCCTGC CGACAGTGCG GCGGAAACCG CCGACATCTA TACGCCTTTG
301 AGCCTGATGT ACGACTTGGA CAAAAACGAT TTGCGCGGGC TGTGCGGCGT
351 ACGCGAACAC AATCCGATGT ACCTTATGCC GCTCTGGTAC AACAAATTCGC
401 CCAACTATGC CCCGGGTTCG CCGACGCGCG GTACGACTGT ACAGGAAAAA
451 TTCGACAGC AGAAACGTGC GGAACCAAAA TTGCAGGTTT CGTTCAAAAG
501 CAAAATTGCC GAAGATTTGT TTAACACCCG CGCGGATCTG TGGTTCGGCT
551 ACAGCCAAAG ATCCGATTGG CAGATTTACA ACCAAGGCAG GAAATCCGCG
601 CCGTTCGCA ATACGGATTA CAAACCTGAA ATTTTCCTGA CCCAGCCTGT
651 GAAGGCGGAT TTGCGTTCG GCGGCAGGCT GCGTATGCTC GGTGCGGGTT
701 TTGTCCACCA GTCCAACGGA CAGAGCCGTC CCGAATCGCG TTCGTGGAAC
751 AGGATTTTCA CCATGGCAGG CATGGAATGG GGCAATTGA CGGTGATTCC
801 GCGCGTGTGG GTGCGTGCCT TCGATCAGAG CCGCGATAAA AACGACAATC
851 CCGATATTGC CGACTATATG GGGTATGGCG ACGTGAAGCT GCAGTACCGC
901 CTGAACGACA GGCAGAATGT GTATTCCGTA TTGCGCTACA ACCCCAAAAC
951 GGGCTACGGC GCGATTGAAG CCGCCTACAC GTTTCGATT AAGGGCAAAC
1001 TCAAAGGCGT GGTACGCGGA TTCCACGGTT ACGGCGAGAG CCTGATCGAC
1051 TACAACCACA AGCAGAACGG TATCGGTATC GGGTTGATGT TCAACGACTT
1101 GGACGGCATC TGA
```

This corresponds to the amino acid sequence <SEQ ID 1788; ORF 582>:

```
m582.pep
1  MRYILLTGLL PMASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGQ
51  EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRGLLGVREH NPMYLMPLWY NNSPNYAPGS PTRGTTVQEK
151 FGQKRAETK LQVSFASKIA EDLFKTRADL WFGYTQRSDW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW GKLTVIPRVW VRAFDQSGDK NDNPDADYDM GYGDVKLQYR
301 LNDQRNVYSV LRYNPKTGYG AIEAAYTFPI KGKLKGVVRG FHGYGESLID
351 YNHKQNGIGI GLMFNDLDGI *
```

m582 / g582 98.6% identity in 370 aa overlap

```

      10      20      30      40      50      60
m582.pep MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
      |||||
g582      MRYILLTGLLPTASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
      |||||
      10      20      30      40      50      60
m582.pep LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRGLLGVREH
      |||||
g582      LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRGLLGVREH
      |||||
      70      80      90      100     110     120
m582.pep NPMYLMPLWYNNNSPNYAPGSPTRGTTVQEKFGQKRAETKLQVSFASKIAEDLFKTRADL
      |||||
g582      NPMYLMPLWYNNNSPNYAPGSPTRGTTVQEKFGQKRAETKLQVSFASKIAENLFKTRADL
      |||||
      130     140     150     160     170     180
m582.pep WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ
      |||||
g582      WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ
      |||||
      190     200     210     220     230     240
m582.pep QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADYDMGYGDVKLQYR
      |||||
g582      QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADYDMGYGDVKLQYR
      |||||
      250     260     270     280     290     300
m582.pep
      |||||
g582
      |||||
      250     260     270     280     290     300
m582.pep
      |||||
g582
      |||||
      310     320     330     340     350     360
```


905

```

m582.pep  LNDQRNVYSLRYNPKTGYGAIEAAYTFPIKGLKGVVRGFHGYGESLIDYNHKQNGIGI
|||||
g582      LNDQRNVYSLRYNPKTGYGAIEAAYTFPIKGLKGVVRGFHGYGESLIDYNHKQNGIGI
              310      320      330      340      350      360

              370
m582.pep  GLMFNDLDGIX
|||||
g582      GLMFNDWDGIX
              370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1789>:

```

a582.seq
1  ATGCGCTATA TTCTTTTGAC AGGACTGTTG CCGATGGCAT CCGCTTTTGG
51  AGAGACCGCG CTGCAATGCG CCGCTTTGAC GGACAATGTT ACGCGTTTGG
101 CGTGTTACGA CAGGATTTT GCGGCACAGC TTCCGTCTTC GGCAGGGCAG
151 GAAGGGCAGG AGTCGAAAGC CGTACTCAAT CTGACGGAAA CCGTCCGCAG
201 CAGCCTGGAT AAGGGCGAGG CGGTCATTGT TGTGAAAAA GGCGGGGATG
251 CGCTTCCTGC CGACAGTGCG GCGGAAACCG CCGACATCTA TACGCCTTTG
301 AGCCTGATGT ACGACTTGA CAAAAACGAT TTGCGCGGGC TGTGGGCGT
351 ACGCGAACAC AATCCGATGT ACCTTATGCC GCTCTGGTAC AACAATTTCG
401 CCAACTATGC CCCGGGTTTC CCGACGCGCG GTACGACTGT ACAGGAAAAA
451 TTCGGACAGC AGAAACGTGC GGAAACCAA TTGCAGGTTT CGTTCAAAAG
501 CAAAATTGCC GAAGATTTGT TAAAACCCG CGCGGATCTG TGGTTCGGCT
551 ACACCCAAAG ATCCGATTGG CAGATTTACA ACCAAGGCAG GAAATCCGCG
601 CCGTTCGCA ATACGATTA CAAACCTGAA ATTTTCCTGA CCCAGCCTGT
651 GAAGGCGGAT TTGCCGTTTC GCGGCAGGCT GCGTATGCTC GGTGCGGGTT
701 TTGTCCACCA GTCCAACGGA CAGAGCCGTC CCGAATCGCG TTCGTGGAAC
751 AGGATTTACG CCATGGCAGG CATGGAATGG GGCAAATTGA CGGTGATTCC
801 GCGCGTGTGG GTGCGTGCGT TCGATCAGAG CCGCGATAAA AACGACAATC
851 CCGATATTGC CGACTATATG GGGTATGGCG ACGTGAAGCT GCAGTACCGC
901 CTGAACGACA GGCAGAATGT GTATTCCGTA TTGCGCTACA ATCCCAAAC
951 GGGCTACGGC GCGATTGAAG CCGCCTACAC GTTTCGATT AAGGGCAAAC
1001 TCAAAGGCGT GGTACGCGGA TTCCACGGTT ACGGCGAGAG CCTGATCGAC
1051 TACAACCACA AGCAGAACGG TATCGGTATC GGGTTGATGT TCAACGACTT
1101 GGACGGCATC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1790; ORF 582.a>:

```

a582.pep
1  MRYILLTGLL PMASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGO
51  EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRGLLGVBREH NPMYLMPLWY NNSPNYAPGS PTRGTTVQEK
151 FGQQKRAETK LQVSFKSKIA EDLFKTRADL WFGYTQRSDW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW GKLTVIPRVW VRAFDQSGDK NDNPDADYM GYGDVKLQYR
301 LNDQRNVYSV LRYNPKTGYG AIEAAYTFPI KGLKGVVRG FHGYGESLID
351 YNHKQNGIGI GLMFNDLDGI *

```

m582/a582 100.0% identity in 370 aa overlap

```

              10      20      30      40      50      60
m582.pep  MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
|||||
a582      MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
              10      20      30      40      50      60

              70      80      90      100     110     120
m582.pep  LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRGLLGVBREH
|||||
a582      LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRGLLGVBREH
              70      80      90      100     110     120

              130     140     150     160     170     180

```

906

```

m582.pep      NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQKRAETKLQVSFKSKIAEDLFKTRADL
|||||
a582          NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQKRAETKLQVSFKSKIAEDLFKTRADL
              130      140      150      160      170      180

              190      200      210      220      230      240
m582.pep      WFGYTQSRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNG
|||||
a582          WFGYTQSRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNG
              190      200      210      220      230      240

              250      260      270      280      290      300
m582.pep      QSRPESRSWNRIYAMAGMEWGKLTVI PRVWVRAFDQSGDKNDNPDIDYMGYGDVKLQYR
|||||
a582          QSRPESRSWNRIYAMAGMEWGKLTVI PRVWVRAFDQSGDKNDNPDIDYMGYGDVKLQYR
              250      260      270      280      290      300

              310      320      330      340      350      360
m582.pep      LNDQRNVYSVLRYPNPKTG YGAIEAAYTFPIKGKLGKGVVRGFHGYGESLIDYNHKQNGIGI
|||||
a582          LNDQRNVYSVLRYPNPKTG YGAIEAAYTFPIKGKLGKGVVRGFHGYGESLIDYNHKQNGIGI
              310      320      330      340      350      360

              370
m582.pep      GLMFNDLDGIX
|||||
a582          GLMFNDLDGIX
              370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1791>:

g583.seq..

```

1   atgataattg accaaagcca aatatttacc catcttgect tctgtgcett
51  ttgcgggatt ggagccgtaa ctgccggcaa tcgactgcat aatcggatgt
101 ataatgccgc cgccgcgcgc ggtattggaa ggggtaacgg gagccagcag
151 cagttcggaa agagcgagac tgtaaccgat gccacgcgtt tttcttccaa
201 aaacggcgat aaacaaatat ccgatacgca tccccagccc tgttttgagc
251 aaaccgcgcg aatcataaac tgcgatggca atcagccaaa tcaacggatt
301 ggcgaacgca ctcaacgcat cgctcatcgc cgcgcccggg ttgtcggcgg
351 ttacgccggt tactgcgacc aaccgcacgg caataatcga cagcgcgccc
401 aacggcataa ccttgccgat aatggcggca atcacaccga caaacatagc
451 cagcagcgtc caagcctgag gcttgacccc gtcgggtacg ggcagtgcca
501 aaaccagggc gcacaatact gcggcaatgg cgaggggtat cggtttgaaa
551 cccaatttca tcatattgac ctccgtaaaa aagaccgtcc cgaaaaatcg
601 gaaaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1792; ORF 583.ng>:

g583.pep..

```

1   MIIDQSQIFT HLAFAFCGI GAVTAGNRLH NRMYNAAAAR GIGRGNGSQQ
51  QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GERTQRIAGR RARFVGGYAG YCDQPDGNNR QRAQRHNLAD NGGNHTDKHS
151 QQRPSLRLLD VYGQCQNQG AQYCGNGEGY RFETQFHHID LRKKDRPEKS
201 EK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1793>:

m583.seq..

```

1   ATGATAGTTG ACCAAAGCCA AATATTTACC CATCTTGCCT TCTGTGCCTT
51  TTGCGGGATT GGAGCCGTAA CTGCCGGCAA TCGACTGCAT AATCGGATGT
101 ATAATGCCGC CGCCGCgcgc GGTATTGGAA GGGGTAACGG GAGCCAGCAG
151 CAGTTCGGAA AGAGCGAGAC TGTAACCGAT GCCCAGCGTT TTTCTTCCAA
201 AAACGGCGAT AAACAAATAT CCGATACGCA TCCCCAGCCC TGTTTTGAGC
251 AAACCGCGCG AAATCATAAC TGCGATGGCA ATCAGCCAAA TCAACGGATT
301 GGCGAACGCA CTCAACGCAT CGCTCATCGC CGCGCCCGGT TTGTGCGCGG
351 TTACGCCGGT TACTGCGACC AACCgcacgg CAATAATCGA CAGCGCGCCC
401 AACGGCATGG CCTTGCCGAT AATGGCGGCA ATCACACCGA CAAACATGGC
451 CAGCAGCGTC CAAGCCTGAG GCTTGACCCC GTCGGGTACG GGCAGTGCCA
501 AAACcagggc GCACAATACT GCGGCAATGG CGAGGGGTAT CGGTTTGAAA

```

907

551 CCCAATTTCA TCATATTGAC CTCCGTAAAA AAGACCGTCC CGAAAAATCG
601 GAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1794; ORF 583>:

m583.pep..

1 MIVDQSQIFT HLAFC AFCGI GAVTAGNRLH NRMYNAAAAR GIGRNGSQQ
51 QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GERTQRIahr RARFVGGYAG YCDQPDGNNR QRAQRHGLAD NGGNHTDKHG
151 QQRPSLRLDP VGYGQCQNQG AQYCGNGEGY RFETQFHHID LRKKDRPEKS
201 EK*

m583 / g583 98.5% identity in 202 aa overlap

m583.pep	10	20	30	40	50	60
	MIVDQSQIFT HLAFC AFCGI GAVTAGNRLH NRMYNAAAAR GIGRNGSQQ QFGKSETVTD					
g583	MIIDQSQIFT HLAFC AFCGI GAVTAGNRLH NRMYNAAAAR GIGRNGSQQ QFGKSETVTD					
	10	20	30	40	50	60
m583.pep	70	80	90	100	110	120
	AQRFSKNGDKQISDTHPQPCFEQTARNHNC DGNQPNQRIGERTQRIahr RARFVGGYAG					
g583	AQRFSKNGDKQISDTHPQPCFEQTARNHNC DGNQPNQRIGERTQRIahr RARFVGGYAG					
	70	80	90	100	110	120
m583.pep	130	140	150	160	170	180
	YCDQPDGNNRQRAQRHGLADNGGNHTDKHGQQRPSLRLDPVGYGQCQNQGAQYCGNGEGY					
g583	YCDQPDGNNRQRAQRHNLADNGGNHTDKHSQQRPSLRLDPVGYGQCQNQGAQYCGNGEGY					
	130	140	150	160	170	180
m583.pep	190	200				
	RFETQFHHIDLRKKDRPEKSEKX					
g583	RFETQFHHIDLRKKDRPEKSEKX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1795>:

a583.seq

1 ATGATAGTTG ACCAAAGCCA AATATTTACC CATCTTGCCT TCTGTGCCTT
51 TTGCGGGATT GGAGCCGTAA CTGCCGGCAA TCGACTGCAT AATCGGATGT
101 ATAATGCCGC CGCCGCGCGC GGTATTGGAA GGGGTAACGG GAGCCAGCAG
151 CAGTTCGGAA AGAGCGAGAC TGTAAACGAT GCCCAGCGTT TTTCTTCCAA
201 AAACGGCGAT AAACAAATAT CCGATACGCA TCCCCAGCCC TGTTTTGAGC
251 AAACCGCGCG AAATCATAAC TCGCATGGCA ATCAGCCAAA TCAACGGATT
301 GGCGAACGCA CTCAACGCAT CGCTCATCGC CGCACCCGGT TTGTCCGGCG
351 TTACGCGGGT TACTGCGACC AACCCGACGG CAATAATCGA CAGCGCACCC
401 AACGCGATGG CTTGCGCGAT AATGGCGGCA ATCACACCGA TAAACATGGC
451 CAGCAGCGTC CAAGCCTGAG GCTTGACCCC GTCGGGTACG GGCAGTGCCA
501 AAACCAAGGC GCACAATACT GCGGCAATGG CGAGGGGTAT CGGTTTGAAA
551 CCCAATTTCA TCATATTGAC CTCCGTAAAA AAGACCGTCC CGAAAAATCG
601 GAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1796; ORF 583.a>:

a583.pep

1 MIVDQSQIFT HLAFC AFCGI GAVTAGNRLH NRMYNAAAAR GIGRNGSQQ
51 QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GERTQRIahr RTRFVGGYAG YCDQPDGNNR QRTQRHGLAD NGGNHTDKHG
151 QQRPSLRLDP VGYGQCQNQG AQYCGNGEGY RFETQFHHID LRKKDRPEKS
201 EK*

m583/a583 99.0% identity in 202 aa overlap

m583.pep	10	20	30	40	50	60
	MIVDQSQIFT HLAFC AFCGI GAVTAGNRLH NRMYNAAAAR GIGRNGSQQ QFGKSETVTD					

908

```

a583      MIVDQSQIFTHLAFCAFCGIGAVTAGNRLHNRMYNAAAARGIGRNGSQQFGKSETVTD
              10      20      30      40      50      60

              70      80      90      100     110     120
m583.pep  AQRFSKNGDKQISDTHPQPCFEQTARNHNCDGNQPNQRIGERTQRIAHRRARFVGGYAG
          |||
a583      AQRFSKNGDKQISDTHPQPCFEQTARNHNCDGNQPNQRIGERTQRIAHRRTRFVGGYAG
              70      80      90      100     110     120

              130     140     150     160     170     180
m583.pep  YCDQPDGNNRQRAQRHGLADNGGNHTDKHGQQRPSLRLDPVGYGQCQNQGAQYCGNGEGY
          |||
a583      YCDQPDGNNRQRTQRHGLADNGGNHTDKHGQQRPSLRLDPVGYGQCQNQGAQYCGNGEGY
              130     140     150     160     170     180

              190     200
m583.pep  RFETQFHHIDLRRKKDRPEKSEKX
          |||
a583      RFETQFHHIDLRRKKDRPEKSEKX
              190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1797>:

g584.seq..

```

1  atgtgcggtt ctattttggc ggcttccctg ctggcggtat cttttccggc
51  ggcggctgag gcattgaatt acaatattgt cgaattttcc gaatcggcgg
101 gtatcgaggt ggctcaggat acaatgtccg cgcgtttcca ggtggcggcg
151 gaaggacggg acaaaaatgc cgtcaatgcc gagtttggtt aaaaattcaa
201 caatttcacc agaaaatcga aaaatggtag ctttaaaacc gaattgggtat
251 cgcgcgagtgc gatgccgcgc tatcaatata ccaacggcag acgcattcaa
301 acaggctggg aggagcgtgc ggaatttaag gcggagggca gggattttga
351 tgctttaaac cgttttattg ctgatgttca gacggatgct tcgcttgaag
401 ataccgattt cagcgtgtcg cgcgaacgcc gaaacgaggt catcgatcag
451 gtcagcaagg atgccgtttt gcgtttcaag gcgcgtgccg aaaaactggc
501 gggcgttctg ggtgcgtccg gttataaaat cgtcaaattg aattttgggc
551 aaatcggcag ccatattgcg ggcgatgggg ctgttcgggc aaaaatgctg
601 cgcgcgatgc cgatggcggc aagcgtcaat atgaagggtg cggattcagc
651 cgcaccgggt gtggaggaaa tcagcatcag catcaatggg acggttcagt
701 tctaa

```

This corresponds to the amino acid sequence <SEQ ID 1798; ORF 584.ng>:

g584.pep Length:..

```

1  MLRSILAASL LAVSFPAAAE ALNYNIVEFS ESAGIEVAQD TMSARFQVAA
51  EGRDKNAVNA EFVKKFNNFT RSKNGSFKT ELVSRSAMPR YQYTNRRRIQ
101 TGWEERAEFK AEGRDFDALN RFIADVQTD SLEDTDFSVS RERRNEVIDQ
151 VSKDAVLRFK ARAEKLAGVL GASGYKIVKL NFGQIGSHIA GDGAVRAKML
201 RAMPMAASVN MKGTDSAAPG VEEISISING TVQF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1799>:

m584.seq..

```

1  ATGTTGCGTC TTGTTTGGC GGCTTCGCTG TCGGCGGTAT CTTTCCGGC
51  AGCGGCTGAA GCATTGAATT ACAATATTGT CGAATTTTCC GAATCGGCGG
101 GTGTCGAGGT GGCTCAGGAT ACAATGTCCG CACGTTTCCA AGTGACGGCG
151 GAAGGACGGG ACAAAAATGC CGTCAATGCT GAGTTTGTTA AAAAAATCAA
201 CAAGTTCATC AGAAAAATCGA AAAATGGTAG CTTTAAACC GAATTGGTAT
251 CGCGCAGTGC GATGCCGCGC TATCAATATA CCAACGGCAG ACGCATTCAA
301 ACAGGCTGGG AGGAGCGTGC GGAATTAAAG GTCGAAGGTA GAGATTTTGA
351 TGAGTTAAAC CGTTTTATTG CCGATATTCA AGCAGATGCC GCGTTGGmAT
401 ATACGGATTT CCATGTGTCT CGCGAACGCC GCAACGAGGT CATCKATCAG
451 GTCAGCAAGG ATGCCGTTTT GCGTTTCAAG GCGCGTGCCG AAAAGTTGGC
501 GGGCGTTTTG GGTGCGTCCG GTTATAAAAT CGTCAAATTG AATTGGGAC
551 ACATCGGCAG CCATATCGCG GGAGGGGGAG CTGCTCAGGC AAAAAAGCTT
601 CGTGCCATGC CGATGGCGGC AAGCGTCAAT ATGGAGGGTG CCGATTCCGC
651 CGCGCCTGGT GTGGAGGAAA TCAGCATCAG CGTCAATGGG ACGGTTTCAGT
701 TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1800; ORF 584>:

m584.pep..

```

1  MLRLVLAASL SAVSFPAAAE ALNYNIVEFS ESAGVEVAQD TMSARFQVTA
51  EGRDKNVNA EFVKKFNKFI RSKNGSFKT ELVSRSAMPR YQYTNRRRIQ
101 TGWEERAEFK VEGRDFDELN RFIADIQADA ALXYTDFHVS RERRNEVIXQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
201 RAMPMAASVN MEGADSAAPG VEEISISVNG TVQF*

```

m584 / g584 89.7% identity in 234 aa overlap

```

              10      20      30      40      50      60
m584.pep    MLRLVLAASLSAVSFPAAAEALNYNIVEFSSESAGVEVAQDTMSARFQVTAEGRDKNVNA
              ||| :||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g584         MLRSILAASLLAVSFPAAAEALNYNIVEFSSESAGIEVAQDTMSARFQVAAEGRDKNVNA
              10      20      30      40      50      60

              70      80      90     100     110     120
m584.pep    EFVKKFNKFIKRSKNGSFKTELVSRSAMPRYQYTNRRRIQTGWEEAEFKVEGRDFDELN
              ||||| :| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g584         EFVKKFNNTFRKSKNGSFKTELVSRSAMPRYQYTNRRRIQTGWEEAEFKAEGRDFDALN
              70      80      90     100     110     120

              130     140     150     160     170     180
m584.pep    RFIADIQADAALXYTDFHVSERRRNEVIXQVSKDAVLRFKARAELAGVLGASGYKIVKL
              ||||| :||| :| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g584         RFIADVQTDASLEDTFVSRRRNEVIDQVSKDAVLRFKARAELAGVLGASGYKIVKL
              130     140     150     160     170     180

              190     200     210     220     230
m584.pep    NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVEEISISVNGTVQFX
              |:| :||||| ||| :| ||||| ||||| ||||| ||||| ||||| |||||
g584         NFGQIGSHIAGDGAVRAKMLRAMPMAASVNMKGTDSAAPGVEEISISINGTVQFX
              190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1801>:

a584.seq

```

1  ATGTTGCGTT CTATTTTGGC GGCTTCCTCG CTG.....
51  .....ATTGT CGAATTTTCT GAATCGGCGG
101 GTGTCGAGGC GGTTCAGGAT ACAATGTCCG CACGTTTCCA AGTGACGGCG
151 GAAGGACGGG ACAAAATGCG CGTCAATGCC GAGTTTGTTA AAAAATTCAA
201 CAATTTTACC AGAAAATCAA AAAATGGTAG CTTTAAACC GAATTGGTAT
251 CGCGCAGTGC GATGCCGCGC TATCAATATA CCAACGGCAG ACGCATTCAA
301 ACAGGTTGGG AGGAGCGTGC GGAATTTAAG GTCGAGGGTA GGAATTTTGA
351 TCGGTTGAAC CGTTTATTG CCGATGTTCA GGCAGATGCC GCGTTGGAAT
401 ATACGGATTT CCATGTGTCG CGCGAACGCC GCAACGAGGT CATCGATCAG
451 GTCAGCAAGG ATGCCGTTT GCGTTTCAAG GCGCGTGCCG AAAAGTTGGC
501 GGGCGTTTTG GGTGCGTCCG GTTATAAAAT CGTCAAATTG AATTTGGGAC
551 ACATCGGCAG CCATATCGCG GGAGGGGGAG CTGCTCAGGC AAAAATGCTT
601 CGTGCCATGC CGATGGCGGC AAGCGTCAAT ATGGAGGGTG CGGATTCCGC
651 CGGCCTGGT GTGGAGGAAA TCAGCATCAG CGTCAATGGG ACGGTTTCAGT
701 TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1802; ORF 584.a>:

a584.pep

```

1  MLRSILAASL L..... IVEFS ESAGVEAVQD TMSARFQVTA
51  EGRDKNVNA EFVKKFNFT RSKNGSFKT ELVSRSAMPR YQYTNRRRIQ
101 TGWEERAEFK VEGRNFDALN RFIADVQADA ALEYTDFHVS RERRNEVIDQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
201 RAMPMAASVN MEGADSAAPG VEEISISVNG TVQF*

```

m584/a584 88.9% identity in 234 aa overlap

```

              10      20      30      40      50      60
m584.pep    MLRLVLAASLSAVSFPAAAEALNYNIVEFSSESAGVEVAQDTMSARFQVTAEGRDKNVNA
              ||| :||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a584         MLRSILAASLL-----IVEFSSESAGVEAVQDTMSARFQVTAEGRDKNVNA
              10      20      30      40

```

910

	70	80	90	100	110	120
m584.pep	EFVKKFNKFIRKSKNGSFKTELVSRSAMPYQYTNRRRIQTGWEERAEFKVEGRDFDELN					
a584	EFVKKFNNFTRKSKNGSFKTELVSRSAMPYQYTNRRRIQTGWEERAEFKVEGRNFDALN					
	50	60	70	80	90	100
	130	140	150	160	170	180
m584.pep	RFIADIQADAALXYTDFHVSRRRNEVIXQVSKDAVLRFKARAELAGVLGASGYKIVKL					
a584	RFIADVQADAALXYTDFHVSRRRNEVIDQVSKDAVLRFKARAELAGVLGASGYKIVKL					
	110	120	130	140	150	160
	190	200	210	220	230	
m584.pep	NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVVEEISISVNGTVQFX					
a584	NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVVEEISISVNGTVQFX					
	170	180	190	200	210	220

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1803>:

g585.seq..

```

1  atgaaactgt  tccaacgcat  tttcgccaca  ttttgcgagg  ttatcgctctg
51  cgcaatcttt  gtggcgagtt  tttctttttg  gctggtgcag  aacacccttg
101  ccgaaaacca  attcaaccaa  cgccgcacca  tcgaaaccac  attgatgggc
151  agcattattt  ccgcattcaa  gacacggggc  gacaacggcg  cgcgcgaaat
201  cctgaccgaa  tggaaaaaca  gccccgtctc  atccgcggtt  tacgtcatac
251  agggcgacga  gaaaaaagac  atcttaaac  gctatatcga  caattacacc
301  atagaacgag  cccggctgtt  tgccgccaac  aacccccatt  ccaaccttgt
351  ccgcacgaa  tacgaccgtt  tcggcggaaga  atacctgttc  ttcattaaag
401  gctgggacaa  ccaccaggca  caacgcctgc  ccagcccgct  gtttatcccg
451  ggccctgcgc  ttgccccgat  ttggcacgaa  ttcacatcat  tctccttcac
501  catcattgtc  ggactgctga  tggcatatat  ccttgccggc  aacattgcca
551  aacccatcag  aatcttaggc  aacggcatgg  acaggggtgc  agaacgagaa
601  cttgaagacc  gcgtttgcca  acaggttcgc  gaccgcgacg  acgaattggc
651  cgatgttgcc  atgcaattcg  acacaatggt  ggaaaaactg  gaataa

```

This corresponds to the amino acid sequence <SEQ ID 1804; ORF 585.ng>:

g585.pep..

```

1  MKLFQIRIFAT  FCAVIVCAIF  VASFSFWLVQ  NTLAENQFNQ  RRTIETTLMG
51  SIISAFKTRG  DNGAREILTE  WKNSPVSSAV  YVIQGDDEKD  ILNRYIDNYT
101  IERARLFAAN  NPHSNLVRIE  YDRFGEEYLF  FIKGWDNHQA  QRLPSPLFIP
151  GLPLAPIWHE  FIILSFIIIV  GLLMAYILAG  NIAKPIRILG  NGMDRVAERE
201  LEDRVCCQVR  DRDDELADVA  MQFDTMVEKL  E*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1805>:

m585.seq..

```

1  ATGAAACTGT  TCCAACGCAT  TTTCGCCACA  TTTTGCGCGG  TTATCGTCTG
51  TGCAATCTTT  GTGGCGAGTT  TTTCTTTCTG  GCTGGTGCGA  AACACCCTTG
101  CCGAAAACCA  GTTCAACCAA  CGCCGCACCA  TCGAAACCAC  TTTGATGGGC
151  AGCATCATTT  CCGCATTCG  GGCACGCGGG  GACGCGGGTG  CGCGCGAAAT
201  CCTGACGGAA  TGGAAAAGCA  GCCCCGTCTC  ATCGGGCGTG  TACGTTATAC
251  AGGGCGACGA  GAAAAAGAT  ATCCTGAACC  GGTATATCGA  CAGCTATACC
301  ATCGAACGCG  CCCGGCTTTT  CGCCGCCGGA  CACCCGCATT  CCAACCTCGT
351  CCATATCGAA  TACGACCGCT  TCGGCGAAGA  ATACCTGTTC  TTCACCAAAG
401  AGCGGACAA  ACTCCAAGCC  CGCCGCCTGC  CCAGCCCCCT  GTTGATCCCC
451  GGCCTGCCGC  TCGCCCCGAT  TTGGCACGAA  CTCATCATAT  TGTCTTCAT
501  CATCATCGTC  GGACTGCTGA  TGGCATATAT  CCTCGCCGGC  AACATTGCCA
551  AACCCATCAG  AATCTTAGGC  AACGGCATGG  ACAGGGTGGC  AAACGGAGAA
601  CTTGAAACCC  GTATCTCCCA  ACAGGTCGAC  GACCGCGACG  ACGAATTGTC
651  CCATCTTGCC  ATCCAATTCT  ACAAAATGGT  GGAAAAACTC  GAAAAACTCG
701  TTGCCAAGA  ACGCCACCTG  CTCCATCACG  TCTCCCATGA  AATGCGTTCT
751  CCCCTTGCGC  GCATGCAGGC  AATTGTCGGA  CTGATTCAGG  CGCAGCCCCA
801  AAAACAGGAG  CAATATCTCA  AACGGCTGGA  AGGCGAACTG  ACCCGCATGG
851  ATACGCTGGC  CGGGGAACCT  TTAACCCCTG  CCCGTCTCGA  AACTTCCAAT
901  ATGGCTTTGG  AAAAAGAAAG  CCTGAAACTC  CTGCCCTTCC  TGGGCAACCT
951  GGTAGAAGAC  AATCAAAGCA  TTGCCCAGAA  AAACGGACAA  ACGGTTACCC
1001  TGTCTGCCGA  CGGAAAAATC  CCCGAAACA  CAACCATCCT  TGCCAACGAA

```

m585.pap..

1	MKLQRIQIFAT	FCAVIVCAIF	VASFQFWLVQ	NTLAENQFNQ	RRTIETTLMG
51	SIISAFRARG	DAGAREILTE	WKDQPVSSGV	YVIQDEKQD	ILNRYIDSYT
101	IERARLFAAG	HPHSNLVHIE	YDRFGEEYLF	FTKDWDKLG	RRLPSPLLLP
151	GLPLAPIWHE	LILLSFIIIV	GLLMAYILAG	NIAPKIRILQ	NGMDRVANGE
201	LETRISQVQD	DRDDELSHLA	QIFDKMVEKL	EKLVAKERHL	LHMVSHMERS
251	PLARMQAIQG	LIQAQPQKQE	QYLRLEGELE	TRMDTLAGEL	LTLRSRLTSN
301	MALEKESLKL	LPFLGNLVED	NQSIAQKNQG	TVTLSADGKI	PENTTILANE
351	SYLYRAFQNV	IRNAVNYSPG	GSTILLNIGQ	DHKHWIIDVT	DNGPGVDQM
401	LPHIFTAFYR	ADSSANKPGE	GLGLALTQHI	IEQHCGKIIA	ENIKPNGLRM
451	RFLPDKKTKG	SKTEKSAN*			

	10	20	30	40	50	60
m585.pep	MKLFQRI	FATFCAVIVCAI	FVASFSFWLVQNT	LAENQFNQRR	TIETTLMGSI	ISAFRARG
g585	MKLFQRI	FATFCAVIVCAI	FVASFSFWLVQNT	LAENQFNQRR	TIETTLMGSI	ISAFKTRG
	10	20	30	40	50	60
m585.pep	70	80	90	100	110	120
	DAGAREILT	EWKDS	PSVSSGVYVI	QGDEKKDIL	NRYIDSYTIER	ARLFAAGHPH
g585	DNGAREILT	EWKNS	PSVSSAVYVI	QGDEKKDIL	NRYIDNYTIER	ARLFAANNPH
	70	80	90	100	110	120
m585.pep	130	140	150	160	170	180
	YDRFGEEYL	FFTKDWDKLQ	ARRLPSP	LLIPGLPLAPI	WHELIILSFI	IIVGLLMAYI
g585	YDRFGEEYL	FFIKGWDNHQA	QRLPSP	LFIPGLPLAPI	WHEFIILSFI	IIVGLLMAYI
	130	140	150	160	170	180
m585.pep	190	200	210	220	230	240
	NIAKP	IRILGN	GMDRV	ANGELE	TRISQQV	DRDDEL
g585	NIAKP	IRILGN	GMDRVA	ERELED	RVCCQV	DRDDEL
	190	200	210	220	230	
m585.pep	250	260	270	280	290	300
	LHHVS	HEMRSP	LARMQA	IVGLIQ	APQKQEQY	LKRLB
g585	LHHVS	HEMRSP	LARMQA	IVGLIQ	APQKQEQY	LKRLB

a585.seq

1	ATGAAACTGT	TCCAACGCAT	CTTCGCCACA	TTTTGCGCGG	TTATCGTCTG
51	TGCAATCTTT	GTGGCGAGTT	TTTCTTTCTG	GCTGGTGCAG	AACACCCTTG
101	CCGAAAAACA	GTTCACCCA	GCCGCGACCA	TCGAAACCA	TTTGATGGGG
151	AGCATCATT	CCGCATTCCG	GGCAGCGGG	GACCGGGTG	CGCGGAAAT
201	CCTGACGGAA	TGGAAAGACA	GCCCCGTCTC	ATCGGGCGTG	TACGTTATAC
251	AGGGCGACGA	GAAAAAAGAT	ATCCTGCACC	GGTATATCGA	CAGCTACACC
301	ATCGAACGCG	CCCGGCTTTT	CGCCGCCGGA	CACCCGCATT	CCAACCTCGT
351	CCATATCGAA	TACGACGGT	TCGGCGAAGA	ATACCTGTTT	TTACCAAAA
401	ACTGGGACAA	ACTCCAAGC	CGCCGCTGCG	CCAGCCCCCT	TTGATCAACC
451	GGCCTGCCGC	TCGCCCGGAT	TTGGCACGAA	CTCATCATAT	TGTCCTTCAT
501	CATCATCGTC	GGACTGTGTA	TGGCGTACAT	CCTCGCGGG	AACATTGCCA
551	AACCCATCAG	AATCTTAGCG	AACGGCATGG	ACAGGGTGGC	AAACGGGAAA
601	CTTGAAACCC	GTATCTCCCA	ACAGGTCGAC	GACCCGACG	ACGAATTGTT

```

651 CCATCTTGCC ATCCAATTCC ACAAATGGT GGAAAACTC GAAAACTCG
701 TTGCCAAGA ACGCCACCTG CTCATCACG TCTCCCATGA AATGCGTTCT
751 CCCCTTGCGC GCATGCAGGC AATTGTCGGA CTGATTCAGG CGCAGCCCCA
801 AAAACAGGAG CAATATCTCA AACGGCTGGA AGGCGAACTG ACCCGCATGG
851 ATACGCTGGC CGGGGAAGT TTAACCCTGT CCCGTCTCGA AACTTCCAAT
901 ATGGCTTTGG AAAAAGAAAG CCTGAACTC CTGCCCTTCC TGGGCAACCT
951 GGTAGAAGAC AATCAAAGCA TTGCCAGAA AAACGGACAA ACGGTTACCC
1001 TGTCTGCCGA CGGAAAAATC CCCGAAAACA CAACCATCCT TGCCAACGAA
1051 AGCTACCTGT ACCGCGCCTT CGACAACGTC ATCCGCAACG CCGTCAACTA
1101 CAGTCCCGAA GGCAGCACCA TCCTGATCAA CATCGGACAA GACCACAAAC
1151 ACTGGATAAT CGACGTTACC GACAACGGCC CCGGCGTGGA CGAAATGCAG
1201 CTCCCGCACA TCTTCACCGC TTTCTACCGT GCAGACTCCA GTGCCAACAA
1251 ACCCGGAACA GGAAGGGGCG TTGCATTGAC CCAACATATT ATTGAACAGC
1301 ACTGCGGCAA AATCATCGCC GAAAACATCA AACCGAACGG TCTGCGGATG
1351 CGCTTTATCC TGCCAAGAA AAAAACCGGT TCCAAAACAG AAAAAAGTGC
1401 GAACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1808; ORF 585.a>:

```

a585.pep
1  MKLFQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG
51  SIISAFRARG DAGAREILTE WKDSPVSSGV YVIQGDEK KD ILHRYIDSYT
101 IERARLFAAG HPHSNLVHIE YDRFGEEYLF FTKDWDKLQA RRLPSPLLI P
151 GLPLAPIWHE LIILSFIIIV GLLMAYILAG NIAKPIRILG NGMDRVANGE
201 LETRISQQVD DRDEL SHLA IQFDKMVEKL EKLVA KERHL LHHVSHEMRS
251 PLARMQAIVG LIQAQPQKQE QYLRLEGE L TRMDTLAGE L LTLSRLETSN
301 MALEKESLKL LPFLGNLVED NQSI AQKNGQ TVTLSADGKI PENTTILANE
351 SYLYRAFDNV IRNAVNY SPE GSTILINIGQ DHKHWIIDVT DNGPGVD EQ
401 LPHIFTAFYR ADSSANKPGT GLGLALTQHI IEQHC GKIIA ENIKPNGLRM
451 RFILPKKKTG SKTEKSAN*

```

m585/a585 99.8% identity in 468 aa overlap

	10	20	30	40	50	60
m585.pep	MKLFQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG SIISAFRARG					
a585	MKLFQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG SIISAFRARG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m585.pep	DAGAREILTEWKDSPVSSGVYVIQGDEK KDILNRYIDSYTIERARLFAAGHPHSNLVHIE					
a585	DAGAREILTEWKDSPVSSGVYVIQGDEK KDILHRYIDSYTIERARLFAAGHPHSNLVHIE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m585.pep	YDRFGEEYLF FTKDWDKLQARRLPSPLLI PGLPLAPIWHE LIILSFIIIVGLLMAYILAG					
a585	YDRFGEEYLF FTKDWDKLQARRLPSPLLI PGLPLAPIWHE LIILSFIIIVGLLMAYILAG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m585.pep	NIAKPIRILGNMGMDRVANGELETRISQQVDDRDEL SHLA IQFDKMVEKLEKLVAKERHL					
a585	NIAKPIRILGNMGMDRVANGELETRISQQVDDRDEL SHLA IQFDKMVEKLEKLVAKERHL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m585.pep	LHHVSHEMRSPLARMQAIVGLIQAQPQKQE QYLRLEGE LTRMDTLAGE L LTLSRLETSN					
a585	LHHVSHEMRSPLARMQAIVGLIQAQPQKQE QYLRLEGE LTRMDTLAGE L LTLSRLETSN					
	250	260	270	280	290	300
	310	320	330	340	350	360
m585.pep	MALEKESLKL LPFLGNLVEDNQSI AQKNGQ TVTLSADGKI PENTTILANESYLYRAFDNV					
a585	MALEKESLKL LPFLGNLVEDNQSI AQKNGQ TVTLSADGKI PENTTILANESYLYRAFDNV					

	310	320	330	340	350	360
m585.pep	370	380	390	400	410	420
	IRNAVNYSPEGSTILINIGQDHKHWIIDVTDNGPGVDEMQLPHIFTAFYRADSSANKPGT					
a585	IRNAVNYSPEGSTILINIGQDHKHWIIDVTDNGPGVDEMQLPHIFTAFYRADSSANKPGT					
	370	380	390	400	410	420
m585.pep	430	440	450	460	469	
	GLGLALTQHIIIEQHCGKIIAENIKPNGLRMRFILPKKKTGSKTEKSANX					
a585	GLGLALTQHIIIEQHCGKIIAENIKPNGLRMRFILPKKKTGSKTEKSANX					
	430	440	450	460		

g586.seq..

This corresponds to the amino acid sequence <SEQ ID 1810; ORF 586.ng>:

g586 . pep . .

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1811>:

m586.seq

This corresponds to the amino acid sequence <SEQ ID 1812; ORF 586>:

m586.pcp

m586 / g586 97.1% identity in 209 aa overlap

m586.pep
MAAHLEEQQELDNFKYFWKTTGKWLFALLILAAALGYLGTYVYNRKVSQNQEEAAVLANI

914

```

g586      MAAHLEEQQELDNFKYFWKTTGKWLFAALLILAAALGYLGTYVYQNRAASQNQEAAAVLANI
           10      20      30      40      50      60

m586.pep  70      80      90      100     110     120
VEKAQSKAPQSEINAELTKLQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWLNSN
g586      VEKAQNKAPQSEINAELSKLQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWLNSN
           70      80      90      100     110     120

m586.pep  130     140     150     160     170     180
QKDSLIALAQAQRLGVVLLQKKYDAALAALDTPVEADFAPLLMETKGDVYAAQGSQEA
g586      QKDSLIALAQAQRLGVVLLQKKYDAALAALDTPVEADFAPLLMETKGDVYAAQKSQEA
           130     140     150     160     170     180

m586.pep  190     200     210
LKNYGQALEKMPQDSVGRELQMKLDSLKX
g586      LKNYGQALEKMPQDSVGRELLQMKLDSLKX
           190     200     210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1813>:

```

a586.seq
1   ATGGCAGCCC ATTTGGAAGA ACAACAAGAG TTGGACAAC TTAATATTTT
51  TTGGAAGAAC ACGGGCAAAT GGCTGTTTGC CGTGCTGATT TTGGCGGCAC
101 TCGGCTACTT GGGATACACG GTTTACCAAA ACCGTGCGGC TTCCCAAAAT
151 CAGGAAGCGG CGGCGGTGCT GGCAAACATC GTGGAAAAGG CGCAAAACAA
201 AGCCCCGCAA AGCGAAATCA ATGCCGAATT GGCCAAGCTC CAACAAGCT
251 ACCCCCATTC CATTTCCGCC GCCCAAGCCA CGCTGATGGC GGCAGCAACC
301 GAATTTGACG CGCAGCGTTA CGATGTTGCC GAAGGCCATT TGAAATGGGT
351 ATTGTCACAC CAAAAAGACA GCCTGATCCA GCGTGTGGCG GCGCAGCGTC
401 TGGGCGTTGT GTTGTGTCAG CAAAAAAAT ACGATGCCGC GCTTGCCGCA
451 CTCGACACGC CGGTTGAAGC GGACTTCGCC CCCCTGCTGA TGGAAACCAA
501 AGGCGATGTC TATGCCGCAC AGGGAAAAAG CCAGGAAGCC TTAATAAACT
551 ACGGACAGGC TTTAGAAAAA ATGCCTCAAG ATTCTGTCGG TCGCGAATTG
601 GTTCAAATGA AACTTGATTC GCTGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1814; ORF 586.a>:

```

a586.pep
1   MAAHLEEQQE LDNFKYFWKT TGKWLFAVLI LAALGYLGTY VYQNRAASON
51  QEAAAVLANI VEKAQNKAPQ SEINAELAKL QSYPHSISA AQATLMAAAT
101 EFDAQRYDVA EGHKLKWLNSN QKDSLIALQA AQLGVVLLQ QKKYDAALAA
151 LDTPVEADFA PLLMETKGDV YAAQGSQEA LKNYGQALEK MPQDSVGREL
201 VQMKLDSLK*

m586/a586 97.6% identity in 209 aa overlap

           10      20      30      40      50      60
m586.pep  MAAHLEEQQELDNFKYFWKTTGKWLFAALLILAAALGYLGTYVYQNRAASQNQEAAAVLANI
           10      20      30      40      50      60
a586      MAAHLEEQQELDNFKYFWKTTGKWLFAVLI LAALGYLGTYVYQNRAASQNQEAAAVLANI
           10      20      30      40      50      60

           70      80      90      100     110     120
m586.pep  VEKAQSKAPQSEINAELTKLQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWLNSN
           70      80      90      100     110     120
a586      VEKAQNKAPQSEINAELAKLQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWLNSN
           70      80      90      100     110     120

           130     140     150     160     170     180
m586.pep  QKDSLIALAQAQRLGVVLLQKKYDAALAALDTPVEADFAPLLMETKGDVYAAQGSQEA
           130     140     150     160     170     180
a586      QKDSLIALAQAQRLGVVLLQKKYDAALAALDTPVEADFAPLLMETKGDVYAAQGSQEA
           130     140     150     160     170     180

```

915

```

                190      200      210
m586.pep      LKNYGQALEKMPQDSVGRELVMKLDLKLX
                |||
a586          LKNYGQALEKMPQDSVGRELVMKLDLKLX
                190      200      210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1815>:

```

g587.seq..
1  atgaaacgta tctttttgcc cgccttgccc gccatcctgc ctttatccgc
51 ttatgccgac ctgcccttga cgattgaaga cataatgacc gacaagggaa
101 aatggaaact ggaaacttcc cttacctatc tgaatagcga aaacagccgc
151 gccgcacttg ccgcaccggg ttacattcaa accggcgcaa cctcgtttat
201 ccccatctcg accgaaattc aagaaaacgg cagcaatacc gatatgctcg
251 ccggcacgct cggtttgccg tacggactga ccggcaatac cgacatttac
301 ggacgaggca gctatctgtg gcacgaagaa cgcaaactcg acggcaacgg
351 caaaacccgc aacaaacgga tgtccgacat atccgcggcg atcagccaca
401 ccttccttaa agacggcaaa aaccccgccc taatcagctt tcttgaaagc
451 acggtttacg aaaaatcgcg caacaaagcc tcgttaatca aaaaaagggg
501 gctttgcccc tttataact taaggataaa ttatgaatat taa

```

This corresponds to the amino acid sequence <SEQ ID 1816; ORF 587.ng>:

```

g587.pep..
1  MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS LTYLNSENNSR
51 AALAAPVYIQ TGATSFIPIP TEIQENGSTNT DMLAGTLGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNGKTR NKRMSDISAG ISHTFLKDGK NPALISFLES
151 TVYEKSRNKA SLIKRGLCP FYNLRINYEY *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1817>:

```

m587.seq..
1  ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCAC
51 TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGAA
101 AATGGAAACT GGAAACTTCC CTTACCTACC TGAACAGCGA AAACAACCGC
151 GCCGAACCTG CCGCACCGGT TTACATTCAA ACCGGCGCAA CCTCGTTTAT
201 CCCCATTCGG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TCGGCACGCT CGGTTTGCGC TACGGACTGA CCGGGAATAC CGACATTTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACCTG ACGGCAACAG
351 CAAAACCCGC AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
401 CTTTCCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATAGA TCCGATTGTC CTTTCCCTCA
551 CCGCCGCTA CCGCATCAAC GGCAGCAAAA CCCTTTCAGA CGGCATCCGC
601 TACAAATCGG GCAACTACCT GCTGCTCAAC CCCAACATCT CATTGCTGTC
651 CAACGACAGA ATCAGCCTGA CCGGAGGCAT CCAATGGCTG GGCAGGCAGC
701 CCGACCGGAC GGACGGCAAA CGGGAATCCT CCAGAAACAC ATCCACCTAC
751 GCCCATTTTC GCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801 ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTCCGAA CTGAAATTTG
851 GCGTACAGCA TACATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1818; ORF 587>:

```

m587.pep..
1  MKRIFLPALP AILPLSTYAD LPLTIEDIMT DKGKWKLETS LTYLNSENNSR
51 AELAAPVYIQ TGATSFIPIP TEIQENGSTNT DMLVGTGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNSKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPIV LSLTAAYRIN GSKTSLSDGIR
201 YKSGNYLLN PNISFAANDR ISLTGGIQWL GRQPDRTDGK RESSRNTSTY
251 AHFGAGFGFT KTTALNASAR FNVSGQSSSE LKFGVQHTF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m587 / g587 95.0% identity in 161 aa overlap

10 20 30 40 50 60

916

```

m587.pep  MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNAELAAPVYIQ
          ||||||||||||||||:||||||||||||||||||||||||||||||:|| |||||||
g587       MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSLTYLNSENNAELAAPVYIQ
          10      20      30      40      50      60

          70      80      90      100     110     120
m587.pep  TGATSFIPITPEIQENGSTNDMLVGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNSKTR
          ||||||||||||||||:||||||||||||||||||||||||||||||:|||
g587       TGATSFIPITPEIQENGSTNDMLAGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNGKTR
          70      80      90      100     110     120

          130     140     150     160     170     180
m587.pep  NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV
          |||||:| ||||||| ||||||| ||||||| ||||||| |||||||
g587       NKRMSDISAGISHTFLKDGKNPALISFLESTVYEKSRNKASLIKKRGLCPFYNLIRINYEY
          130     140     150     160     170     180

          190     200     210     220     230     240
m587.pep  LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK
g587       X

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1819>:

```

a587.seq
1  ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCGC
51 TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGCA
101 AATGGAAACT GGAAACTTCC CTTACCTACC TGAACAGCGA AAACAACCGC
151 GCCGAACTTG CCGCACCGGT TTACATCCAA ACCGGCGCAA CCTCGTTTAT
201 CCCCATTCCG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TTGGCAGCT CGGTTTGCGC TACGGACTGA CCGGGAATAC CGACATTTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACCTCG ACGGCAACGG
351 CAAAACCCGA AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
401 CCTTCCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATCGA CCCCCTCGTC CTCTCATTGA
551 CCGCTGCCTA CCGTATCAAC GGCAGCAAAA CCCTTTCAAG CAACACCAAA
601 TACAAAGCAG GCAATTACTG GATGCTGAAT CCCAATATAT CCTTCGCCGC
651 CAACGACAGA ATCAGCCTCA CGGGCGGCAT CCAATGGCTG GGCAAGCAGC
701 CCGACCGTCT GGACGGCAAA AAAGAATCCG CAAGAAACAC ATCCACCTAT
751 GCCCATTTCG GCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801 ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTTCCGAA CTGAAATTTG
851 GCGTACAGCA TACGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1820; ORF 587.a>:

```

a587.pep
1  MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS LTYLNSENNR
51 AELAAPVYIQ TGATSFIPIT PEIQENGSTN DMLVGTGLRL YGLTGNTDIY
101 GSGSYLWHEE RKLDGNGKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPVV LSLTAAYRIN GSKTLSSNTK
201 YKAGNYWMLN PNISFAANDR ISLTGGIQWL GKQPDRLDGK KESARNTSTY
251 AHFGAGFGFT KTTALNASAR FNVSGQSSE LKFGVQHTF*

```

m587/a587 95.2% identity in 289 aa overlap

```

          10      20      30      40      50      60
m587.pep  MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNAELAAPVYIQ
          ||||||||||||||||:||||||||||||||||||||||||||||||:|||
a587       MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSLTYLNSENNAELAAPVYIQ
          10      20      30      40      50      60

          70      80      90      100     110     120
m587.pep  TGATSFIPITPEIQENGSTNDMLVGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNSKTR
          ||||||||||||||||:||||||||||||||||||||||||||||||:|||
a587       TGATSFIPITPEIQENGSTNDMLVGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNGKTR
          70      80      90      100     110     120

```

917

	130	140	150	160	170	180
m587.pep	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV					
a587	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPVV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m587.pep	LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK					
a587	LSLTAAYRINGSKTLSSNTKYKAGNYWMLNPNISFAANDRISLTGGIQWLGRQPDRLDGK					
	190	200	210	220	230	240
	250	260	270	280	290	
m587.pep	RESSRNTSTYAHFGAGFGFTKTALNASARFNVSGQSSSELKFGVQHTFX					
a587	KESARNTSTYAHFGAGFGFTKTALNASARFNVSGQSSSELKFGVQHTFX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1821>:

```

g588.seq
1  atgcttaaac atctcgcat cctactgccc gccatgatgt tcgccctccc
51  cgcccagacc gccgtcctaa gccctatca ggaaaccggc tgcacctacg
101 aaggcgggat cggaagac gggcttcctt caggcaaagg catatggcgt
151 tgccgggatg ggcgcggtta taccggttca ttcaaaaacg gcaaattcga
201 cgggcaaggc gtttataacc ttgccgcgg ccgcgaagta tttctcgagc
251 cgttcaattc cgacagtacc aaattccgca atatggcatt gtcgggcacg
301 ttcaacaag gcttggcaca cggcagggtt gccgcctcgc aaaacggcga
351 aaccctcttt tattatgaaa tgcgaacacg gcatgattaa

```

This corresponds to the amino acid sequence <SEQ ID 1822; ORF 588.ng>:

```

g588.pep..
1  MLKHLAFLLP AMMFALPAQT AVLSPYQETG CTYEGGIGKD GLPSGKGIWR
51  CRDGRGYTGS FKNGKFDGQG VYTVAAGREV FLEPFNSDST KFRNMALSGT
101 FKQGLAHGRF AASQNGETLF YYEMRTRHD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1823>:

```

m588.seq..
1  ATGCTTAAAC ATCTCGCATT CCTACTGCCC GCCATGATGT TCGCCCTCCC
51  CACTTCGGCC GCCGTCTGA CTCCTATCA AGAACCAGGC TGCACCTACG
101 ACGGCAATGT CGGCAAAGAC GGTAAACCCG CCGGCAAAGG CACATGGCGC
151 TGCCAAGACG GCGCAACTA TACCGGTTCT TTTAAAAACG GCAAATTCGA
201 CGGGCAAGGC GTTTATACCG TTGCCGCCAA CCGCGAAATA TTTATCGAAC
251 CGTTCAATTC CGACAGTACC AAATTCCGCA ACATGGTACT CTCGGGCACG
301 TTCAAAAAAG GCTTGGCACA CGGCAGATTT ACCGTCTCGC AAAACGGCGA
351 AACCCTCTTC ATTATGAAAT GCGAAAACGG CATGATTAAA GAAGTGAAC
401 TGCCCAAAAA CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1824; ORF 588>:

```

m588.pep..
1  MLKHLAFLLP AMMFALPTSA AVLTSYQEPG CTYDGNVGKD GKPAKGKTWR
51  CQDGRNYTGS FKNGKFDGQG VYTVAANREI FLEPFNSDST KFRNMVLSGT
101 FKKGLAHGRF TVSQNGETLF IMKCENGMK EVKLPKNK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m588 / g588 82.5% identity in 120 aa overlap

10 20 30 40 50 60

918

```

m588.pep    MLKHLAFLLPAMMFALPTSAAVLTSYQEPGCTYDGNVGKDGKPKAGKGTWRCQDGRNYTGS
g588        MLKHLAFLLPAMMFALPAQTAVLSPYQETGCTYEGGIGKDGKPSGKGIWRCRDGRGYTGS
              10      20      30      40      50      60

              70      80      90     100     110     120
m588.pep    FKNGKFDGQGVYTVAAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
g588        FKNGKFDGQGVYTVAAAGREVLFEPFNSDSTKFRNMALSGTFKQGLAHGRFAASQNGETLF
              70      80      90     100     110     120

              130     139
m588.pep    IMKCENGMIKEVKLPKNKX
g588        YYEMRTRHDX
              130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1825>:

```

a588.seq
1  ATGCTTAAAC ATCTCGCATT CCTACTGCCC GCCATGATGT TCGCCCTCCC
51 CGCCGCGTCC GCCGTTCTGA CTTCTATCA AGAACCCGGC TGCACCTACG
101 AAGGCGATGT CGGCAAAGAC GGTAACCCG CCGGCAAAGG CACATGGCGC
151 TGCCAAGACG GGCGCAACTA TACCGGTTCTG TTTAAAAATG GCAAATTCGA
201 CGGACAAGGC GTTTATACCG TTGCCGCCAA CCGCGAAATA TTTATCGAAC
251 CGTTCAATTC CGACAGTACC AAATTCCGCA ACATGGTACT CTCGGGCACA
301 TTCAAAAAG GCTTGGCACA CGGCAGATTT ACCGTCTCGC AAAACGGCGA
351 AACCCTCTTC ATTATGAAAT GCGAAAACGG CATGATTAAA GAAGTGAAGC
401 TGCCCCAAAA CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1826; ORF 588.a>:

```

a588.pep
1  MLKHLAFLLP AMMFALPAAS AVLTSYQEPG CTYEGDVGKD GKPAGKGTWR
51  CQDGRNYTGS FKNGKFDGQG VYTVAANREI FIEPFNSDST KFRNMVLSGT
101 FKKGLAHGRF TVSQNGETLF IMKCENGMIK EVKLPKNK*

m588/a588    96.4% identity in 138 aa overlap

              10      20      30      40      50      60
m588.pep    MLKHLAFLLPAMMFALPTSAAVLTSYQEPGCTYDGNVGKDGKPKAGKGTWRCQDGRNYTGS
a588        MLKHLAFLLPAMMFALPAASAVLTSYQEPGCTYEGDVGKDGKPKAGKGTWRCQDGRNYTGS
              10      20      30      40      50      60

              70      80      90     100     110     120
m588.pep    FKNGKFDGQGVYTVAAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
a588        FKNGKFDGQGVYTVAAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
              70      80      90     100     110     120

              130     139
m588.pep    IMKCENGMIKEVKLPKNKX
a588        IMKCENGMIKEVKLPKNKX
              130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1827>:

```

g589.seq..
1  atgcaacaaa aaatccggtt ccaaactcgag gcgatgacct gtcaggcatg
51  tgcttcgcgc attgaaaaag tggtgaacaa aaaagatttt gtcgaatcgg
101 cgggagtgaa ctttgccagt gaggaagcgc aggttacgtt tgacggcagc
151 aaaacctcgg ttgccgacat tgccaaaatc attgagaaaa ccggttacgg
201 cgcgaaggaa aaaacggaag atacattgcc gcaacctgaa gcagaacacc
251 atatcgctg gcggttggtg cttttgctga ccatcaatat cccgttcctt

```

919

```

301 atcgggtatgg tagggatgat gctaaaaggg ctgaattgga caccggcacga
351 ttggatgatt ccgcctgtat ggcagtttgt actggcaagc atagtgaac
401 tttggctggc aatcccgttt tacaaaagcg cgtgggcaag cattaagggc
451 gggctggcga atatggacgt actcgttacc atcggcacgg tgctgattta
501 cctgtattcc gtttatatgc tgtttttcag ttcgcatgcg gcgcacggta
551 tggcgcatgt gtattttgaa gcgggcgtag tggatcgcg ttttgtgtcg
601 ctgggtaagt ttttggaaca ccgcacaaa aaatccagcc tgaacagctt
651 gggcttactg ctaaaactca cgccgaccca agtcaacgtg caacgcaacg
701 gcgaatggaa acaactgccc atcgaccaag tgcaaatcgg cgaccttacc
751 cgcaccaacc acggcggaacg catcgtgtgc gacggcatta tcgaaagcgg
801 cagcgggttg gcggacgaaa gccaccttac cggcgaatcc aatcccgaag
851 agaaaaaggc gggcggaaca gtgttgccgg gcgcgctgat gaccgaagcg
901 agcgtggtgt accgcgccgc gcagctcggc agccaaaccc tgctcggcga
951 catgatgaac gcgctctctg aagcacaagg cagttaaagca ccgattgcgc
1001 gcgtggccga taaagcggcg gcggtatttg tgccaaactgt cgtgggcatc
1051 gcgcttctga cttttatcgt tgcttggtcg attaaggcg attggacggt
1101 cgcactgatg cagcgcgttg ccgttttggg gattgcctgc ccgtgcgcg
1151 tcggtctggc gacccctgcc gcgattatgg tcggcatggg caaagcgggtg
1201 aaacacggca tttggtttaa agacgcggcg gcaatggagg aagcagccca
1251 cgtcgatgcc gtcgtattgg acaaaaccgg tacgctgacc gaaggcaggc
1301 cgcaggttgc cgcggtttat tacgttcccg acagcggctt tgacgaagac
1351 gctttgtacc gcatcgccgc cgccgtcgag caaaacgccc cccaccgct
1401 cgcccgccgc atcgtctccg ccgcacaagc gcgcggtttg gagattcccg
1451 ctgcacaaaa tgcgcaaacg gttgtcggag caggcattac cgccgaagtg
1501 gaaggcgtgg gtttggtgaa atcaggcaaa gccgaatttg ccgaactgac
1551 cttgccgaag ttttcagacg gcggtttggg aatcgccagt gcggttaccg
1601 tatctgtaaa cggcaaacgg atcggcgcat tcgcactctc cgacgcgttg
1651 aaagccgata ccgccaagc cataggccgt ctgaaaaaac acaatatcga
1701 tgtctatatt atgagcggcg ataaccaaaag tacggtcgaa tacgtcgcca
1751 aacaactggg catcgcacac gccttcggta atatgagtc gtgcgacaaa
1801 gccgccgaag tgcagaaact caaagccgcc ggcaaaaccc tggcgatggt
1851 cggcgacggc atcaacgacg cgcccgcgct tgccgcccgc aacgtcagct
1901 tcgccatgaa aggcgggtgc gacgttgccg aacacaccgc ctccgccacg
1951 ctgatgcagc attcgggtcaa tcagctcgcc gatgccctgc tgatatcgca
2001 ggcaacgttg gaaaacatca agcaaaacct atttttcgcc ttcttctaca
2051 atatatggg cattccgctc gccgcgctcg gctttttaaa tcccgtcata
2101 gcaggcgcg caatggcggc aagctcggtt tcggtatttg gcaatgcctt
2151 gcgcctgaaa tgggtaaaaa tcgattga

```

This corresponds to the amino acid sequence <SEQ ID 1828; ORF 589.ng>:

g589.pep..

```

1  MQQKIRFQIE AMTCQACASR IEKVLNKKDF VESAGVNFAS EEAQVTFDGS
51  KTSVADIANK IEKTGYGAKE KTEDTLPQPE AEHHIGWRLW LLLTINIPFL
101 IGVMGMLKLG LNWTRHDWMI PPVWQFVLAS IVQLWLAIPF YKSAWASIKG
151 GLANMDVLVT IGTVSIYLYS VYMLFFSSHA AHGMAHVYFE AGVMFIFVS
201 LGKFLHRTK KSSLNSLGLL LKLTPTQVNV QRNGEWKQLP IDQVQIGDLI
251 RTNHGERIAA DGIIESGSGW ADESHLTGES NPEEKKAGGK VLAGALMTEG
301 SVVYRAAQLG SQTLLGDMMN ALSEAQGSKA PIARVADKAA AVFVPTVVGI
351 ALLTFIVAWL IKGDWTVAlM HAVAVLVIAc PCALGLATPA AIMVGMGKAV
401 KHGIWFKDAA AMEEAAHVDA VVLDKTGTLT EGRPQVAAYV YVPDSGFDED
451 ALYRIAAAVE QNAAHPLARA IVSAAQARGL EIPAAQNAQT VVGAGITAEV
501 EGVGLVKSGK AEFAELTLPK FSDGVWEIAS AVTVSVNGKP IGAFALSDAL
551 KADTAEAIGR LKKHNIDVYI MSGDNQSTVE YVAKQLGIAH AFGNMSPCDK
601 AAEVQKLKAA GKTVMVGDG INDAPALAAA NVSFAMKGGa DVAEHTASAT
651 LMQHSVNQLA DALLISQATL ENIKQNLFFA FFYNILGIPL AALGFLNPVI
701 AGAAMAASSV SVLGNALRLK WVKID*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1829>:

m589.seq..

```

1  ATGCAACAAA AAATCCGTTT CCAAATCGAA GGCATGACCT GCCAGGCCTG
51  CGCTTCGCGC ATTGAAAAAG TGTGTAACAA AAAAGATTTT GTCGAATCGG
101 CGGGGGTAAA CTTCGCCAGC GAAGAGGCGC AGGTAGTGTT TGACGACAGC
151 AAAACCTCAG TAGCCGACAT TGCCAAAATC ATTGAGAAAA CCGGTTACGG
201 CGCGAAGGAA AAAACGGAAG ATACATTGCC GCAACCCGAA GCAGAACACC
251 ATATCGGCTG GCGGCTGTGG CTGCTGTTCA CCATCAACGT CCCGTTCTTT

```

920

```

301 ATCGGCATGG CGGGGATGAT GATCGGCAGA CACGATTGGA TGATTCCGCC
351 GTTGTGGCAG TTCGCATTGG CAAGCGTGGT GCAGCTTTGG CTGGCAATCC
401 CGTTTTACAA AAGCGCGTGG GCGAGCATT AAGGCGGACT GGCGAATATG
451 GACGTGCTGG TTACCATCGG CACGGTCTCG ATTTACCTGT ATTCCGTCTA
501 TATGCTGTTT TTCAGCCCGC ACGCGGCGTA CGGTATGGCG CATGTGTATT
551 TTGAAGTGGG CGTGATGGTG ATCGGTTTTG TGTCAC TGGG TAAATTTTTG
601 GAACACCGTA CCAAAAAATC CAGCCTCAAC AGCTTGGGCT TGCTGCTCAA
651 ACTTACACCA ACCCAAGTCA ACGTGCAACG CAACGCGGAA TGGAAACAGC
701 TTCCCATCGA CCAAGTGCAA ATCGGCGACC TTATCCGCGC CAACCACGGC
751 GAACGCATTG CCGCAGACGG CATCATTGAA AGCGGCAGCG GTTGGGCGGA
801 CGAGAGCCAT CTTACCGGCG AATCCAATCC TGAAGAAAAA AAGGCGGGCG
851 GCAAAGTGTT GCGGCGGCGG TTAATGACCG AAGGCAGTGT GGTGTACCGC
901 GCCACGCAGC TCGGCAGCCA AACCAGCTC GGCACATGA TGAACGCGCT
951 CTCTGAAGCA CAAGGCAGTA AAGCACCGAT TGC GCGCGTA GCCGATAAAG
1001 CGGCTGCGGT ATTCGTGCCT GCCGTCGTGG GCATTGCGTT GTTGACTTTT
1051 ATTGTTACTT GGCTGATTAA GGGCGATTGG ACGGTTGCGC TGATGCACGC
1101 CGTCGCCGTT TTGGTGATTG CCTGCCCGTG CCGCTGGGT CTGGCAACCC
1151 CTGCCGCGAT TATGGTCGGT ATGGGCAAAG CGGTAAACA CGGTATTTGG
1201 TTTAAAGACG CGGCAGCAAT GGAGGAAGCC GCCACGTCG ATGCCGTCGT
1251 GTTGGACAAA ACCGGTACGC TGACCGAAGG CAGCCCGCAG GTTGCCGCGC
1301 TTTATTGCGT TCCCGACAGC GGCTTTGACG AAGACGCTTT GTACCGATC
1351 GCCGCCGCCG TCGAACAAAA CGCCGCCCAT CCGCTCGCCC GTGCCATCGT
1401 CTCCGCCGCC CAAGCGCGCG GTTGGACAT TCCCGCGCA CAAAACGCAC
1451 AAACCGTTGT CCGCGCAGGC ATTACCGCCG AAGTGGAAGG CGTGGGTTTG
1501 GTGAAAGCAG GCAAAGCCGA ATTTGCCGAA CTGGCCTTGC CGAAGTTTTT
1551 AGACGGCGTT TGGGATATTG CAAGCATTGT TCGGCTCTCA GTCCGATACA
1601 AACCACATCG CGCATTTCGA CTTGCCGACG CGTTGAAAGC CGATACCGCC
1651 GAAGCCATAG GCCGTCTGAA AAAACACAAT ATCGATGTCT ATATTATGAG
1701 CGGCGACAAC CAAGGCACGG TCGAATACGT CGCCAAACAA CTGGGCATCG
1751 CACACGCCTT CGGCAACATG AGTCCGCGCG ATAAAGCTGC CGAAGTGCAA
1801 AAACCTCAAAG CCGCCGGCAA AACCGTGCGG ATGGTCGGCG ACGGCATCAA
1851 CGACGCGCCC GCGCTTGCCG CCGCTAACGT CAGCTTCGCC ATGAAAGGCG
1901 GAGCGGACGT TGCCGAACAT ACCGCATCCG CCACGCTGAT GCAGCATTCT
1951 GTCAACCAAC TCGCCGATGC TCTGCTGGTG TCGCAAGCCA CTTTGAAAAA
2001 CATCAAGCAA AACCTGTTTT TCGCCTTCTT CTACAATATT TTGGGCATTCT
2051 CTCTCGCCGC GCTTGGCTTT TTAAATCCCG TCATCGCTGG CGCGGCAATG
2101 GCGGCAAGCT CGGTTTCCGT GTTGAGCAAT GCCTTGCGCC TGAACGGGT
2151 AAAATCGAT TAG

```

This corresponds to the amino acid sequence <SEQ ID 1830; ORF 589>:

```

m589.pep..
  1  MQQKIRFQIE GMTQCACASR IEKVLNKKDF VESAGVNFAS EEAQVVFDDSD
 51  KTSVADIANK IEKTGYGAKE KTEDTLQPQE AEHHIGWRLW LLFTINVPFL
101  IGMAGMMIGR HDWMIPPLWQ FALASVVQLW LAIPFYKSAW ASIKGGLANM
151  DVLVTIGTVS IYLYSVYMLF FSPHAAYGMA HVYFEVGMVM IGFVSLGKFL
201  EHRTKKSSLN SLGLLLKLTP TQVNVQRNGE WKQLPIDQVQ IGDILIRANHG
251  ERIAADGIIE SGSGWADESH LTGESNPEEK KAGGKVLAGA LMTEGSVVYR
301  ATQLGSQTQL GDMMNALSEA QGSKAPIARV ADKAAAVFVP AVVGIALLTF
351  IVTWLIKGDW TVALMHAVAV LVIACPCALG LATPAAIMVG MGKAVKHGIW
401  FKDAAMEEAA AHVDAVVLDK TGTLTGEGSPQ VAAVYCVDPD GFDEDALYRI
451  AAAVEQNAAH PLARAIVSAA QARGLDIPAA QNAQTVVGAG ITAEVEGVGL
501  VKAGKAFAE LALPKFLDGV WDIASIVAVS VDNKPIGAFA LADALKADTA
551  EAIGRLKKHN IDVYIMSGDN QGTVEYVAKQ LGIAHAFGNM SPRDKAAEVQ
601  KLKAAGKTVA MVGDGINDAP ALAAANVSFA MKGGADVAEH TASATLMQHS
651  VNQLADALLV SQATLKNIKQ NLFFAFFYNI LGIPLAALGF LNPVIAGAAM
701  AASSVSVLSN ALRLKRVKID *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m589 / g589 94.2% identity in 725 aa overlap

```

              10      20      30      40      50      60
m589.pep      MQQKIRFQIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADIANKI
              |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```


921

```
g589      MQQKIRFQIEAMTCQACASRIEKVLNKKDFVESAGVNFASEEAQVTFDGSKTSVADIAKI
           10      20      30      40      50      60

           70      80      90      100     110
m589.pep  IEKTGYGAKEKTEDTLPOPEAEHHIGWRLWLLFTINVPFLIGMAGMMIG-----RHDWMI
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g589      IEKTGYGAKEKTEDTLPOPEAEHHIGWRLWLLLTINIPFLIGMVGMMMLKGLNWTNRHDWMI
           70      80      90      100     110     120

           120     130     140     150     160     170
m589.pep  PPLWQFALASVVQLWLAIIPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
           ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
g589      PPVWQFVLASIVQLWLAIIPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSSHA
           130     140     150     160     170     180

           180     190     200     210     220     230
m589.pep  AYGMAHVYFEVGMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWKQLP
           |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g589      AHGMAHVYFEAGVMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWKQLP
           190     200     210     220     230     240

           240     250     260     270     280     290
m589.pep  IDQVQIGDLIRANHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLGALMTEG
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g589      IDQVQIGDLIRTNHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLGALMTEG
           250     260     270     280     290     300

           300     310     320     330     340     350
m589.pep  SVVYRATQLGSQTQLGDMMNALSEAQGSKAPIARVADKAAAVFVPAVVGIALLTFFIVTWL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g589      SVVYRAAQLGSQTLLGDMMNALSEAQGSKAPIARVADKAAAVFVPTVVVGIALLTFFIVAWL
           310     320     330     340     350     360
```

922

	360	370	380	390	400	410
m589.pep	IKGDWTVALMHAVAVLVIAACPCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
g589	IKGDWTVALMHAVAVLVIAACPCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
	370	380	390	400	410	420
	420	430	440	450	460	470
m589.pep	VVLDKTGTLTEGSPQVAAYVCVPDSGFDEDALYRIAAAVEQNAAHPLARAIVSAAQARGL					
g589	VVLDKTGTLTEGRPQVAAYVVPDSGFDEDALYRIAAAVEQNAAHPLARAIVSAAQARGL					
	430	440	450	460	470	480
	480	490	500	510	520	530
m589.pep	DIPAAQNAQTVVGAGITAEVEGVGLVKAGKAFAELALPKFLDGVWDIASIVAVSVDNKP					
g589	EIPAAQNAQTVVGAGITAEVEGVGLVKSAGKAFAELTLPKFSDGVWEIASAVTVSVNGKP					
	490	500	510	520	530	540
	540	550	560	570	580	590
m589.pep	IGAFALADALKADTAEAIGRLLKHNIDVYIMSGDNQGTVEYVAKQLGIAHAFGNMSPRDK					
g589	IGAFALSDALKADTAEAIGRLLKHNIDVYIMSGDNQSTVEYVAKQLGIAHAFGNMSPCDK					
	550	560	570	580	590	600
	600	610	620	630	640	650
m589.pep	AAEVQKLKAAGKTVAMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA					
g589	AAEVQKLKAAGKTVAMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA					
	610	620	630	640	650	660
	660	670	680	690	700	710
m589.pep	DALLVSQATLKNIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSVSVLGNALRLK					
g589	DALLISQATLENIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSVSVLGNALRLK					
	670	680	690	700	710	720
	720					
m589.pep	RVKIDX					
g589	WVKIDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1831>:

```

a589.seq
1   ATGCAACAAA AAGTCCGTTT CCAAATCGAA GGCATGACCT GCCAGGCATG
51  TGCTTCGCGC ATTGAAAAAG TGTTGAACAA AAAAGATTTT GTCGAATCGG
101 CGGGGGGTAAA CTTCCGCCAGC GAAGAGGCTC AGGTAGTGTT TGACGACAGC
151 AAAACCTCAG TAGCCGACAT TGCCAAATC ATTGAGAAAA CCGGTTACGG
201 CGCGAAGGAA AAAACGGAAG ATACATTGCC GCAACCCGAA GCAGAACACC
251 ATATCGGCTG GAGGTTGTGG CTTTGTCTGG CCATCAATAT CCCGTTCTTT
301 ATCGGTATGG TAGGGATGAT GCTAAAAGGG CTGAATTGGA CACGGCATGA
351 TTGGATGTTG TCGCCCTTGT TGCAGTTTGC ATTGGCGAGT GTGGTGCAGC
401 TTTGGCTGGC GGTGCCATTT TACAAAAGCG CGTGGGCGAG CATTAAAGGC
451 GGGCTGGCGA ATATGGACGT ACTCGTTACC ATCGGCACGG TCTCGATTTA
501 CCTGTATTCC GTCTATATGC TGTTTTTCAG CCCGCACGCG GCGTACGGTA
551 TGGCGCATGT GTATTTTGAA GTAGGCATAA TGGTGATTGG TTTTGTGTCA
601 CTGGGTAAAT TTTTGGAACA CCGCACAAA AAATCCAGCC TGAACAGCTT
651 GGGCTTGCTG CTCAAACCTA CGCCAACCCA AGTCAACGTG CAACGCGATG
701 GCGAATGGCG GCAGCTACCC ATCGACCAAG TGCAAATCGG CGACCTAATC
751 CGCGCCAATC ACGGCGAACG CATTGCCGCC GACGGCATCA TAGAAAGCGG
801 CAGCGGCTGG GCGGACGAAA GCCATCTTAC CGGCGAATCC AATCCCGAAG
851 AGAAAAAGGC AGGCGGCAAA GTATTGGCGG GCGCGCTGAT GACTGAAGGC
901 AGCGTGGTGT ACCGCGCCGC GCAGCTCGGC AGCCAAACCC TGCTCGGCGA
951 CATGATGAAC GCGCTCTCCG AAGCGCAAGG CAGTAAAGCA CCGATTGCGC
1001 GTGTGGCGGA CAAGGCGGCG GCGGTATTCG TGCTGCGCGT TGTGGGCATC
1051 GCACTTTTGA CTTTTATCGC TACTTGGCTG ATTAAGGGCG ATTGGACGCT
1101 CGCATTGATG CACGCCGTCG CCGTTTTGGT GATTGCCTGC CCGTGTGCAC

```

923

```

1151 TCGGTTTGGC AACCCCTGCT GCGATTATGG TCGGTATGGG CAAAGCGGTT
1201 AAACACGGTA TTTGGTTTAA AGACGCGGCA GCAATGGAAG AAGCCGCCCA
1251 CGTTGATGCC GTCGTGCTGG ACAAAACCGG CACGCTGACC GAAGGCAAGC
1301 CGCAGGTTGC CGCCGTTTAT TGTGTTCCCG ACAGCGGCTT TGACGAAGAC
1351 GCTTTGTACC GCATCGCCGC CGCCGTCGAA CAAAACGCCG CCCATCCGCT
1401 CGCCCGTGCC ATCGTCTCCG CCGCCCAGGC GCGCGGTTTG GAGATTCCCA
1451 CCGCACAAAA TGCCCAAACC ATTGTCGGCG CGGGCATTAC CGCCGAAGTA
1501 AAAGGCGCGG GTTGGTAAA AGCAGGCAAA GCCGAATTTG CCGAACTGAC
1551 CTTGCCGAAG TTTTCAGACG GCGTTTGGGA AATCGCCAGT GTGGTTGCCG
1601 TATCTGTAAG CGGCAAACCT ATCGGCGCAT TCGCACTCGC CGACGCGTTG
1651 AAAGCCGATA CGCCGAAGC CATAGGCCGT CTGAAAAAAC ACAATATCGA
1701 TGCTATATT ATGAGCGGCG ATAACCAAGG CACGGTCGAG TACGTCGCCA
1751 AACAACTGGG CATCGCACAC GCCTTCGGTA ATATGAGTCC GCGCGACAAA
1801 GCCGCCGAAG TGCAGAAACT CAAAGCCGCC GGCAAACCG TGCGCATGGT
1851 CGGCGACGGC ATCAACGACG CGCCGCGCCT CGCCGCCGCC AACGTCAGCT
1901 TCGCCATGAA AGCGGTTGCA GACGTTGCCG AACACACCGC ATCCGCCACA
1951 CTGATGCAGC ATTCGGTCAA CCAGCTCGCC GATGCGCTAT CGGTATCGCG
2001 AGCGACGTTG AAAAACATCA AGCAAAACCT GTTTTTCGCC TTCTTCTACA
2051 ATATTTTGGG CATTCCGCTC GCCGCGCTCG GCTTTTTTAA CCCCCTCATC
2101 GCAGGCGCGG CAATGGCGGC AAGCTCGGTT TCCGTGTTGA GCAACGCCTT
2151 GCGCCTGAAA CGGGTAAAAA TCGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1832; ORF 589.a>:

a589.pep

```

1  MQQKVRFAQIE GMTQCACASR IEKVLNKKDF VESAGVNFAS EEAQVVFDDSD
51  KTSVADIANK IEKTGYGAKE KTEDTLPQPE AEHHIGWRLW LLLAINIPFL
101 IGMVGMMLKG LNWTRHDWML SPLLQFALAS VVQLWLAVPF YKSAWASIKG
151 GLANMDVLVT IGTVSIYLYS VYMLFFSPHA AYGMHVYFE VGIMVIGFVS
201 LGKFLEHRTK KSSLNSLGLL LKLTPTQVNV QRDGEWRQLP IDQVQIGDLI
251 RANHGERIAA DGIIESGSW ADESHLTGES NPEKKAGGK VLAGALMTEG
301 SVVYRAAQLG SQTLLGDMN ALSEAQGSKA PIARVADKAA AVFVPAVVGI
351 ALLTFIATWL IKGDWTLALM HAVAVLVIAC PCALGLATPA AIMVGMGKAV
401 KHGIWFKDAA AMEEAAHVDA VVLDKTGTLT EGKQPQAAVY CVPDSGFDED
451 ALYRIAAAVE QNAAHPLARA IVSAAQARGL EIPTAQNAQT IVGAGITAEV
501 KGAGLVKAGK AEFAELTLPK FSDGVWEIAS VVAVSVNGKP IGAFALADAL
551 KADTAEAIGR LKKHNIDVYI MSGDNQGTVE YVAKQLGIAH AFGNMSPRDK
601 AAEVQKLKAA GKTVMVGDG INDAPALAAA NVSFAMKGGG DVAEHTASAT
651 LMQHSVNQLA DALSVSRATL KNIKQNLFFA FFYNILGIPL AALGLFNPVI
701 AGAAMAASSV SVLSNALRLK RVKID*

```

m589/a589 94.9% identity in 725 aa overlap

```

10 20 30 40 50 60
m589.pep MQQKIRFQIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADIANK
||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
a589 MQQKVRFAQIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADIANK
10 20 30 40 50 60

70 80 90 100 1 110
m589.pep IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLFTINVPFLIGMAGMMIG----RHDWMI
|||||||||||||||||||||||||||||||||||||||||:|||||:|||||:|||||
a589 IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLAINIPFLIGMVGMMMLKGLNWTRHDWML
70 80 90 100 110 120

120 130 140 150 160 170
m589.pep PPLWQFALASVVQLWLAIPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
|| |||||||||||||||||||||||||||||||||||||||||||||||||||
a589 SPLLQFALASVVQLWLAVPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
130 140 150 160 170 180

180 190 200 210 220 230
m589.pep AYGMHVYFEVGMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWKQLP
|||||||||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a589 AYGMHVYFEVGIMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRDGEWRQLP
190 200 210 220 230 240

```

924

m589.pep	240	250	260	270	280	290
	IDQVQIGDLIRANHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLGALMTEG					
a589	250	260	270	280	290	300
	IDQVQIGDLIRANHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLGALMTEG					
m589.pep	300	310	320	330	340	350
	SVVYRATQLGSQTQLGDMMNALSEAQGSKAPIARVADKAAAVFVPAVVGIALLTFIIVTWL					
a589	310	320	330	340	350	360
	SVVYRAAQLGSQTLLGDMMNALSEAQGSKAPIARVADKAAAVFVPAVVGIALLTFIATWL					
m589.pep	360	370	380	390	400	410
	IKGDWTVALMHAVAVLVIA PCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
a589	370	380	390	400	410	420
	IKGDWTVLALMHAVAVLVIA PCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
m589.pep	420	430	440	450	460	470
	VVLDKTGTLTGEGSPQVAAYVCVPDSGFDEDALYRIAAAVEQNAAHPLARAIVSAAQARGL					
a589	430	440	450	460	470	480
	VVLDKTGTLTGEGKQVAAYVCVPDSGFDEDALYRIAAAVEQNAAHPLARAIVSAAQARGL					
m589.pep	480	490	500	510	520	530
	DIPAAQNAQTIVGAGITAEVEGVGLVKAGKAEFAELALPKFLDGVWDIASIVAVSVDNKP					
a589	490	500	510	520	530	540
	EIPTAQNQTIVGAGITAEVKGAGLVKAGKAEFAELTLPKFSDGVWEIASVAVSVNGKP					
m589.pep	540	550	560	570	580	590
	IGAFALADALKADTAEAIIGRLKKHNIDVYIMSGDNQGTVEYVAKQLGIAHAFGNMSPRDK					
a589	550	560	570	580	590	600
	IGAFALADALKADTAEAIIGRLKKHNIDVYIMSGDNQGTVEYVAKQLGIAHAFGNMSPRDK					
m589.pep	600	610	620	630	640	650
	AAEVQKLKAAGKTVAMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA					
a589	610	620	630	640	650	660
	AAEVQKLKAAGKTVAMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA					
m589.pep	660	670	680	690	700	710
	DALLVSQATLKNIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSVSVLSNALRLK					
a589	670	680	690	700	710	720
	DALSVSRATLKNIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSVSVLSNALRLK					
m589.pep	720					
	RVKIDX					
a589	RVKIDX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1833>:

g590.seq..

```

1  atgaaaaaac ctttgatttc agttgcggca gtattgctcg gcgttgcttt
51  ggggtacacct tattatttgg gtgtcaaagc agaagaaagt ctgacgcagc
101 agcaaaaaat attgcagaaa acgggctttt tgaccgtcga atcgaccag
151 tatgatcgag gctggtttac ctctacggaa acgacgggtca tccgtctgaa
201 acccgagttg ctgcataatg cgcagaaata cctgccggat aacttgaaaa
251 tagtgttgga acagccggtt acgctggtta accatatcac gcacggccct
301 ttcgccggcg gattcggcac gcaggcgcac attgaaaccg agttcaaata
351 cgcgcctgaa acggaaaaag ttttggaacg cttttttggg aaacaagttc
401 cggtttccct tgccaatacc gtttatttca acggcagcgg taaaatggaa
451 gtcagtggtc cgcgtttcga ttatgaagaa ctgtcgggca tcaggctgca

```

```

501 ctgggaagggc ctgacggggg aaacgggttta tcaaaaaggt ttcaaaagct
551 accgcaacag ctatgatgcg cccttggttca aaatcaagct ggcagacaaa
601 ggcgatgccc cgtttgaaaa agcgcatctt gattcggaaa cttcagacgg
651 catcaatccc cttgctttgg gcagcagcaa tctgactttg gaaaaatttt
701 cgctcgaatg gaaagagggg gtcgattaca acgtcaaatt gaacgaactg
751 gtcaacctcg ttaccgattt gcagatcggc gcgtttatca atcccaacgg
801 cagcatcgca ccttccaaaa tcgaagtcgg caagctggct ttttcaacca
851 agaccggggg atcgggcccgcg tttatcgaca gcgaagggcg gttccgtttc
901 gatacgttgg tgtacggcga tgaataatac ggcccgtcgg acatccatat
951 cgctgccgaa cacctcgatg cttctgcctt aaccgtattg aaacgcaagt
1001 ttgcacaaat ttctgccaaa aaaatgactg aggaacaaat ccgcaatgat
1051 ttgattgccc cagtcaaaag cgatgccttc ggattattta cccatgaccc
1101 ggtactaaat atcaaaattt tccgtttcac cctgcctcag gaaaaaattg
1151 atgtggggcg aaaaatcatg tttaaaggca tgaagaagga agatttgaac
1201 caattgggac tgatgttaaa gaaaaccgag gcaaacatca gaatgagtat
1251 tcctcaaaaa atgttggaag atttgccggt aagtcaggct ggaatatatt
1301 tcagtgtaaa tgccgaagat gaggcggaag ccagagcaag cattgccgat
1351 attaatgaaa cattgcgcct gatgggtggc agtacggctc aaagtatggc
1401 aagggaaaaa tatcttactt tagacggtaa tcagattgat acggtcattt
1451 cctttaaaaa caacgccctg aagttaaacc ggaaaacgct gcaaatgaa
1501 cccgatcctg attttgacga gggagatatg gtttccggcc agccgcatta
1551 a

```

This corresponds to the amino acid sequence <SEQ ID 1834; ORF 590.ng>:

g590.pep..

```

1 MKKPLISVAA VLLGVALGTP YYLGVKAES LTQQQKILQK TGFLTVESHQ
51 YDRGWFTSTE TTVIRLKP EL LHNAQKYL PD NLKIVLEQPV TLVNHITHGP
101 FAGGFGTQAH IETEFKYAPE TEKVLERFFG KQVPVSLANT VYFNGSGKME
151 VSVPAFYDYE LSGIRLHWEG LTGETVYQKG FKSYSNSYDA PLFKIKLADK
201 GDAAFEKAHF DSETSDGINP LALGSSNLTL EKFSLEWKEG VDYNVKLNEL
251 VNLVTDLQIG AFINPNGSIA PSKIEVGKLA FSTKTGESGA FIDSEGRFRF
301 DTLVYGEKEY GPLDIHIAAE HLDASALTVL KRKFAQISAK KMTTEEQIRND
351 LIAAVKG DAS GLFTHDPVLN IKIFRFTLPQ GKIDVGGKIM FKGMMKEDLN
401 QLGLMLKKTE ANIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEARASIA D
451 INETLRLMVD STVQSMAREK YLTLDGNQID TVISLKNNAL KLNKKT LQNE
501 PDPDFDEGDM VSGQPH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1835>:

m590.seq (partial) ..

```

1 .. TGGTTTACCT CTATGGAAC GACGGTCATC CGTCTGAAAC CCGAGTTGCT
51 GAATAATGCC CGAAATACC TGCCGGATAA CCTGAAAACA GTGTTGGAAC
101 AGCCGGTTAC GCTGGTTAAC CATATCACGC ACGGCCCTTT CGCCGGCGGA
151 TTCGGCAGCG AGGCGTACAT TGAACCCGAG TTCAAATACG CGCCTGAAAC
201 GGAAAAAGTT CTGGAACGCT TTTTGGAAA ACAAGTCCCG GCTTCCCTTG
251 CCAATACCGT TTATTTTAAC GGCAGCGGTA AAATGGAAGT CAGTGTTCCT
301 GCCTTCGATT ATGAAGAGCT GTCGGGCATC AG. CTGCACT GGGAAKGCCT
351 GACGGGAGAA ACGGTTTATC AAAAAGGTTT CAAAAGCTAC CGGAACGGCT
401 ATGATGCCCC CTGTGTTAAA ATCAAGCTGG CAGACAAAGG CGATGCCGCG
451 TTTGAAAAAG TGCAATTCGA TTCGGAAACT TCAGACGGCA TCAATCCGCT
501 TGCTTTGGGC AGCAGCAATC TGACCTTGGA AAAATTCTCC CTAGAATGGA
551 AAGAGGGTGT CGATTACAAC GTCAAGTTAA ACGAACTGGT CAATCTTGTT
601 ACCGATTGTC AGATTGGCGC GTTTATCAAT CCAACGGCA GCATCGCACC
651 TTCCAAAATC GAAGTCGGCA AACTGGCTTT TTCAACCAAG ACCGGGGAAT
701 CAGGCGCGTT TATCAACAGT GAAGGGCAGT TCCGTTTCGA TACACTGGTG
751 TACGGCGATG AAAAATACGG CCCGCTGGAC ATCCATATCG CTGCCGAACA
801 CCTCGATGCT TCTGCCTTAA CCGTATTGAA ACGCAAGTTT GCACAAATTT
851 CCGCCAAAAA AATGACCGAG GAACAAATCC GCAATGATTT GATTGCCGCC
901 GTCAAAGGAG AGGCTTCCGG ACTGTTTACC AACAAATCCC TATTGGACAT
951 TAAAACTTTC CGATTACACG TGCCATCGGG AAAAAATCGAT GTGGGCGGAA
1001 AAATCATGTT TAAAGACATG AAGAAGGAAG ATTTGAATCA ATTGGGTTTG
1051 ATGCTGAAGA AAACCGAAGC CGACATCAGA ATGAGTATTC CCAAAAAAAT
1101 GCTGGAAGAC TTGGCGGTCA GTCAAGCAGG CAATATTTTC AGCGTCAATG
1151 CCGAAGATGA GGCGGAAGGC AGGGCAAGTC TTGACGACAT CAACGAGACC
1201 TTGCGCCTGA TGGTGGACAG TACGGTTCAG AGTATGGCAA GGGAAAAATA
1251 TCTGACTTTG AACGCGGACC AGATTGATAC TGCCATTTC CTGAAAAACA
1301 ATCAGTTGAA ATTGAACGGT AAAACGTTGC AAAACGAACC GGAGCCGGAT
1351 TTTGATGAAG GCGGTATGTT TTCAGAGCCG CAGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1836; ORF 590>:

m590.pep..(partial)

```

1  .WFTSMETTVI RLKPELLNNA RYLPDNLKT VLEQPVTLVN HITHGPFAGG
51  FGTQAYIETE FKYAPETEKV LERFFGKQVP ASLANTVYFN GSGKMEVSVP
101 AFDEEELSGI XLHWEXLTGE TVYQKGFKSY RGYDAPLFK IKLADKGDAA
151 FEKVHFDSET SDGINPLALG SSNLTLEKFS LEWKEGVDYN VKLNELVNLV
201 TDLQIGAFIN PNGSIAPSKI EVGKLAFSTK TGESGAFINS EGQFRFDTLV
251 YGDEKYGPLD IHIAAEHLDA SALTVLKRKF AQISAKKMT E QIRNDLIAA
301 VKGEASGLFT NNPVLDIKTF RFTLPSGKID VGGKIMFKDM KKEDLNQLGL
351 MLKKTEADIR MSIPQKMLED LAVSQAGNIF SVNAEDEAEG RASLDDINET
401 LRLMVDSTVQ SMAREKYLT L NGDQIDTAIS LKNNQLKLNG KTLQNEPEPD
451 FDEGGMVSEP QQ*

```

m590 / g590 93.1% identity in 462 aa overlap

```

                                10      20      30
m590.pep                      WFTSMETTIVIRLKPPELLNNARKYLPDNLKT
                                |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
g590      VKAEESLTQQQKILQKTGFLTVESHQYDRGWFTSTETTIVIRLKPPELLHNAQKYLDPNLKI
                                30      40      50      60      70      80

                                40      50      60      70      80      90
m590.pep      VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPASLANTVYFN
                                |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
g590      VLEQPVTLVNHITHGPFAGGFGTQAHIETEFKYAPETEKVLERFFGKQVPVSLANTVYFN
                                90      100     110     120     130     140

                                100     110     120     130     140     150
m590.pep      GSGKMEVSVPAPDYEEELSGIXLHWEXLTGETVYQKGFKSYRNGYDAPLFKIKLADKGDAA
                                |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
g590      GSGKMEVSVPAPDYEEELSGIRLHWEGLTGETVYQKGFKSYRNSYDAPLFKIKLADKGDAA
                                150     160     170     180     190     200

                                160     170     180     190     200     210
m590.pep      FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVDYNVKLNELVNLVTDLQIGAFIN
                                |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
g590      FEKAHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVDYNVKLNELVNLVTDLQIGAFIN
                                210     220     230     240     250     260

                                220     230     240     250     260     270
m590.pep      PNGSIAPSKIEVGKLAFSTKTGESGAFINSEGQFRFDTLVYGDKEYGPLDIHIAAEHLDA
                                |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
g590      PNGSIAPSKIEVGKLAFSTKTGESGAFIDSEGRFRFDTLVYGDKEYGPLDIHIAAEHLDA
                                270     280     290     300     310     320

                                280     290     300     310     320     330
m590.pep      SALTVLKRKFAQISAKKMTTEEQIRNDLIAAVKGEASGLFTNNPVLDIKTFRFTLPSGKID
                                |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
g590      SALTVLKRKFAQISAKKMTTEEQIRNDLIAAVKGDASGLFTHDPVLNLIKIFRFTLPQGKID
                                330     340     350     360     370     380

                                340     350     360     370     380     390
m590.pep      VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEG
                                |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
g590      VGGKIMFKDMKKEDLNQLGLMLKKTEANIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEG
                                390     400     410     420     430     440

                                400     410     420     430     440     450
m590.pep      RASLDDINETLRLMVDSTVQSMAREKYLTLDGNDQIDTAISLKNNQLKLNGKTLQNEPEPD
                                |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
g590      RASIADINETLRLMVDSTVQSMAREKYLTLDGNQIDTVISLKNALKLNGKTLQNEPDPP
                                450     460     470     480     490     500

                                460
m590.pep      FDEGGMVS-EPQQX
                                |||  |||  |||  |||
g590      FDEGDMVSGQPHX
                                510

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1837>:

```
a590.seq
1  ATGAAAAAAC CTTTGATTTC GGTGCGGCA GCATTGCTCG GCGTTGCTTT
51  GGGCACGCCT TATTATTGCG GTGTCAAAGC CGAAGAAAGC TTGACGCAGC
101 AGCAAAAAAT ATTGCAGGAA GCGGGCTTCT TGACCGTCGA ATCGCACCAA
151 TATGAGCGCG GCTGGTTTAC CTCTACGAA ACGACGGTCA TCCGCTTGAA
201 ACCCGAGTTG CTGCATAATG CGCAGAAATA CCTGCCGGAT AACCTGAAAA
251 CAGTGTGGA ACAGCCGGTT ACGCTGGTAA ACCATATCAC GCACGGTCCT
301 TTTGCCGGCG GATTTCGGCAC GCAGGCGTAC ATTGAAACCG AGTTCAAATA
351 CGCGCCTGAA ACGGAAAAAG TTCTGGAACG CTTTTTGGGA AAACAAGTCC
401 CGGTTTCCCT TGCCAATACC GTTTATTTTA ACGGCAGCGG TAAAATGGAA
451 GTCAGTGTTC CCGCCTTCGA TTATGAAGAG CTGTCGGGCA TCAGGCTGCA
501 CTGGGAAGGC CTGACGGGAG AAACGGTTTA TCAAAAAGGT TTCAAAAGCT
551 ACCGGAACGG CTATGATGCC CCCTTGTTTA AAATCAAGCT GGCAGACAAA
601 GGCGATGCCG CGTTTGAAAA AGTGCATTTT GATTCGGAAA CTTCAGACGG
651 CATCAACCCG CTTGCTTTGG GCAGCAGCAA TCTGACCTTG GAAAAATTTT
701 CCTTAGAATG GAAAGAGGGT GTCGATTACA ACGTCAAGTT AAACGAAGCT
751 GTCAATCTTG TTACCGATTT GCAGATTGGC GCGTTTATCA ATCCCAACGG
801 CAGCATCGCA CCTTCCAAAA TCGAAGTCGG CAAGCTGGCT TTTTCAACCA
851 AGACCGGGGA ATCGGGCGCG TTTATCGATA GCGAAGGGCA GTTCCGTTTT
901 GGCACGCTGG TTTACGGCGA TGAAAAATAC GGCCCTCTGG ACATCCATAT
951 CGCTGCCGAA CACCTCGATG CTTCTGCCTT AACCGTATTG AAACGCAAGT
1001 TTGCACGAAT TTCTGCCAAA AAAATGACTG AAGAACAAAT CCGCAATGAT
1051 TTGATTGCGG CAGTCAAAGG CGAGGCTTCC GGATTATTTA CCCATAACCC
1101 AGTATTGGAC ATTAAACTT TCCGATTAC GCTGCCATCG GGAAAAATCG
1151 ATGTGGGCGG AAAAATCATG TTTAAAGACA TGAAGAAGGA AGATTTGAAC
1201 CAATTGGGTT TGATGCTGAA GAAAACCGAA GCCGACATCA GAATGAGTAT
1251 TCCCCAAAAA ATGCTGGAAG ACTTGGCGGT CAGTCAAGCA GGCAATATTT
1301 TCAGCGTCAA TGCCGAAGAT GAGGCGGAAG GCAGGGCAAG TCTTGACGAC
1351 ATCAACGAGA CCTTGCGCCT GATGGTGGAC AGTACGGTTC AGAGTATGGC
1401 AAGGGAAAAA TATCTGACTT TGAACGGCGA CCAGATTGAT ACTGCCATTT
1451 CTCTGAAAAA CAATCAGTTG AAATTGAACG GTAAACGTT GCAAAACGAA
1501 CCGGAGCCGG ATTTTGATGA AGGCGGTATG GTTTCAGAGC CGCAGCAGTA
1551 A
```

This corresponds to the amino acid sequence <SEQ ID 1838; ORF 590.a>:

```
a590.pep
1  MKKPLISVAA ALLGVALGTP YYLGVKAEES LTQQQKILQE AGFLTVESHO
51  YERGWFSTTE TTVIRLKPPEL LHNAQKYLDP NLKTVLEQPV TLVNHITHGP
101 FAGGFGTQAY IETEFKYAPE TEKVLERFFG KQVPVSLANT VYFNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNGYDA PLFKIKLADK
201 GDAAFEKVHF DSETSDGINP LALGSSNLTL EKFSLEWKEG VDYNVKLNEL
251 VNLVTDLQIG AFINPNGSIA PSKIEVGKLA FSTKTGESGA FIDSEGQFRF
301 GTLVYGDEKY GPLDIHIAAE HLDASALTVL KRKFARISAK KMTEEQIRND
351 LIAAVKGEAS GLFTHNPVLD IKTFRFTLPS GKIDVGGKIM FKDMKKEDLN
401 QLGLMLKKTE ADIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEGRASLDD
451 INETLRLMVD STVQSMAREK YLTLNGDQID TAISLKNQNL KLNGKTLQNE
501 PEPDFDEGGM VSEPPQ*

m590/a590 97.8% identity in 462 aa overlap

m590.pep
10 20 30
WFTSMETTIVIRLKPPELLNNARKYLPDNLKT
|||||

a590
30 40 50 60 70 80
VKAEEESLTQQQKILQEAGFLTVESHOYERGWFSTETTIVIRLKPPELLHNAQKYLDPDNLKT

m590.pep
40 50 60 70 80 90
VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPASLANTVYFN
|||||

a590
90 100 110 120 130 140
VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPVSLANTVYFN

m590.pep
100 110 120 130 140 150
GSGKMEVSVPAFDYEEELSGIXLHWEXLTGETVYQKGFKSyrNGYDAPLFIKIKLADKGDAA
```

928

```

|||||
a590      GSGKMEVSVPAFDYEELSGIRLHWEGLTGETVYQKGFKSYRNGYDAPLFKIKLADKGDAA
          150      160      170      180      190      200

          160      170      180      190      200      210
m590.pep  FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVDYNVKLNELVNLVTDLQIGAFIN
          |||||
a590      FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVDYNVKLNELVNLVTDLQIGAFIN
          210      220      230      240      250      260

          220      230      240      250      260      270
m590.pep  PNGSIAPSKIEVGKLAFFSTKTGESGAFINSEGGFRFDLTVYGDEKYGPLDIHIAAEHLDA
          |||||
a590      PNGSIAPSKIEVGKLAFFSTKTGESGAFIDSEGGFRFGLTVYGDEKYGPLDIHIAAEHLDA
          270      280      290      300      310      320

          280      290      300      310      320      330
m590.pep  SALTVLKRKFAQISAKKMTEEQIRNDLIAAVKGEASGLFTNNPVLDIKTFRFTLPSPGKID
          |||||
a590      SALTVLKRKFARISAKKMTEEQIRNDLIAAVKGEASGLFTNPNVLDIKTFRFTLPSPGKID
          330      340      350      360      370      380

          340      350      360      370      380      390
m590.pep  VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEAG
          |||||
a590      VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEAG
          390      400      410      420      430      440

          400      410      420      430      440      450
m590.pep  RASLDDINETLRLMVDSTVQSMAREKYLTNLNGDQIDTAISLKNQNLKLNKTLQNEPEPD
          |||||
a590      RASLDDINETLRLMVDSTVQSMAREKYLTNLNGDQIDTAISLKNQNLKLNKTLQNEPEPD
          450      460      470      480      490      500

          460
m590.pep  FDEGGMVSEPQQX
          |||||
a590      FDEGGMVSEPQQX
          510

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1839>:

m590-1.seq

```

1  ATGAAAAAAC CTTTGATTTC GGTGCGGCA GCATTGCTCG GCGTTGCTTT
51  GGGCACGCCT TATTATTGCG GTGTCAAAGC CGAAGAAAGC TTGACGCAGC
101 AGCAAAAAAT ATTGCAGGAA ACGGGCTTCT TGACCGTCGA ATCGCACCAA
151 TATGAGCGCG GCTGGTTTAC CTCTATGGAA ACGACGGTCA TCCGCTCGAA
201 ACCCGAGTTG CTGAATAATG CCCGAAAATA CCTGCCGGAT AACCTGAAAA
251 CAGTGTTGGA ACAGCCGGTT ACGCTGGTTA ACCATATCAC GCACGGCCCT
301 TTCGCCGCGC GATTCGGCAC GCAGGCGTAC ATTGAAACCG AGTTCAAATA
351 CGCGCCTGAA ACGGAAAAAG TTCTGGAACG CTTTTTTGGA AAACAAGTCC
401 CGGCTTCCCT TGCCAATACC GTTTATTTTA ACGGCAGCGG TAAAAATGGAA
451 GTCAGTGTTC CCGCCTTCGA TTATGAAGAG CTGTCGGGCA TCAGGCTGCA
501 CTGGGAAGGC CTGACGGGAG AAACGGTTTA TCAAAAAGGT TTCAAAAGCT
551 ACCGGAACGG CTATGATGCC CCCTTGTTTA AAATCAAGCT GGCAGACAAA
601 GCGCATGCCG CGTTTGAAAA AGTGCATTTC GATTCGGAAA CTTCAGACGG
651 CATCAATCCG CTGCTTTTGG GCAGCAGCAA TCTGACCTTG GAAAAATTCT
701 CCCTAGAATG GAAAGAGGGT GTCGATTACA ACGTCAAGTT AAACGAAGTG
751 GTCAATCTTG TTACCGATTG GCAGATTGGC GCGTTTATCA ATCCCAACGG
801 CAGCATCGCA CCTTCCAAAA TCGAAGTCGG CAAACTGGCT TTTTCAACCA
851 AGACCGGGGA ATCAGGCGCG TTTATCAACA GTGAAGGGCA GTTCCGTTTC
901 GATACACTGG TGTACGGCGA TGAAAAATAC GGCCCGCTGG ACATCCATAT
951 CGCTGCCGAA CACCTCGATG CTTCTGCCTT AACCGTATTG AAACGCAAGT
1001 TTGCACAAAT TTCCGCCAAA AAAATGACCG AGGAACAAAT CCGCAATGAT
1051 TTGATTGCCG CCGTCAAAGG AGAGGCTTCC GGACTGTTCA CCAACAATCC
1101 CGTATTGGAC ATTAAAACTT TCCGATTACG GCTGCCATCG GGAAAAATCG
1151 ATGTGGGCGG AAAAATCATG TTAAAGACA TGAAGAAGGA AGATTTGAAT
1201 CAATTGGGTT TGATGCTGAA GAAAACCGAA GCCGACATCA GAATGAGTAT

```


929

```

1251 TCCCCAAAAA ATGCTGGAAG ACTTGGCGGT CAGTCAAGCA GGCAATATTT
1301 TCAGCGTCAA TGCCGAAGAT GAGGCGGAAG GCAGGGCAAG TCTTGACGAC
1351 ATCAACGAGA CCTTGCCTCT GATGGTGGAC AGTACGGTTC AGAGTATGGC
1401 AAGGGAAAAA TATCTGACTT TGAACGGCGA CCAGATTGAT ACTGCCATTT
1451 CTCTGAAAAA CAATCAGTTG AAATTGAACG GTAAAACGTT GCAAAACGAA
1501 CCGGAGCCGG ATTTTGATGA AGGCGGTATG GTTTCAGAGC CGCAGCAGTA
1551 A

```

This corresponds to the amino acid sequence <SEQ ID 1840; ORF 590-1>:

m590-1.pep

```

1 MKKPLISVAA ALLGVALGTP YYLGVKAEES LTQQQKILQE TGFLTVESHO
51 YERGWFSTME TTVIRLKPEL LNNARKYLPD NLKTVLEQPV TLVNHITHGP
101 FAGGFGTQAY IETEFKYAPE TEKVLERFFG KQVPASLANT VYFNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNGYDA PLFKIKLADK
201 GDAAFEKVHF DSETSDGINP LALGSSNLTL EKFSLEWKEG VDYNVKLNEL
251 VNLVTDLQIG AFINPNNGSIA PSKIEVGKLA FSTKTGESGA FINSEGQFRF
301 DTLVYGDEKY GPLDIHIAAE HLDASALTVL KRKFAQISAK KMTEEQIRND
351 LIAAVKGEAS GLFTNNPVLD IKTFRFTLPS GKIDVGGKIM FKDMKKEDLN
401 QLGLMLKKTE ADIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEGRASLDD
451 INETLRMLVD STVQSMAREK YLTNGDQID TAISLKNQNL KLNKTLQNE
501 PEPDFDEGGM VSEPQQ*

```

m590-1/g590 93.6% identity in 516 aa overlap

	10	20	30	40	50	60
m590-1.pep	MKKPLISVAA	ALLGVALGTP	YYLGVKAEES	LTQQQKILQE	TGFLTVESHO	YERGWFSTME
g590	MKKPLISVAA	VLLGVALGTP	PYYLGVKAEES	LTQQQKILQKT	TGFLTVESHO	YDRGWFTSTE
	10	20	30	40	50	60
	70	80	90	100	110	120
m590-1.pep	TTVIRLKPEL	LNNARKYLPD	NLKTVLEQPV	TLVNHITHGP	FAGGFGTQAY	IETEFKYAPE
g590	TTVIRLKPELL	HNAQKYL	PDNLKIVLEQ	PVTLVNHITHGP	FAGGFGTQAH	IETEFKYAPE
	70	80	90	100	110	120
	130	140	150	160	170	180
m590-1.pep	TEKVLERFFG	KQVPASLANT	VYFNGSGKME	VSVPAFDYEE	LSGIRLHWEG	LTGETVYQKG
g590	TEKVLERFFG	KQVPVSLANT	VYFNGSGKME	VSVPAFDYEE	LSGIRLHWEG	LTGETVYQKG
	130	140	150	160	170	180
	190	200	210	220	230	240
m590-1.pep	FKSYRNGYDA	PLFKIKLADK	GDAAFEKVHF	DSETSDGINP	LALGSSNLTL	EKFSLEWKEG
g590	FKSYRNSYDA	PLFKIKLADK	GDAAFEKAH	FDSETSDGINP	LALGSSNLTL	EKFSLEWKEG
	190	200	210	220	230	240
	250	260	270	280	290	300
m590-1.pep	VDYNVKLNEL	VNLVTDLQIG	AFINPNNGSIA	PSKIEVGKLA	FSTKTGESGA	FINSEGQFRF
g590	VDYNVKLNEL	VNLVTDLQIG	AFINPNNGSIA	PSKIEVGKLA	FSTKTGESGA	FDSEGRFRF
	250	260	270	280	290	300
	310	320	330	340	350	360
m590-1.pep	DTLVYGDEKY	GPLDIHIAAE	HLDASALTVL	KRKFAQISAK	KMTEEQIRND	LIAAVKGEAS
g590	DTLVYGDEKY	GPLDIHIAAE	HLDASALTVL	KRKFAQISAK	KMTEEQIRND	LIAAVKGDAS
	310	320	330	340	350	360
	370	380	390	400	410	420
m590-1.pep	GLFTNNPVLD	IKTFRFTLPS	GKIDVGGKIM	FKDMKKEDLN	QLGLMLKKTE	ADIRMSIPQK
g590	GLFTHDPVLN	IKIFRFTLPQ	GKIDVGGKIM	FKGMKKEDLN	QLGLMLKKTE	ANIRMSIPQK
	370	380	390	400	410	420
	430	440	450	460	470	480
m590-1.pep	MLEDLAVSQA	GNIFSVNAED	EAEGRASLDD	INETLRMLVD	STVQSMAREK	YLTNGDQID
g590	MLEDLAVSQA	GNIFSVNAED	EAEARASIAD	INETLRMLVD	STVQSMAREK	YLTLDGNQID
	430	440	450	460	470	480
	490	500	510			
m590-1.pep	TAISLKNQNL	KNKTLQNE	PEPDFDEGGM	VSEPQQX		

[illegible]

g591.seq

1	TTGCAAAACC	TTCTAGCTTT	TATCTTCGCC	ATCCTGATTT	TGGTCAGCCT
51	GCACGAATTC	GGACACTACA	TCGTGCGCCG	GTTGTGCGGC	GTCAAGGTTG
101	TGCGTTTTTC	GCTCGGCTTC	GGCAAAACCG	TTTTTACC	AAAGCGCGGC
151	GACACCGAAT	GGTGCCTCGC	CCCGATTCCG	TTGGGCGGCT	ACGTCAAAAT
201	GGTCGATACG	CGCGAAGGCG	AAGTATCAGA	AGCCGATTTA	CCCTACGCTT
251	TTGACAAACA	ACACCCCGCC	AAGCGCATCG	CCATCGTGCg	CGCCGGTCCG
301	CTGACCAACC	TCGCActggc	ggTTTTTGCTg	TACGGACTGa	gctTtctctt
351	cggcqttaac	GAACTGCGGC	Cctatgtcgg	cacaqtcaaa	cccgacacc

931

```

401 ttgccgCCCG CACCGGCTTC caaagcggcg acaaAATACa atccgtcaac
451 ggcgtTtccg tCCAAGACTG GAGCAGCGCG CAAACCGAAA TCGTcctcAA
501 CCTCGAAGCC Ggcaaagtcg ccgtcggcgT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCAtcgAT GCCGCAGGCA CGCCGGAAGC CGGTAAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGGAAAAAG GCAGCCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCCTCGC ctcATGGCAG
751 GAATGggcaa acctgACccg cCAAAGCCCg ggcAAAAAAA Tcaccctgac
801 ctacgAaCGC GCcggacaaa cccaTAccgc CGACATCCGC CccgATactg
851 TCGAACagcc cgACCACACC CTGATCgggc gcgTCGGCCT CCGtcggcaG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAAA AACCCTTTCC CACTCGTGGA
1001 CAACCCTCAA ATTTTTCGGC AAATAATCA GCGGCAACGC CTCTGTCAGC
1051 CATATTTCCG GGCCGCTGAC CATTGCCGAC ATTGCCGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGGAATTTT AGCGTTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTGCTG CCCGTCCCCG TTTTGGACGG CGGGCACCTC
1201 GTGTTTTATA CTGTCGAATG GATACGCGGC AAACCTTTGG GCGAACGCGT
1251 CCAAAACATC GGTTCGCGCT TCGGGCTCGC CCTGATGATG CTGATGATGG
1301 CGGCCGCCTT CTTCAACGAC GTTACCCGGC TGATCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1842; ORF 591.ng>:

g591.pep..

```

1 LQTLAIFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFTRKRG
51 DTEWCLAPIP LGGYVKMVDI REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTVE PDTVAARTGF QSGDKIQSVN
151 GVSVDWSSA QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLTYER AGQHTADIR PDTVEQPDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVR AFGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVLNLL PVPVLDGGHL
401 VFYTVIEWIRG KPLGERVQNI GLRFLALMM LMMAAAFFND VTRLIG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1843>:

m591.seq

```

1 TTGCACACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGGTCAGCCT
51 GCACGAGTTC GGACACTACA TCGTTGCCAG ATTGTGCGGC GTCAAAGTCG
101 TACGCTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCCTCGC CCCGATTCCG TTGGGCGGTT ACGTCAAAT
201 GGTGATACG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCCTACGCTT
251 TTGACAAACA ACACCCCGCC AAGCGCATCG CCATCGTCGC CGCCGGCCCA
301 CTGACCAACC TCGCACTGGC GGTTTTGCTG TACGGACTGA GCTTTTCCTT
351 CCGCGTAACC GAACTGCGCC CCTACGTCGG CACAGTCGAA CCCGACACCA
401 TTGCCGCCCG CGCCGGCTTC CAAAGCGGCG ACAAATACA ATCCGTCAAC
451 GGCACACCCG TTGCAGATTG GGGCAGCGCG CAAACCGAAA TCGTCCTCAA
501 CCTCGAAGCC GGCAAAGTCG CCGTCGGCGT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATCGAT GCCGCAGGCA CGCCGGAAGC CGGTAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGGAAAAAG GCAGCCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCCTCGC CTCATGGCAA
751 GAATGGGCAA ACCTGACCCG CCAAAGCCCC GGCAAAAAAA TCACCCTGAA
801 CTACGAACGC GCCGGACAAA CCCATACCGC CGACATCCGC CCCGATCTG
851 TCGAACAGTC CGACCACACC CTGATCGGGC GCGTCGGCCT CCGTCCGAG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAAA AACCCTTTCC CACTCGTGGA
1001 CAACCCTCAA ATTTTTCGGC AAATAATCA GCGGCAACGC CTCCGTGAGC
1051 CATATTTCCG GGCCGCTGAC CATTGCCGAC ATTGCCGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGGAATTTT AGCACTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTACTG CCCGTCCCTG TTTTGGACGG CGGGCACCTC
1201 GTGTTTTATA CTGCCGAATG GATACGCGGC AAACCTTTGG GCGAACGCGT
1251 CCAAAACATC GGTTCGCGCT TCGGGCTCGC CCTCATGATG CTGATGATGG
1301 CGGTGCGCTT CTTCAACGAC GTTACCCGGC TGCTCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1844; ORF 591>:

m591.pep..

932

```

1  LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFFTRKRG
51 DTEWCLAPIP LGGYVKMVDV REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTV E PDTIARAGF QSGDKIQSVN
151 GTPVADWGS QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLNYER AGQTHADIR PDTVEQSDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVRA FGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVNLNL PVPVLDGGHL
401 VFYTAEWIRG KPLGERVQNI GLRFGALMM LMMAVAFFND VTRLIG*

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m591 / g591 97.3% identity in 446 aa overlap

	10	20	30	40	50	60
m591.pep	LHTLLAFIFA	ILILVSLHEF	GHYIVARLCG	VKVVRFSVGF	GKPFFFTRKRG	DTEWCLAPIP
g591	LQTLAFIFA	ILILVSLHEF	GHYIVARLCG	VKVVRFSVGF	GKPFFFTRKRG	DTEWCLAPIP
	10	20	30	40	50	60
m591.pep	LGGYVKMVDV	REGEVSEADL	PYAFDKQHPA	KRIAIVAAGP	LTNLALAVLL	YGLSFSFGVT
g591	LGGYVKMVDV	REGEVSEADL	PYAFDKQHPA	KRIAIVAAGP	LTNLALAVLL	YGLSFSFGVT
	70	80	90	100	110	120
m591.pep	ELRPYVGTV	EPDTIARAGF	QSGDKIQSVN	GTPVADWGS	QAQTEIVLNLEA	GKVAVGVQTA
g591	ELRPYVGTV	EPDTVAARTG	FQSGDKIQSVN	GVSVQDWSSA	QAQTEIVLNLEA	GKVAVGVQTA
	130	140	150	160	170	180
m591.pep	SGAQTVRTID	AAGTPEAGKI	AKNQGYIGLM	PFKITTVAGG	VEKGSPEAKA	GLKPGDRLTA
g591	SGAQTVRTID	AAGTPEAGKI	AKNQGYIGLM	PFKITTVAGG	VEKGSPEAKA	GLKPGDRLTA
	190	200	210	220	230	240
m591.pep	ADGKPIASWQ	EWANLTRQSP	GKKITLNYER	AGQTHADIR	PDTVEQSDHT	LIGRVGLRPQ
g591	ADGKPIASWQ	EWANLTRQSP	GKKITLTYER	AGQTHADIR	PDTVEQPDHT	LIGRVGLRPQ
	250	260	270	280	290	300
m591.pep	PDRAWDAQIR	RSYRPSVVRA	FGMGWEKTVS	HSWTTLKFFG	KLISGNASVS	HISGPLTIAD
g591	PDRAWDAQIR	RSYRPSVVRA	FGMGWEKTVS	HSWTTLKFFG	KLISGNASVS	HISGPLTIAD
	310	320	330	340	350	360
m591.pep	IAGQSAELGL	QSYLEFLALV	SISLGVNLNL	PVPVLDGGHL	VFYTAEWIRG	KPLGERVQNI
g591	IAGQSAELGL	QSYLEFLALV	SISLGVNLNL	PVPVLDGGHL	VFYTVIEWIRG	KPLGERVQNI
	370	380	390	400	410	420
m591.pep	GLRFGALMM	LMMAVAFFND	VTRLIGX			
g591	GLRFGALMM	LMAAAFFND	VTRLIGX			
	430	440				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1845>:
a591.seq

933

```

1   TTGCACACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGGTCAGCCT
51  GCACGAATTC GGACACTACA TCGTCGCCAG ATTGTGCGGC GTCAAGGTTG
101 TGCCTTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCCTCGC CCCGATTCCG TTGGGCGGTT ACGTCAAAAT
201 GGTGACACAG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCCTACGCTT
251 TTGACAAACA ACACCCCGCC AAGCGCATCG CCATCGTCGC CGCCGGCCCG
301 CTGACCAACC TCGCACTGGC GGTTTTGCTG TACGGACTGA GCTTTTCCTT
351 CGGCGTTACC GAACTGCGCC CCTATGTCGG CACAGTCGAA CCCGACACCA
401 TTGCCGCCCG CGCCGGCTTC CAAAGCGGCG ACAAATACA ATCCGTC AAC
451 GGCACACCCG TTGCAGATTG GGGCAGCGCG CAAACCGAAA TCGTCCTCAA
501 CCTCGAAGCC GGCAAAGTCG CCGTCGGCGT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATCGAT GCCGCAGGCA CGCCGGAAGC CGGTAAATC
601 GCAAAAACCC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGGAAAAAG GCAGCCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCATCGC CTCATGGCAA
751 GAATGGGCAA ACCTGACCCG CCAAAGCCCC GGCAAAAAAA TCACCCTGAC
801 CTACGAACGC GCCGGACAAA CCCATACCGC CGACATCCGC CCCGATACTG
851 TCGAACAGCC CGACCACACC CTGATCGGGC GCGTCGGCCT CCGTCCGCAG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAAA AACCGTTTCC CACTCGTGGA
1001 CAACCTCAA ATTTTTCGGC AAACCTAATCA GCGGCAACGC CTCCTGACG
1051 CATATTTCCG GTCCGCTGAC CATTGCCGAT ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGAATTTTTT GGCCTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTGCTG CCCGTCCCCG TTTTGGACGG CGGCCACCTC
1201 GTGTTTTATA CTGCCGAATG GATACGCGGC AAACCTTTGG GCGAACGCGT
1251 CCAAAACATC GGTTTTCGCT TCGGGCTTGC CCTCATGATG CTGATGATG
1301 CGGTGCGCTT CTTCAACGAC GTTACCCGGC TGCTCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1846; ORF 591.a>:

```

a591.pep
1   LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFTRKRKG
51  DTEWCLAPIP LGGYVKMVD T REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTV PDTIAARAGF QSGDKIQSVN
151 GTPVADWGS A QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLTyer AGQHTADIR PDTVEQPDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVRA FGMWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVNLNL PVPVLDGGHL
401 VFYTAEWIRG KPLGERVQNI GLRFGALMM LMMAVAFFND VTRLLG*

```

m591/a591 99.6% identity in 446 aa overlap

```

10      20      30      40      50      60
m591.pep LHTLLAFIFAILILVSLHEFGHYIVARLCGVKVVRFSGFGKPFTRKRGDTEWCLAPIP
|||||
a591     LHTLLAFIFAILILVSLHEFGHYIVARLCGVKVVRFSGFGKPFTRKRGDTEWCLAPIP
10      20      30      40      50      60

70      80      90      100     110     120
m591.pep LGGYVKMVDTREGEVSEADLPYAFDKQHPAKRIAIVAAGPLTNLALAVLLYGLSFSFGVT
|||||
a591     LGGYVKMVDTREGEVSEADLPYAFDKQHPAKRIAIVAAGPLTNLALAVLLYGLSFSFGVT
70      80      90      100     110     120

130     140     150     160     170     180
m591.pep ELRPYVGTVPEPDTIAARAGFQSGDKIQSVNGTPVADWGSQAQTEIVLNLEAGKVAVGVQTA
|||||
a591     ELRPYVGTVPEPDTIAARAGFQSGDKIQSVNGTPVADWGSQAQTEIVLNLEAGKVAVGVQTA
130     140     150     160     170     180

190     200     210     220     230     240
m591.pep SGAQTVRTIDAAGTPEAGKIAKNQGYIGLMPFKITTVAGGVEKGSPEAKAGLKPGDRLTA
|||||
a591     SGAQTVRTIDAAGTPEAGKIAKNQGYIGLMPFKITTVAGGVEKGSPEAKAGLKPGDRLTA
190     200     210     220     230     240

```

934

	250	260	270	280	290	300
m591.pep	ADGKPIASWQEWANLTRQSPGKKITLNYERAGQHTADIRPDTVEQSDHTLIGRVGLRPQ					
a591	ADGKPIASWQEWANLTRQSPGKKITLTYERAGQHTADIRPDTVEQPDHTLIGRVGLRPQ					
	250	260	270	280	290	300
	310	320	330	340	350	360
m591.pep	PDRAWDAQIRRSYRPSVVRAFGMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
a591	PDRAWDAQIRRSYRPSVVRAFGMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
	310	320	330	340	350	360
	370	380	390	400	410	420
m591.pep	IAGQSAELGLQSYLEFLALVSISLGVNLLPVPVLDGGHLVFYTAEWIRGKPLGERVQNI					
a591	IAGQSAELGLQSYLEFLALVSISLGVNLLPVPVLDGGHLVFYTAEWIRGKPLGERVQNI					
	370	380	390	400	410	420
	430	440				
m591.pep	GLRFGALMMLMMAVAFNDVTRLLGX					
a591	GLRFGALMMLMMAVAFNDVTRLLGX					
	430	440				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1847>:

g592.seq..

```

1  atgattccgg acgtgttcgg tcagattttt tcgggcgcggt tcaaattcga
51  cgcggcagca ggcggccttac tcggcggtct gatttcgcaa acgatgatga
101 tgggcatcaa acgcggcctg tattccaacg aggcgggtat gggttccgcg
151 ccgaacgcgc ccgcccgcgc cgaagtgaac caccctgttt cgcaaggat
201 gattcaaatg ctgggcgtgt ttgtcgatcc catcatcggt tgttcttgca
251 ccgccttcat catcttgatt taccaacagc cttatggcga tttgagcggg
301 gcggcgctga cgcaggcggc gattgtcagc caagtggggc aatggggcgc
351 gggtttcctc gccgtcatcc tgtttatggt tgccctttcc accggttatcg
401 gcaactatgc ctatgccgag tccaacgtcc aattcatcaa aagccattgg
451 ctgattaccg ccgttttccg tatgctgggt ttggcgtggg tctatttcgg
501 cgcggttgcc aatgtgcctt tggctcggga tatggcggat atggcgatgg
551 gcatcatggc gtggatcaac ctgcgcgcca tcctgctgct ctgcgcattg
601 gcgtttatgc tgctgcgcga ttacaccgcc aagctgaaaa tgggcaaaga
651 ccccgagttc aaactttccg aacatccggg cctgaaacgc cgcatacaat
701 ccgatgttg gtaa

```

This corresponds to the amino acid sequence <SEQ ID 1848; ORF 592.ng>:

g592.pep ..

```

1  MIPDVFGQIF SGAFKFDAAA GGLLGLISQ TMMGIKRL YSNEAGMGSA
51  PNAAAAAEVK HPVSQGMQM LGVFVDTIIV CSCTAFILI YQQPYGDLG
101 AALTQAIVS QVGQWAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW
151 LITAVFRMLV LAWVYFGAVA NVPLVDMAD MAMGIMAWIN LVAILLSPL
201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1849>:

m592.seq ..

```

1  ATGATTCCGG ACGTGTTCGG TCAGATTTT TCGGGCGCGT TCAAATTCGA
51  CGCGGCAGCA GCGCGCTTAC TCGGCGGTCT GATTTCGCAA ACGATGATGA
101 TGGGCATCAA ACGCGGCCTG TATTCCAACG AGGCGGGTAT GGGTTCGCG
151 CCGAACGCCG CCGCCGCCGC CGAAGTGAAA CACCCTGTTT CGCAAGGTAT
201 GATTCAAATG CTGGGCGTGT TTGTCGATAC CATCATCGTT TGTCTCTGCA
251 CCGCCTTCAT CATCTTGATT TACCAACAGC CTTACGGCGA TTTGAGCGGT
301 GCGGCGCTGA CGCAGCGGCG GATTGTCAGC CAAGTGGGGC AATGGGCGC
351 GGGCTTCCTC GCCGTCATCC TGTTTATGTT TGCCTTTTCC ACCGTTATCG
401 GCAACTATGC CTATGCCGAG TCCAACGTCC AATTATCAA AAGCCATTGG
451 CTGATTACCG CCGTTTTCGG TATGCTGGTT TTGGCGTGGG TCTATTTCCG
501 CGCGGTTGCC AATGTGCCTT TGGTCTGGGA TATGGCGGAT ATGGCGATGG
551 GCATTATGGC GTGGATCAAC CTTGTCGCCA TCCTGCTGCT CTCGCCCTTG

```

935

601 GCGTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA
 651 CCCCAGTTTC AAACCTTCCG AACATCCGGG CCTGAAACGC CGTATCAAAT
 701 CCGACGTTTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1850; ORF 592>:

m592.pep ..
 1 MIPDVFGQIF SGAFKFDAAA GLLGGLISQ TMMGIKRL YSNEAGMGS
 51 PNAAAAAEVK HPVSQGMQIM LGVFVDTIIV CSCTAFIILI YQPPYGDLSG
 101 AALTQAAIVS QVGQWGAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW
 151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL
 201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW*

m592 / g592 100.0% identity in 237 aa overlap

	10	20	30	40	50	60
m592.pep	MIPDVFGQIFSGAFKFDAAA	GLLGGLISQTMMGIKRL	YSNEAGMGSAPNA	AAAAAEVK		
g592	MIPDVFGQIFSGAFKFDAAA	GLLGGLISQTMMGIKRL	YSNEAGMGSAPNA	AAAAAEVK		
	10	20	30	40	50	60
	70	80	90	100	110	120
m592.pep	HPVSQGMQIMLGVFVDTIIV	CSCTAFIILIYQPPYGDLS	GAAALTQAAIVSQVGQWGAGFL			
g592	HPVSQGMQIMLGVFVDTIIV	CSCTAFIILIYQPPYGDLS	GAAALTQAAIVSQVGQWGAGFL			
	70	80	90	100	110	120
	130	140	150	160	170	180
m592.pep	AVILFMFAFSTVIGNYAYAES	SNVQFIKSHWLITAVFRMLV	LAWVYFGAVANVPLVWDMAD			
g592	AVILFMFAFSTVIGNYAYAES	SNVQFIKSHWLITAVFRMLV	LAWVYFGAVANVPLVWDMAD			
	130	140	150	160	170	180
	190	200	210	220	230	
m592.pep	MAMGIMAWINLVAILLLSPL	AFMLLRDYTAKLKM	GKDPEFKLSEHPGLKRRIKSDVW			
g592	MAMGIMAWINLVAILLLSPL	AFMLLRDYTAKLKM	GKDPEFKLSEHPGLKRRIKSDVW			
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1851>:

a592.seq
 1 ATGATTCCGG ACGTGTTCGG TCAGATTTTT TCGGGCGCGT TCAAATTCGA
 51 CGCGGCAGCA GGCGGCTTAC TCGGCGGTCT GATTTCGCAA ACGATGATGA
 101 TGGGCATCAA ACGCGGCCCTG TATTCCAACG AGGCGGGTAT GGTTCCGCG
 151 CCGAACGCCG CCGCCGCCGC CGAAGTGAAG CACCCTGTTT CGCAAGGTAT
 201 GATTCAAATG CTGGGCGTGT TTGTCGATAC CATCATCGTT TGTCTTGCA
 251 CCGCCTTCAT CATCTTGATT TACCAACAGC CTTACGGCGA TTTGAGCGGT
 301 GCGGCGCTGA CGCAGGCGGC GATTGTCAGC CAAGTGGGGC AATGGGGCGC
 351 GGGCTTCCTC GCCGTCATCC TGTATTGTT TGCCTTTTCC ACCGTTATCG
 401 GCAACTATGC CTATGCCGAG TCCAACGTCC AATTCATCAA AAGCCATTGG
 451 CTGATTACCG CCGTTTTCCG TATGCTGGTT TTGGCGTGGG TCTATTTCCG
 501 CGCGGTTGCC AATGTGCCTT TGGTCTGGGA TATGGCGGAT ATGGCGATGG
 551 GCATTATGGC GTGGATCAAC CTTGTCGCCA TCCTGCTGCT CTCGCCCTTG
 601 GCGTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA
 651 CCCCAGTTTC AAACCTTCCG AACATCCGGG CCTGAAACGC CGTATCAAAT
 701 CCGACGTTTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1852; ORF 592.a>:

a592.pep
 1 MIPDVFGQIF SGAFKFDAAA GLLGGLISQ TMMGIKRL YSNEAGMGS
 51 PNAAAAAEVK HPVSQGMQIM LGVFVDTIIV CSCTAFIILI YQPPYGDLSG
 101 AALTQAAIVS QVGQWGAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW
 151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL
 201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW*

m592/a592 100.0% identity in 237 aa overlap

936

	10	20	30	40	50	60
m592.pep	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMMMGIKRGLYSNEAGMGSAPNAAAAAEVK					
a592	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMMMGIKRGLYSNEAGMGSAPNAAAAAEVK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m592.pep	HPVSQGMIOQLGVFVDTIIVCSCTAFIILIYQQPYGDLSGAALTQAAIVSQVGQWGAGFL					
a592	HPVSQGMIOQLGVFVDTIIVCSCTAFIILIYQQPYGDLSGAALTQAAIVSQVGQWGAGFL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m592.pep	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFERMLVLAWVYFGAVANVPLVWDMAD					
a592	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFERMLVLAWVYFGAVANVPLVWDMAD					
	130	140	150	160	170	180
	190	200	210	220	230	
m592.pep	MAMGIMAWINLVAILLSPLAFMLLRDYTAKLMGKDPEFKLSEHPGLKRRIKSDVWX					
a592	MAMGIMAWINLVAILLSPLAFMLLRDYTAKLMGKDPEFKLSEHPGLKRRIKSDVWX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1853>:

```

g593.seq..
1  atgcttgaac tgaacggact ctgcaaatgc ttcggcggca aaacggtcgc
51  cgacaacatc tgcctgactg tcgggcgcgg caaaatactc gccgtactgg
101 ggcggtcggg ctgcggcaaa tccaccctgc tgaatatgat tgcgggcatc
151 gtccggccgg acggcgcgca aattcggctg aacggggaaa acattacctg
201 tatgccgccc gaaaaacgcc gtatctcgct gatgtttcaa gattacgcgc
251 tgtttcccca tatgagtgcg ctgaaaataa cggcattcgg tttgaaaatg
301 caaaaaatgc cgaaagccga agccgaacgc ctcgccttgt cggcacttgc
351 cgaagtgcgg ctggaaaacg aggcgcaccg caagcctgaa aaactttccg
401 gaggcgagaa gcaacggttg gcactggcgc gcgctttggt tgtccgcctc
451 tccctgctgt tgetggatga atcgttttcc agtttggaca cgcatttgcg
501 cgaccggctg cgccgtatga ccgccgaacg catccgcaag ggcggcatcc
551 ctgccgtttt ggtaacgcac tcgcccgaag aggcctgcac ggcggcggac
601 gaaatcgccg tcatgcacga ggggaaaatc cttcaatgcg gtacgcccga
651 aaccttgatt caaacgcctg ccggcggtga ggtcgcccgt ctgatggggc
701 tgcccaatac cgacgatgac cgccatattc cgcaaaatgc cgtgtgcttg
751 gacaatcatg gaacggaatg ccgtctgctg tccctcgtec gcctgcccga
801 ctgcgtccgg ctttcgcccg tccatcccga acacggcgag ctgaccttaa
851 acctgactgt cggacaacat acggacggta tttccggaaa cggtagcgtc
901 cgcattccgc tcgatgaagg gcgtatcgtc cgtttccgat ga

```

This corresponds to the amino acid sequence <SEQ ID 1854; ORF 593.ng>:

```

g593.pep..
1  MLELNLCKC FGGKTVADNI CLTVGRGKIL AVLGRSGCGK STLLNMIAGI
51  VRPDGGEIRL NGENITCMPP EKRRISLMFQ DYALFPHMSA LENTAFGLKM
101 QKMPKAEAEER LALSALAEVG LENEHRKPE KLSGGEKQRL ALARALVVRP
151 SLLLLDESFS SLDTHLRDRL RRMTAERIRK GGIPAVLVTH SPEEACTAAD
201 EIAVMHEGKI LQCGTPETLI QTPAGVQVAR LMGLPNTDDD RHIPQNAVCL
251 DNHGTECRLL SLVRLPDSL RLSAVHPEHGE LTLNLTVGQH TDGISNGTV
301 RIRVDEGRIV RFR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1855>:

```

m593.seq
1  ATGCTTGAAC TGAACGGACT CTGCAAACGC TTCGGAATA AAACCGTCGC
51  CGACAACATC TGCCTGACTG TCGGGCGCGG CAAAATACTC GCCGTTTGG
101 GCGGTCGGG CTGCGGAAAA TCCACCCTGC TGAATATAAT TGCGGGGATT
151 GTCCGGCCGG ACGGCGGGGA AATATGGCTG AACGGAGAAA ACATTACCCG

```


937

```

201 TATGCCGCC GAAAAACGCC GTATCTCGCT GATGTTTCAA GATTACGCGC
251 TGTTCCTCCA TATGAGTGCG CTGGAAAATG CGGCATTCCG TTTGAAAATG
301 CAAAAAATGC CGAAAGCCGA AGCCGAACGC CTCGCCATGG CGGCACTTGC
351 CGAAGTCGGA CTGGAAAACG AGGCGCACCG CAAGCCTGAA AAACCTTTCCG
401 GAGGCGAGAA GCAACGGCTG GCGTTGGCGC GCGCTTTGGT TGTCCGCCCT
451 TCCCTGCTGC TGTGGACGA ATCGTTTTC AGTTTGGACA CGCATTTGCG
501 CGGCACGCTG CGCCGTATGA CTGCCGAACG TATCCGAAAC GCGCGCATCC
551 CTGCCGTTTT GGTAAACGCAT TCGCCCGAAG AAGCCTGTAC GACGGCAGAC
601 GAAATCGCCG TGATGCATAA AGGGAGGATT CTACAATACG GTACGCCCGA
651 AACATTGGTC AAAACACCAT CCTGCGTGCA GGTGCGCCGA CTGATGGGTT
701 TGCCCAATAC CGACGATAAC CGCCATATTC CGCAACATGC GGTGCGTTTC
751 GACCAAGACG GCATGGAGTG CCGCGTATTA TCCCGTACCT GTTTGCCCGA
801 ATCGTTCAGC CTGTCGTCC TCCATCCGGA ACACGGCATC CTGTGGCTGA
851 ACCTCGATAT GCGGCACGCC GGGGCGGTAT CGGGCAAGGA TACGGTACGC
901 ATCCATATCG AAGAACGGGA AATCGTCCGC TTCCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1856; ORF 593>:

```

m593.pep ..
  1 MLELNLCKR FGNKTVADNI CLTVGRGKIL AVLGRSGCGK STLLNIIAGI
 51 VRPDGGEIWL NGENITRMPP EKRRISLMFQ DYALFPHMSA LENAALVVRP
101 QKMPKAEAEER LAMAALAEVG LENEHRKPE KLSGGEKQRL ALARALVVRP
151 SLLLLDESFS SLDTHLRGTL RRMTAERIRN GGIPAVLVTH SPEEACTTAD
201 EIAVMHKGRI LQYGPETLV KTPSCVQVAR LMGLPNTDDN RHIPQHVRFE
251 DQDGMCECVL SRTCLPESFS LSVLHPEHGI LWNLDMRHA GAVSGKDTVR
301 IHIEEREIVR FR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m593 / g593 83.4% identity in 313 aa overlap

	10	20	30	40	50	60
m593.pep	MLELNLCKRFGNKTVDNICLTVGRGKILAVLGRSGCGKSTLLNIIAGIVRPDGGGEIWL					
g593	MLELNLCKCFGGKTVADNICLTVGRGKILAVLGRSGCGKSTLLNMIAGIVRPDGGGEIRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m593.pep	NGENITRMPPEKRRISLMFQDYALFPHMSALENAALVVRPSLLLLDESFS					
g593	NGENITCMPPEKRRISLMFQDYALFPHMSALENTAFGLKMQKMPKAEAEERLALSALAEVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m593.pep	LENEHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFS					
g593	LENEHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m593.pep	GGIPAVLVTHSPEEACTTADEIIVMHKGRIQLQYGPETLVKTPSCVQVARLMGLPNTDDN					
g593	GGIPAVLVTHSPEEACTTADEIIVMHKGRIQLQYGPETLVKTPSCVQVARLMGLPNTDDN					
	190	200	210	220	230	240

	250	260	270	280	290	299
m593.pep	RHIPQHAVRFDQDGM	ECRVLSRTCLPESF	SLSVLHPEHGILWL	NLDM-RHAGAVSGKD	TV	
	: : :	: : :	: ::	: : : :	:	
g593	RHIPQNAVCLDNHGT	ECRLLSLVRLPDSL	RLRSVAVHPEHGEL	TNLTVGQHTDGISG	NGTV	
	250	260	270	280	290	300
	300	310				
m593.pep	RIHIEEREIVRFRX					
	:: :					
g593	RIRVDEGRIVRFRX					
	310					

```
a593.seq
1  ATGCTTGAAC  TGAACGGACT  CTGCAAACGC  TTCGGCGGCA  AAACGGTTGC
51  CGACGATATC  TGCCTGACTG  TCGGGCGCGG  CAAATACTC  GCCGTTTGG
101 GCGGTCGGG  TCGCGGCAAA  TCCACCTGCT  TCGAATATGAT  TCGGGCATCG
151 GTCCGGCCGG  ACGGCGGGGA  AATATGGCTG  AATGGGGAAA  CATTACCCG
201 TATGCCGCC  GAAAAACGCC  GTATTTCTGCT  GATGTTTCAA  GATTACGCGC
251 TGTTTCCCA  TATGAGTGCA  CTGGAATAATG  CGGCATTTCG  TTTGAAAATG
301 CAAAAAATGC  CGAAAGCCGA  AGCCGAAAGC  CTCGCCATGG  CGGCACTTGC
351 CGAAGTCGGA  CTGGAATAACG  AGGCGCACCG  CAAGCCTGAN  AAACCTTCCG
401 GAGGCGAAAA  GCAACGGTTG  GCACTGGCGC  GCGCTTTGGT  TGTCCGCCCT
451 TCCCTGCTGC  TGTTGGACGA  ATCGTTTTCC  AGTTTGGACA  CGCATTTGCG
501 CGACCGGCT  CGCCGCATGA  CTGCCGAACG  TATCCGCAAG  GCGGCGATCC
551 CTGCCGTTT  TGTATACGCAT  TCGCCCGAAG  AGGCCCTGCAC  GCGCGCAGAC
601 GAAATCGCC  TCGATCGACGA  GGGGAAATC  GTTCAATGCG  GTACGCCCGA
651 AACCTTGGT  CAAACGCCTG  CCGGCGTGCA  GGTTCGCCAT  CTGATGGGGC
701 TGCCCAATAC  CGACGATGAC  CGCCATATTC  CGCAACATGC  GGTGCGTTTC
751 GACCAAGAC  GCATGGAATG  CCGCGTATTA  TCCCCTACCT  GTTTGCCCGA
801 ATCGTTTCA  CTGTCCGTCC  TGCATCCGGA  ACACGGCATC  CTGTGGCTGA
851 ACCTCGATAT  GCGCGACGCC  TGGAAATAT  CGGGAACAGA  TACGGTACGC
901 ATCCATATCG  AAGACAGGGA  AATCGTCCGC  TTCCGCTGA
```

a593.pep

1	MLELNLCKR	FGGKTVADDI	CLTVGRGKIL	AVLGRSGCGK	STLLNMIAGI
51	VRPDGGEIWL	NGENITRMPP	EKRISLMFQ	DYALFPHMSA	LENAAFGLMK
101	QKMPKAAEAS	LAMAALAEVG	LENAHRKPX	KLSGGEKQRL	ALARALVVRP
151	SLLLLDESFS	SLDTHLRDRL	RRMTAERIRK	GGIPAVLVTH	SPEEACTAAD
201	EIAVMHEGKI	LQCGTPETLV	QTPAGVQVAH	LMGLPNTDDD	RHIPOHAVRF
251	DQDGMECRVL	SRCTLPESFS	LSVLHPHEGI	LWLNLDMPHA	GEISGNDTVR
301	IHEDREIVR	FR*			

	10	20	30	40	50	60
m593.pep	MLELNLGCKRFRGKNTVADNICLTVGRGKILAVLGRSGCGKSTLLNIIAGIVRPDGGGEIWL					
a593	MLELNLGCKRFRGGKTVADDICLTVGRGKILAVLGRSGCGKSTLLNMIAGIVRPDGGGEIWL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m593.pep	NGENITRMPPEKRRISLMFQDYALFPHMSALENAAFGLKMQKMPKAEAEERLAMAALAEVG					
a593	NGENITRMPPEKRRISLMFQDYALFPHMSALENAAFGLKMQKMPKAEAESLAMAALAEVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m593.pep	LENEAHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFSLLDTHLRGTLRRMTAERIRN					
a593	LENEAHRKPXKLSGGEKQRLALARALVVRPSLLLLDESFSLLDTHLRDRLRRMTAERIRK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m593.pep	GGIPAVLVTHSPPEEACTTADEIAVMHKGRILQYGTPTLVKTPSCVOVARLMGLPNTDDN					

939

```

|||||:|||||:|:| | |||||:|:| | |||||:|||||:
a593  GGIPAVLVTHSP EEACTAADEI AVMHEGKILQCGT PETLVQTPAGVQVAHLMGLPNTDDD
      190      200      210      220      230      240

      250      260      270      280      290      300
m593.ppep RHIPQHAVRFDQDGM ECRVLSRTCLPESFSLSVLHPEHGILWLNLDMRHAGAVSGKDTV
a593  RHIPQHAVRFDQDGM ECRVLSRTCLPESFSLSVLHPEHGILWLNLDMPHAGEISGNDTV
      250      260      270      280      290      300

      310
m593.ppep IHIEEREIVRFRX
      ||||:|||||
a593  IHIEDREIVRFRX
      310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1859>:

```

g594.seq..
1  atgggtgcag ataccgatgg cgacaaggat gttcggctta atcgaacggg
51  tctcgttttt agcatactcc ggctgctgtt ccgcacgcga attgggatcg
101 gtaagttcgc cgttcaggcc tttcaggtct ttaagctgct gatctgtacg
151 gttgagcacc caaatcgggt tgccttgcca ctccgcggtc agcagctgac
201 ccgcttcgat tttactgaca tccacctcga cggcagcacc ggaggccttg
251 gctttttccg aagggaaaaa actggccaca aacggcggtg ccacacccaa
301 tgctgccact ccgcccgcg cgcaggtcgc aagtgtcagg aaacggcggc
351 ggccgttggt gatttcttga ttatccatta ttcagtcgtc ctaatatattt
401 gggaatgccg agccattaaa cattgcaatt ttaccaggtt tgcagtgata
451 ctcaaagcat tatttaaaat aaggtaa

```

This corresponds to the amino acid sequence <SEQ ID 1860; ORF 594.ng>:

```

g594.pep
1  MGADTDGDKD VRLNRTGLVF SILRLLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHPNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFRREK TGHKRRCHTQ
101 CCHSARAAGR KCQETAAAVV DFLIIHYSVV LIFWECRAIK HCNFTQFAVI
151 LKALFKIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1861>:

```

m594.seq
1  ATGGGTGCAG ATACCGATGG CGACAAGGAT GTTCGGCTTA ATCGAACGGG
51  TCTCGTTTTT AGCATACTCC GGCTGCTGTT CCGCATCGGA ATTGGGATCG
101 GTAAGTTCGC CGTTCAGGCC TTTCAGGTCT TTAAGCTGCT GATCTGTACG
151 GTTGAGCACC CAAATCGGTT TGCCTTGCCA CTCGGCGGTC AGCAGCTGAC
201 CCGCTTCGAT TTTACTGACA TCCACCTCGA CGGCAGCACC GGCGGCCTTG
251 GCTTTTCCG AAGGGAAAAA ACTGGCCACA AACGGCGTTG CCACACCCAA
301 TGCTGCCACT CCGCCCGCGC CGCAGGTGCG GAGTGTGAGG AAACGGCGGC
351 GGCCGTGTGT GATTCTTGA TTATCCATTA TTCAGTCGTC CTAATATTTT
401 GGGAATACCG AGCCATTAAA CGTTGCAATT TTACCCAGTT TGCAGTGATA
451 CTCAAAGCAT TATTTAAAT AAGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1862; ORF 594>:

```

m594.pep
1  MGADTDGDKD VRLNRTGLVF SILRLLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHPNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFRREK TGHKRRCHTQ
101 CCHSARAAGR ECQETAAAVV DFLIIHYSVV LIFWEYRAIK RCNFTQFAVI
151 LKALFKIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m594 / g594 98.1% identity in 158 aa overlap

940

	10	20	30	40	50	60
m594.pep	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
g594	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m594.pep	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
g594	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRKQETAAAVV					
	70	80	90	100	110	120
	130	140	150	159		
m594.pep	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
g594	DFLIHYSVVLIFWECRAIKHCNFTQFAVILKALFKIRX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1863>:

```

a594.seq
1  ATGGGTGCAG ATACCGATGG CGACAAGGAT GTTCGGCTTA ATCGAACGGG
51  TCTCGTTTTT AGCATACTCC GGCTGCTGTT CCGCATCGGA ATTGGGATCG
101  GTAAGTTCGC CGTTCAGGCC TTTCAGGTCT TTAAGCTGCT GATCTGTACG
151  GTTGAGCACC CAAATCGGTT TGCCTTGCCA CTCGGCGGTC AGCAACTGAC
201  CCGCTTCGAT TTTACTGACA TCCACCTCGA CGGCAGCACC GGCAGCCTTG
251  GCTTTTCCG AAGGGAAAAA ACTGGCCACA AACGGCGTTG CCACACCCAA
301  TGCTGCCACT CCGCCCGCGC CGCAGGTGCG GAGTGTCAGG AAACGGCGGC
351  GGCCGTGTGTT GATTTCCTGA TTATCCATTA TTCAGTCGTC CTAATATTTT
401  GGGAAATACCG AGCCATTAAA CGTTGCAATT TTACCCAGTT TGCAGTGATA
451  CTCAAAGCAT TATTTAAAT AAGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1864; ORF 594.a>:

```

a594.pep
1  MGADTDGDKD VRLNRTGLVF SILRLLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHPNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFRREK TGHKRRCHTQ
101  CCHSARAAGR ECQETAAAVV DFLIIHYSV LIFWEYRAIK RCNFTQFAVI
151  LKALFKIR*

```

m594/a594 100.0% identity in 158 aa overlap

	10	20	30	40	50	60
m594.pep	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
a594	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m594.pep	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
a594	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
	70	80	90	100	110	120
	130	140	150	159		
m594.pep	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
a594	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1865>:

```

g595.seq.
1  atgagaaaat tcaatttgac cgcattgtcc gtgatgcttg ccttggtttt
51  gaccgcgtgc cagccgccgg aggcggagaa agccgcgccg gccgcgtccg
101  gtgagaccca atccgccaa cgaaggcggtt cggtcggtat cgccgtcaac

```

```
151 gacaatgcct gcgaaccgat gaatctgacc gtgccgagcg gacaggttgt
201 gttcaatatt aaaaacaaca gcggccgcaa gctcgaatgg gaaatcctga
251 agggcggtgat ggtggtggac gaacgcgaaa atatcgcccc ggggctttcc
301 gacaaaatga accgtaacct gctgccgggc gaatacgaaa tgacctgcgg
351 ccttttgacc aatccgcgcg gcaagctggt ggtagccgac agcggcttta
401 aagacaccgc caacgaagcg gatttgaaa aactgcccc accgctcgcc
451 gactataaaag cctacgttca aggcgagggt aaagagctgg cggcgaaaac
501 caaaaccttt accgaagccg tcaaagcagg cgacattgaa aaggcgaat
551 ccctgtttgc cgccaccgc gtccattacg aacgcacga accgattgcc
601 gagcttttca gcgaactcga ccccgtcac gatgctgtg aagacgactt
651 caaagacggt gcgaaagatg ccgggtttac cggcttcac cgtatcgaac
701 acgccctttg ggtggaaaaa gacgtatccg gcgtgaagga aaccgcggcc
751 aaactgatga ccgatgtcga agccctgcaa aaagaaatcg acgattggc
801 gttccctccg ggcaaagtgg tcggcggcgc gtccgaactg attgaagaag
851 cggcggggcag taaaatcagc ggcgaagaag accgttacag ccacaccgat
901 ttgagcgact tccaagctaa tgcggacgga tctaaaaaaa tcgtcgattt
951 gttccgtccg ttgattgagg caaaaaaca agccttggtg gaaaaaaccg
1001 ataccaactt caaacaggtc aacgaaatc tggcgaaata ccgcacaaaa
```

942

1051 gacggttttg aaacctacga caagctgagc gaagccgacc gcaaagcatt
 1101 acaggctcct attaacgcgc ttgccgaaga ccttgcccaa cttcgcgga
 1151 tactcggtt gaaataa

This corresponds to the amino acid sequence <SEQ ID 1866; ORF 595.ng>:

g595.pep ..
 1 MRKFNLALS VMLALGLTAC QPPEAEKAAP AASGETQSAN EGGSVGI AVN
 51 DNACEPMNLT VPSGQVVFNI KNNSGRKLEW EILKGVMVVD ERENIAPGLS
 101 DKMNRNLLPG EYEMTCGLLT NPRGKLVVAD SGFKDTANEA DLEKLQPLA
 151 DYKAYVQGEV KELAAKTKTF TEAVKAGDIE KAKSLFAATR VHYERIEPIA
 201 ELFSELDPVI DACEDDFKDG AKDAGFTGFH RIEHALWVEK DVSGVKETAA
 251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEAAGSKIS GEEDRYSHTD
 301 LSDFQANADG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
 351 DGFETYDKLS EADRKALQAP INALAEDLAQ LRILGLK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1867>:

m595.seq
 1 ATGAGAAAAT TCAATTGAC CGCATGTGCC GTGATGCTTG CCTTAGGTTT
 51 GACCGCGTGC CAGCCGCCGG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
 101 GTGAGGCGCA AACCGCCAAC GAGGGCGGTT CGGTCAATAT CGCCGTCAAC
 151 GACAATGCCT GCGAACCGAT GGAAGTACC GTGCCGAGCG GACAGGTTGT
 201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
 251 AAGCGGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
 301 GATAAAATGA CCGTACCCCT GTTGCCGGGC GAATACGAAA TGACTTGCGG
 351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA
 401 AAGACACCGC CAACGAAGCG GATTGGAAA AACTGTCCCA ACCGCTCGCC
 451 GACTATAAAG CCTACGTTCA AGGCGAGGTT AAAGAGCTGG TGGCGAAAAC
 501 CAAAACCTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGCGGAAAT
 551 CCCTGTTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
 601 GAGCTTTTCA GCGAACTCGA CCCCGTCATC GATGCGCGTG AAGACGACTT
 651 CAAAGACGGC GCGAAAGATG CCGGATTAC CCGCTTTCAC CGTATCGAAT
 701 ACGCCCTTTG GGTGGAAAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
 751 AAAGTATGTA CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGATTGGC
 801 GTTTCCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGAACTG ATTGAAGAAG
 851 TGGCGGGCAG TAAATCAGC GGCGAAGAAG ACCGGTACAG CCACACCGAT
 901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCTAAAAAAA TCGTCGATTT
 951 GTTCCGTCCG CTGATCGAGG CCAAAAACAA AGCCTTGTTG GAAAAAACCG
 1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
 1051 GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
 1101 ACAGGCCTCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTGCGGGCA
 1151 TACTCGGCTT GAAATAA

This corresponds to the amino acid sequence <SEQ ID 1868; ORF 595>:

m595.pep
 1 MRKFNLALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSI AVN
 51 DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGVMVVD ERENIAPGLS
 101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
 151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
 201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
 251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEVAGSKIS GEEDRYSHTD
 301 LSDFQANVDG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
 351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRILGLK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m595 / g595 95.4% identity in 388 aa overlap

	10	20	30	40	50	60
m595.pep	MRKFNLALS	VMLALGLTAC	QPPEAEKAAP	AASGEAQTAN	EGGSVSI	AVNDNACEPMELT
g595	MRKFNLALS	VMLALGLTAC	QPPEAEKAAP	AASGETQSAN	EGGSVGI	AVNDNACEPMNLT
	10	20	30	40	50	60
	70	80	90	100	110	120

943

m595.pep	VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT
g595	VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMNRNLLPGEYEMTCGLLT
	70 80 90 100 110 120
m595.pep	130 140 150 160 170 180
	NPRGKLVVTD SGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE
g595	NPRGKLVVAD SGFKDTANEADLEKLPQPLADYKAYVQGEVKELAAKTKTFTEAVKAGDIE
	130 140 150 160 170 180
m595.pep	190 200 210 220 230 240
	KAKSLFADTRVHYERIEPIAE L FSELD PVIDAREDDFKD GAKDAGFTGFHRIEYALWVEK
g595	KAKSLFAATRVHYERIEPIAE L FSELD PVIDACEDDFKD GAKDAGFTGFHRIEHALWVEK
	190 200 210 220 230 240
m595.pep	250 260 270 280 290 300
	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVG GASELIEEVAGSKISGEEDRYSHTD
g595	DVSGVKETAAKLMTDVEALQKEIDALAFPPGKVVG GASELIEEAAGSKISGEEDRYSHTD
	250 260 270 280 290 300
m595.pep	310 320 330 340 350 360
	LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTD TNFKQVNEILAKYRTK DGFETYDKLG
g595	LSDFQANADGSKKIVDLFRPLIEAKNKALLEKTD TNFKQVNEILAKYRTK DGFETYDKLS
	310 320 330 340 350 360
m595.pep	370 380 389
	EADRKALQASINALAEDLAQLRGILGLKX
g595	EADRKALQAPINALAEDLAQLRGILGLKX
	370 380

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1869>:

```

a595.seq
1  ATGAGAAAAT TCAATTTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
51  GACCGCGTGC CAGCCGCCGG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
101 GTGAGGCGCA AACCGCCAAC GAGGGCGGTT CGGTCAGTAT CGCCGTC AAC
151 GACAATGCCT GCGAACCGAT GGAAGTACC GTGCCGAGCG GACAGGTTGT
201 GTTCAATATT AAAAACACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
301 GATAAAATGA CCGTCACCCT GTTGCCGGGC GAATACGAAA TGACTGCGG
351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTTGGAAA AACTGTCCCA ACCGCTCGCC
451 GACTATAAAG CCTATGTCA AGGCGAAGTC AAAGAGCTGG TGGCGAAAAC
501 CAAAACCTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAT
551 CCCTGTTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCCCCTCATC GATGCGCGTG AAGACGACTT
651 CAAAGACGGC GCGAAAGATG CCGGATTTAC CGGCTTCCAC CGTATCGAAT
701 ACGCCCTTTG GGTGGAAAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
751 AAAGTATGAT CCGATGTCTG AGCCCTGCAA AAAGAAATCG ACGCATTGGC
801 GTTTCTCTCG GGCAAGGTGG TCGGCGGCGC GTCCGAAGT ATTGAAGAAG
851 TGGCGGGCAG TAAAATCAGC GGCGAAGAAG ACCGGTACAG CCACACCGAT
901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCGAAAAAAA TCGTCGATTT
951 GTTCCGTCCT TTGATCGAGA CCAAAAACAA AGCCTTGTTG GAAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
1051 GACGGTTTGA AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
1101 ACAGGCCTCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTGCGGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1870; ORF 595.a>:

```

a595.pep
1  MRKFNL TALS VMLALGLTAC QPPEAEKAAP AASGEAQ TAN EGGSVSI AVN
51  DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGMVVD ERENIAPGLS

```

944

```

101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
251 KLMTDVEALQ KEIDALAFPP GKVVGASEL IEEVAGSKIS GEEDRYSHTD
301 LSDFQANVDG SKKIVDLFRP LIETKNKALL EKTDNFKQV NEILAKYRTK
351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK*

```

m595/a595 99.7% identity in 388 aa overlap

	10	20	30	40	50	60
m595.pep	MRKFNL	TALSVMLALGLT	ACQPPEAEKA	APASGEAQTANEGGS	SVSIAVNDNACEP	MELT
a595	MRKFNL	TALSVMLALGLT	ACQPPEAEKA	APASGEAQTANEGGS	SVSIAVNDNACEP	MELT
	10	20	30	40	50	60
	70	80	90	100	110	120
m595.pep	VPSGQV	VFNKNNSGRKLEWEIL	KGVMVVDERENI	APGLSDKMTVTLLPGEY	EMTCGLLT	
a595	VPSGQV	VFNKNNSGRKLEWEIL	KGVMVVDERENI	APGLSDKMTVTLLPGEY	EMTCGLLT	
	70	80	90	100	110	120
	130	140	150	160	170	180
m595.pep	NPRGKL	VVTD SGFKDTANEA	DLEKLSQPLADY	KAYVQGEVKELVAK	TKTFTEAVKAGDIE	
a595	NPRGKL	VVTD SGFKDTANEA	DLEKLSQPLADY	KAYVQGEVKELVAK	TKTFTEAVKAGDIE	
	130	140	150	160	170	180
	190	200	210	220	230	240
m595.pep	KAKSLF	ADTRVHYERIEPIA	ELFSELDPVIDARE	DDFKDGA	KDAGFTGFHRIEYALWVEK	
a595	KAKSLF	ADTRVHYERIEPIA	ELFSELDPVIDARE	DDFKDGA	KDAGFTGFHRIEYALWVEK	
	190	200	210	220	230	240
	250	260	270	280	290	300
m595.pep	DVSGVKEIAAKLMTD	VEALQKEIDALAFPP	GKVVGASELIEEVAGSKIS	GEEDRYSHTD		
a595	DVSGVKEIAAKLMTD	VEALQKEIDALAFPP	GKVVGASELIEEVAGSKIS	GEEDRYSHTD		
	250	260	270	280	290	300
	310	320	330	340	350	360
m595.pep	LSDFQANVDGSKKIVDL	FRPLIEAKNKALLEKTD	NFKQVNEILAKYRTK	DGFETYDKLG		
a595	LSDFQANVDGSKKIVDL	FRPLIETKNKALLEKTD	NFKQVNEILAKYRTK	DGFETYDKLG		
	310	320	330	340	350	360
	370	380	389			
m595.pep	EADRKALQAS	INALAEDLAQLRGILGLKX				
a595	EADRKALQAS	INALAEDLAQLRGILGLKX				
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1871>:

g596.seq. (partial).

```

1  ..atgctgctct tggacgagcc gaccaaccac ttggatgctg aatcggtgga
51  atggctggag caattcctcg tgcgcttccc cggcacagtg gtcgcggtaa
101 cgcacgaccg ctacttctc gacaacgccg ccgaatggat tttggaactc
151 gaccgctggac acggcattcc gtggaaaggc aattactcgt cttggctgga
201 gcagaaagaa aaacgcttgg aaaacgaggc gaaatccgaa gccgcgcgcg
251 tgaaggcgat gaagcaggaa ttggaatggg tgcgccaaaa tgccaaaggc
301 cgccaagcca agcccaaagc gcgtttggcg cgttttgaag aaatgagcaa
351 ctacgaatac caaaaacgca acgaaactca ggaaatcttt atccctgttg
401 ccgagcggtt gggtaacgaa gtgattgaat ttgtgaatgt ttccaaatcg

```


945

```

451      ttcggcgata aagtgtgat tgacggtttg agcttcaaag tgccggcgagg
501      cgcgattgtc ggcatcatcg gcccgaacgg cgcggtataa tcgacgctgt
551      tcaaaatgat tcggggcaaa gagcagcccg attcgggcca agtgaaaatc
601      gggcaaacgg tgaaaatgag cttgattgac caaagccgag aagggtttgca
651      aaacgacaaa accgtgttcg acaacattgc cgaaggtcgc gatattttgc
701      aggtcggaca gtttgaaatc cccgcccggc aatatttggg acgcttcaac
751      tttaaaggca gcgaccaaag caaaatcgca aggcagcttt ccggcgcgca
801      acgcgccgct ctgcacttgg caaaaacctt gttgggaggc ggcaatgtgt
851      tgctgctgga cgaaccgtcc aacgatctcg acgtggaaac cctgcgcgag
901      ttggaagacg cattgttggg atttgccggc agcgtgatgg tgatttcgca
951      cgaccgctgg tttctcgacc gcatagccac gcatatcttg gcgtgtgaag
1001     gcgactccaa atgggtgttc ttcgacggca actatcaaga atacgaagcc
1051     gacaagaaac gccgactcgg caaagaaggc gcgaaaccga aacgcatcaa
1101     atacaaaccg gtaacgcgtt aa

```

This corresponds to the amino acid sequence <SEQ ID 1872; ORF 596.ng>:

g596.pep (partial).

```

1      ..MLLLDEPTNH LDAESVEWLE QFLVRFPGT VAVTHDRYFL DNAAEWILEL
51     DRGHGIPWKG NYSSWLEQKE KRLNEAKSE AARVKAMKQE LEWVRONAKG
101    RQAKPKARLA RFEEMSNEYE QKRNETQEIF IPVAERLGNE VIEFVNVSKS
151    FGDKVLIDGL SFKVPAGAIV GIIGPNGAGK STLFKMIAGK EQPDSGEVKI
201    GQTVKMSLID QSREGLQNDK TVFDNIAEGR DILQVQFEI PARQYLGRFN
251    FKGSQSKIA RQLSGGERGR LHLAKTLLGG GNVLLLDDEPS NDLDVETLRA
301    LEDALLEFAG SVMVISHDRW FLDRIATHIL ACEGDSKWVF FDGNYQEYEA
351    DKRRLGKEG AKPKRIKYKP VTR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1873>:

m596.seq..

```

1      ATGTCCCAAC AATACGTCTA TTCTATGCTG CGCGTGAGCA AGGTTGTGCC
51     GCCGCAGAAA ACCATCATTA AAGATATTTC CCTTCTTTC TTCCCCGGCG
101    CGAAAATCGG CCTGCTCGGT TTGAACGGCG CGGGCAAGTC CACCGTGCTG
151    CGGATTATGG CGGGCGTGGA TAAGGAATTT GAGGGCGAAG CCGTGCCGAT
201    GGGCGGCATC AAAATCGGCT ACCTGCCGCA AGAGCCTGAG CTGTATCCGG
251    AAAAAACCGT GCGCGAGGAA GTGGAAGCG GTTGGGCGA AGTGGCTGCC
301    GCGCAGAAAC GTTTGGAAGA AGTGTATGCC GAGTACGCCA ATCCTGATGC
351    GGATTTTGAC GCGTTGGCAG AAGAGCAGGG CCGCTTGGA GCGATTATTG
401    CGGCAGGTTT GTCCACGGGC GCGGCTGCGG AACACGAATT GGAATCGGCC
451    GCCGACGCGC TGCGCTGCC GGAATGGGAT GCCAAAATCG ATAATTGTGTC
501    CGGCGGTGAA AAACGCCGCG TTGCCTTGTG CAAACTCTTG TTGAGCAAGC
551    CCGATATGCT TTTGCTGGAC GAGCCGACCA ACCACTTGA TGCGGAATCG
601    GTCGAGTGGC TGGAGCAATT TCTCGTGC GC TCCCCGGCA CAGTCGTTGC
651    GGTAACGCAC GACCGCTACT TCCTCGACAA CGCCGCCGAA TGATTTTGG
701    AACTCGACCG CGGCCATGGT ATTCCGTGGA AAGGCAATTA CTCGTCTTGG
751    CTGGAGCAGA AAGAAAAACG CTTGGAACG GAGGCAAAAT CCGAAGCCGC
801    GCGCGTGAAG GCGATGAAGC AGGAATTGGA ATGGGTGCGC CAAAATGCCA
851    AAGGCCGCCA AGCCAAGTCC AAAGCGCGTT TGGCTCGTTT TGAAGAAATG
901    AGCAACTACG AATACCAAAA ACGCAATGAA ACGCAGGAAA TCTTTATTCC
951    CGTTGCCGAG CGTTTGGGTA ACGAAGTGAT TGAATTTGTA AATGTTTCCA
1001   AATCGTTTCG CGATAAAGTG CTGATTGACG ATTTGAGCTT CAAAGTGCCT
1051   GCGGGCGCGA TTGTCGGCAT CATCGGCCCG AACGGCGCGG GTAAATCTAC
1101   GCTGTTCAAA ATGATTTTCG GCAAAGAGCA GCCTGATTCC GCGAGGTGA
1151   AAATCGGACA AACCGTGAAT ATGAGCTTGA TTGACCAAAG CCGCAAGGT
1201   TTGCAAAACG ACAAACCGT GTTCGACAA ATTGCCGAAG GCCGCGACAT
1251   TTTGCAGGTT GGTCAAGTTG AAATTCCCGC CCGCCAATAT TTGGGCGGTT
1301   TCAACTTCAA AGGCAGCGAC CAAAGCAAAA TTGCAGGTCA ATTGTCTGGC
1351   GCGCAACGCG GTCGTCTGCA CTTGGCAAAA ACCTTGTTGA GCGCGGCAA
1401   TGTATTGCTG CTGGATGAAC CGTCTAACGA CCTTGACGTG GAAACCTGTC
1451   GCGCGTTGGA AGACGCATTG TTGGAATTTG CCGGCAGCGT GATGGTGATT
1501   TCGCACGACC GTTGGTTCC TCGACGCATC GCCACGCATA TCTTGGCGTG
1551   TGAAGGCGAC TCTAAATGGG TGTTCTTCGA CGGCAACTAT CAGGAATACG
1601   AAGCCGACAA GAAACGCCGT TTGGGCGAAG AAGGCGCGAA ACCGAAACGC
1651   ATCAATACA AACCGGTAAC GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1874; ORF 596>:

m596.pep..

946

```

1  MSQQYVYSML RVSKVVPPOK TIIKDISLSF FPGAKIGLLG LNGAGKSTVL
51  RIMAGVDKEF EGEAVPMGGI KIGYLPQEPE LDPEKTVREE VESGLGEVAA
101 AQKRLEEVYA EYANPDADF ALAEEQGRLE AIIAAGSSTG GGAHEHELEIA
151 ADALRLPEWD AKIDNLSGGE KRRVALCKLL LSKPDMLLLD EPTNHLDAES
201 VEWLEQFLVR FPGTVVAVTH DRYFLDNAAE WILELDRGHG IPWKGNYSW
251 LEQKEKRLN EAKSEAARVK AMKQELEWVR QNAKGRQAKS KARLARFEEM
301 SNYEYQKRNE TQEIFIPVAE RLGNEVIEFV NVSKSFGDKV LIDDLSEFKVP
351 AGAIVGIIGP NGAGKSTLFK MISGKEQPDG GEVKIGQTVK MSLIDQSREG
401 LQNDKTVFDN IAEGRDILQV GQFEIPARQY LGRFNFKGSD QSKIAGQLSG
451 GERGLHLAK TLLSGGNVLL LDEPSNDLDV ETLRALEDAL LEFAGSVMVI
501 SHDRWFLDRI ATHILACEGD SKWVFFDGNV QEYEADKRRR LGEEGAKPKR
551 IKYKPVTR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

```

m596  g596      98.4% identity in 373 aa overlap

      160      170      180      190      200      210
m596.pep  LPEWDAKIDNLSGGEKRRVALCKLLLSKPDMLLLDEPTNHLDAESVEWLEQFLVRFPQTV
g596      MLLLDEPTNHLDAESVEWLEQFLVRFPQTV
              10      20      30

      220      230      240      250      260      270
m596.pep  VAVTHDRYFLDNAAEWILELDRGHGIPWKGNYSWLEQKEKRLNEAKSEAARVKAMKQE
g596      VAVTHDRYFLDNAAEWILELDRGHGIPWKGNYSWLEQKEKRLNEAKSEAARVKAMKQE
              40      50      60      70      80      90

      280      290      300      310      320      330
m596.pep  LEWVRQNAKGRQAKSKARLARFEEMSNYEYQKRNETQEIFIPVAERLGNEVIEFVNVSKS
g596      LEWVRQNAKGRQAKPKARLARFEEMSNYEYQKRNETQEIFIPVAERLGNEVIEFVNVSKS
              100      110      120      130      140      150

      340      350      360      370      380      390
m596.pep  FGDKVLIDDLSEFKVPAGAIVGIIGPNAGKSTLFKMISGKEQPDGSEVKIGQTVKMSLID
g596      FGDKVLIDGLSEFKVPAGAIVGIIGPNAGKSTLFKMIAGKEQPDGSEVKIGQTVKMSLID
              160      170      180      190      200      210

      400      410      420      430      440      450
m596.pep  QSREGLQNDKTVFDNIAEGRDILQVGQFEIPARQYLGRFNFKGSDQSKIAGQLSGGERGR
g596      QSREGLQNDKTVFDNIAEGRDILQVGQFEIPARQYLGRFNFKGSDQSKIARQLSGGERGR
              220      230      240      250      260      270

```

	460	470	480	490	500	510
m596.pep	LHLAKTLLSGGNVLLDDEPSNDLDVETLRALEDALLEFAGSVMVISHDRWFLDRIATHIL					
	:					
g596	LHLAKTLLGGGNVLLDDEPSNDLDVETLRALEDALLEFAGSVMVISHDRWFLDRIATHIL					
	280	290	300	310	320	330
	520	530	540	550	559	
m596.pep	ACEGDSKWVFFDGNVQEYEADKKRRLGEEGAKPKRIKYKPVTRX					
g596	ACEGDSKWVFFDGNVQEYEADKKRRLGKEGAKPKRIKYKPVTRX					
	340	350	360	370		

a596.seq

1	ATGTCCCAAC	AATACGTCTA	TTCATGCTG	CGCGTGAGCA	AGGTTGTGCC
51	GCCGCAGAAA	ACCATCATT	AAGATATTT	CCTTTCTTT	TTCCCCGGCG
101	CGAAAATCGG	TTGGCTCGGT	TTGAACGGCG	CGGGCAAGTC	CACCGTGCAT
151	CGGATTATGG	CGGGCGTGG	TAAAGAATTT	GAGGGCGAAG	CCGTGCCAGT
201	GGGCGGTATT	AAAATCGGCT	ACCTGCCGCA	AGAGCCTGAG	CTTGATCCGG
251	AAAAAACCGT	GCGTGAGGAA	GTGGAAAGCG	GTTTGGGCGA	AGTGGCTGCC
301	GCGCAGAAAC	GTTTGGAGGA	AGTGTATGCC	GAGTACGCCA	ATCCCGATGC
351	GGATTTTGAC	GCGTTGGCGG	AAGAGCAGGG	CGGTTTGGAA	GCGATTATTG
401	CGCGGGGTTT	GTCACGGGG	GGCGGTGCGG	AACACGAATT	GGAATTCGCT
451	GCCGACGCGC	TGCGCCTGCC	GGAATGGGAT	GCCAAAATCG	ATAATTTGTC
501	CGGCGGTGAA	AAACGCCGCG	TCGCTTTGTG	CAAACCTCTT	TTGAGCAAGC
551	CCGATATGCT	TTTGCTGGAC	GAGCCGACCA	ACCACCTTGA	TGCGGAATCG
601	GTCGAGTGGC	TGGAGCAATT	TCTCGTGCCG	TTCCCCGGTA	CAGTCGTTTG
651	CGTAACACAC	GACCGCTACT	TCTCTGACAA	CGCCGCCGAA	TGGATTTTGG
701	AACTCGACCG	CGGGCACGGT	ATTCCGTGGA	AAGGAAATTA	CTCGTCTTGG
751	TTGGAGCAGA	AAGAAAAACG	TTTGGAANA	GAGGCGAAT	CCGAAGCCGC
801	GCGCGTGAAA	GCGATGAAG	AGGAATTTGA	ATGGGTGCGC	CAAAATGCCA
851	AAGGCGCTCA	AGCCAAGTCC	AAAGCGCGTT	TGGCGCGTTT	TGAAGAAATG
901	AGCAACTATG	AATACCAAAA	ACGCAATGAA	ACGCAAGAAA	TCTTCATTCC
951	CGTCGCCGAG	CGTTTGGGTA	ACGAAGTGAT	TGAATTTGTG	AATGTTTCCA
1001	AATCGTTTCG	CGACAAAGTG	CTGATTGACG	ATTTGAGCTT	CAAAGTGCCT
1051	GCGGGCGCGA	TTGTCCGGAT	CATCGGTCCG	AACGGCGCGG	GTAATTCGAC
1101	ACTGTTTAAA	ATGATTTCGG	CGAAAGAGCA	GCCCGATCTC	GGTGAAGTGA
1151	AAATCGGGCA	AACCGTGAAA	ATGAGCTTGA	TTGACCAAAG	CCCGCAAGGT
1201	TTGCAAAACG	ACAAAACCGT	GTTCGACAAC	ATTGCCGAAG	GTGCGGATAT
1251	TTTACAGGTC	GGGCAGTTTG	AAATCCCCGC	CCGCCAATAT	TTGGGACGCT
1301	TCAATTTCAA	AGGCACGCAC	CAAAGCAAAA	TCACGGGGCA	GCTTTCCGGC
1351	GGCAACGCG	GACGTTTGCA	CTTGGCAAAA	ACCTTGTGTG	CGGTTGGCAA
1401	TGTGTTTGCT	CTGGACGAAC	CGTCCAACGA	CCTCGACGTG	GAAACCTTCG
1451	GCGCGTTGGA	AGACGCATTG	CTGGAATTTG	CCGGCAGCGT	GATGGTGATT
1501	TCGCACGACC	GCTGGTTTCT	CGACCGTATT	GCTACGCATA	TCTTGGCTTG
1551	CGAAGGCGAC	TCCAAATGGG	TGTTCTTTGA	CGGCAACTAT	CAGGAATACG
1601	AAGCGCACAA	GAAACGCCGA	CTCGGCGAAG	AAGGCACGAA	ACCGAAACGC
1651	ATCAAATACA	AACCGGTAA	GCGTTAA		

a596.pcp

1	MSQQYVYSML	RVSKVPPQK	TIKDISLSF	FPAKIGLLG	LNGAGKSTVL
51	RIMAGVDKEF	EGEAVPMGGI	KIGYLPQEPE	LDPEKTVREE	VESGLGEVAA
101	AQKRLEEVYA	EYANPDADFD	ALAEEQGRLE	AIIAAGSSTG	GGAEHELEIA
151	ADALRLPEWD	AKIDNLSGGE	KRRVALCKLL	LSKPDMLLLD	EPTNHLDAES
201	VEWLEQFLVR	FPGTVAVTH	DRYFLDNAE	WILELDRGHG	IPWKNGYSWS
251	LEQKEKRLN	EAKSEARVK	AMKQELWEVR	QNAKGRQAKS	KARLNARFEEM
301	SNYEYQKRNE	TQEIFIPVAE	RLGNEVIEFV	NVSKSFGDKV	LIDDLSEFKVP
351	AGAIVGIIGP	NGAGKSTLFK	MIAGKEQPDS	GEVKIGQTVK	MSLIDQSREG
401	LQNDKTVFDN	IAEGRDILQV	GQFEIPARQY	LGRFNFKGSD	QSKITGQLSG
451	GERGRHLHLAK	TLLGGGNVLL	LDEPSNDLDV	ETLRALEDAL	LEFAGSVMVI
501	SHDRWFLDRI	ATHILACEGD	SKWVFFDGNV	QEYEAADKKRR	LGEEGTKPKR
551	IKYKPVTR*				

m596/a596 99.3% identity in 558 aa overlap

948

m596.pep	10	20	30	40	50	60
	MSQQYVYSMLRVSKVVPQKTIIKDISLSFFPGAKIGLLGLNGAGKSTVLRIMAGVDKEF					
a596	MSQQYVYSMLRVSKVVPQKTIIKDISLSFFPGAKIGLLGLNGAGKSTVLRIMAGVDKEF					
	10	20	30	40	50	60
m596.pep	70	80	90	100	110	120
	EGEAVPMGGIKIGYLPQEPELDPEKTVREEVESGLGEVAAAQKRLEEVYAEYANPDADF					
a596	EGEAVPMGGIKIGYLPQEPELDPEKTVREEVESGLGEVAAAQKRLEEVYAEYANPDADF					
	70	80	90	100	110	120
m596.pep	130	140	150	160	170	180
	ALAEQGRLEAIIAAGSSTGGGAHELEIAADALRLPEWDAKIDNLSGGEKRRVALCKLL					
a596	ALAEQGRLEAIIAAGSSTGGGAHELEIAADALRLPEWDAKIDNLSGGEKRRVALCKLL					
	130	140	150	160	170	180
m596.pep	190	200	210	220	230	240
	LSKPDMLLLDEPTNHLDAESVEWLEQFLVRFPGTVVAVTHDRYFLDNAAEWILELDRGHG					
a596	LSKPDMLLLDEPTNHLDAESVEWLEQFLVRFPGTVVAVTHDRYFLDNAAEWILELDRGHG					
	190	200	210	220	230	240
m596.pep	250	260	270	280	290	300
	IPWKGNYSWLEQKEKRLNEAKSEAARVKAMKQELEWVRQNAKGRQAKSKARLARFEEM					
a596	IPWKGNYSWLEQKEKRLNEAKSEAARVKAMKQELEWVRQNAKGRQAKSKARLARFEEM					
	250	260	270	280	290	300
m596.pep	310	320	330	340	350	360
	SNYEYQKRNETQEIFIPVAERLGNEVIEFVNVSKSFGDKVLIDDLSEFKVPAGAIVGIIGP					
a596	SNYEYQKRNETQEIFIPVAERLGNEVIEFVNVSKSFGDKVLIDDLSEFKVPAGAIVGIIGP					
	310	320	330	340	350	360
m596.pep	370	380	390	400	410	420
	NGAGKSTLFLKMISGKEQPDSEVKIGQTVKMSLIDQSREGLQNDKTVFDNIAEGRDILQV					
a596	NGAGKSTLFLKMIAGKEQPDSEVKIGQTVKMSLIDQSREGLQNDKTVFDNIAEGRDILQV					
	370	380	390	400	410	420
m596.pep	430	440	450	460	470	480
	GQFEIPARQYLGRFNFKGSQSKIAGQLSGGERGRHLAKTLLSGGNVLLLDEPSNDLDV					
a596	GQFEIPARQYLGRFNFKGSQSKITGQLSGGERGRHLAKTLLSGGNVLLLDEPSNDLDV					
	430	440	450	460	470	480
m596.pep	490	500	510	520	530	540
	ETLRALEDALLEFAGSVMVISHDRWFLDRIATHILACEGDSKWVFFDGNVQYQYADKKRR					
a596	ETLRALEDALLEFAGSVMVISHDRWFLDRIATHILACEGDSKWVFFDGNVQYQYADKKRR					
	490	500	510	520	530	540
m596.pep	550	559				
	LGEEGAKPKRIKYKPVTRX					
a596	LGEEGAKPKRIKYKPVTRX					
	550					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1877>

g597.seq

```

1  ATGCTGCTTC ATGTCAGCAA TTCCCTCAAA CAGCTTCAGG AAGAGCGTAT
51  CCGCCAAGAA CGTATCCGCC AAGAGCGTAT CCGTCAGGCG CGCGGCAACC
101 TTGCTTCCGT CAACGCAAA CAGCGCGAGG CTTGGGACAA ATTCCAAAAA

```

```

151 CTCAATACCG AGCTGAACCG TTTGAAAACG GAAGTCGCCG CTACGAAAGC
201 GCAGATTTCC CGTTTCGTAT CGGGGAACCTA TAAAAACAGC CGGCCGAATG
251 CGGTGCGCCT GTTCTCGAAA AACGCCGAAC CGGGTCAGAA AAACCGCTTT
301 TTGCGTTATA CGCGTTATGT AAACGCCTCC AATCGGGAAG TTGTCAAGGA
351 TTTGAAAAAA CAGCAGAAGG CTTTGGCGGT ACAAGAGCAG AAAATCAACA
401 ATGAGCTTGC CCGTTTGAAG AAAATTCAGG CAAACGTGCA ATCCCTGCTG
451 AAAAAACAGG GTGTAACCGA TCGCGCGGAA CAGACGGAAA GCCGCAGACA
501 GAATGCCAAA ATCTCCAAAG ATGCCGAAA ACTGCTGGAA CAGAAAGGGA
551 ACGAGCAGCA GCTGAACAAG CTCTTGAGCA ATTTGgagaa aaAAAAagcc
601 gaacaccgCA TtcaggAtgc ggAagcaaaa agaAAATTGG CTGAagcCaa
651 actGgcggca gccgAAAAAG CCAGAAAAGA AGCGGCGCAG CAGAAGGCTG
701 AAGCGCGACG TCGGGAATG TCCAACCTGA CCGCCGAAGA CAGGAACATC
751 CAAGCGCCTT CGGTATATGG TATCGGCAGT GCCGACGgTT TCAGCCGCAT
801 GCAGGGACGT TTGAAAAAAC CGGTGACGG TGTGCCGACC GGGCTTTTCG
851 GGCAGAACCG GAGCGGcgC GATGTTTGA AAGCGGTGT CTATTCCACT
901 GCGCTGCAA CGGTGAAAG CATTGCGCcg gGAACggtaa GCTATGCGGA
951 cgaGTTGGAC GGTACCGCA AAGTGGTCGT GATCGATCAC GGCAGAACT
1001 ACATCAGCAT CTATGCCGGT TTGAGCGAAA TTTCCGCCG CAAGGGTTAT
1051 ACGGTGCGGG CAGGAAGCAA AATCGGCACG AGCGGGTTCG TGCCGGACGG
1101 GGAAGAGGGG CTTTACCTGC AAATACGTTA TCGAGGTCAG GTGTTGAACC
1151 CTTCCGGGCTG GATACGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1878; ORF 597>:

g597.pep

```

1 MLLHVSNSLK QLQEEIRIQE RIRQERIROA RGNLASVNRK QREAWDKFQK
51 LNTLNLRLKT EVAATKAQIS RFVSGNYKNS RPNAVALFLK NAEPGQKNRF
101 LRYTRYVNAS NREVVKDLEK QQKALAVQEQ KINNELARLK KIQANVQSLL
151 KKQGVTDAAE QTESRRQNAK ISKDARKLLE QKGNEQQLNK LLSNLEKKKA
201 EHRIQDAEAK RKLAEAKLAA AEKARKEAAQ QKAEARRAEM SNLTAEDRNI
251 QAPSVMGIGS ADGFSRMQGR LKKPVDGVPT GLFGQNRSGG DVWKGVFYST
301 APATVESIAP GTVSYADELD GYGKVVVIDH GENYISIIYAG LSEISAGKGY
351 TVAAGSKIGT SGSLPDGEEG LYLQIRYRQ VLNPSGWIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1879>:

m597.seq

```

1 ATGCTGCTTC ATGTCAGCAA TTCCCTCAAA CAGCTTCAGG AAGAGCGTAT
51 CCGCCAAGAG CGTATCCGTC AGGCGCGCGG CAACCTTGCT TCCGTCAACC
101 GCAAACAGCG CGAGGCTTGG GACAAGTTCC AAAAACTCAA TACCGAGCTG
151 AACCGTTTGA AACCGGAAGT CGCCGCTACG AAAGCGCAGA TTTCCCGTTT
201 CGTATCGGGG AACTATAAAA ACAGCCAGCC GAATGCGGTT GCCCTGTTCC
251 TGA AAAACGC CGAACCGGT CAGAAAACC GCTTTTTCG TTATACGCGT
301 TATGTAAACG CCTCCAATCG GGAAGTTGTC AAGGATTGGA AAAAACAGCA
351 GAAGGCTTTG GCGGTACAAG AGCAGAAAAT CAACAATGAG CTTGCCCGTT
401 TGAAGAAAAT TCAGGCAAAC GTGCAATCTC TGCTGAAAAA ACAGGGTGTA
451 ACCGATGCGG CGGAACAGAC GGAAGCCGC AGACAGAATG CCAAAATCGC
501 CAAAGATGCC CGAAAACCTG TGAACAGAA AGGGAACGAG CAGCAGCTGA
551 AAGAGCTCTT GAGCAATTG GAGAAGAAA AGGCCGAACA CCGATTTCAG
601 GATGCGGAAG CAAAAGAAA ATTGGCTGAA GCCAGACTGG CGGCAGCCGA
651 AAAAGCCAGA AAAGAAGCGG CGCAGCAGAA GGTGAAGCA CGACGTGCGG
701 AAATGTCCAA CCTGACCGCC GAAGACAGGA ACATCCAAG GCCTTCGGTT
751 ATGGGTATCG GCAGTGCCGA CGGTTTCAGC CGCATGCAAG GACGTTTGAA
801 AAAACCGGTT GACGGTGTGC CGACCGGACT TTTCGGGCGA AACC GGAGCG
851 GCGGCGATAT TTGAAAGGC GTGTTCTATT CCACTGCACC GGCAACGGTT
901 GAAAGCATTTG CGCCGGGAAC GGTAAGCTAT GCGGACGAGT TGGACGGCTA
951 CGGCAAAGTG GTCGTGGTGC ATCAGGCGCA GAACTACATC AGCATCTATG
1001 CCGGTTTGGG CGAAATTTCC GTCGGCAAGG GTTATATGGT CGCGGCAGGA
1051 AGCAAAATCG GCTCGAGCGG GTCGCTGCCG GACGGGGAAG AGGGGCTTTA
1101 CCTGCAAATA CGTTATCAAG GTCAGGTATT GAACCTTCG AGCTGGATAC
1151 GTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1880; ORF 597>:

m597.pep

```

1 MLLHVSNSLK QLQEEIRIQE RIRQARGNLA SVNRKQREAW DKFQKLNTEL
51 NRLKTEVAAT KAQISRFVSG NYKNSQPNV ALFLKNAEPG QKNRFLRYTR
101 YVNASNREVV KDLEKQOKAL AVQEQKINNE LARLKKIQAN VQSLKKQGV
151 TDAAEQTESR RQNAKIAKDA RKLLEQKGNE QQLNKLNSL EKKKAEHRIQ
201 DAEAKRLAE ARLAAAEKAR KEAAQQAEEA RRAEMSNLTA EDRNIQAPSV
251 MIGSADGFS RMQRLKKPV DGVPTGLFGQ NRSGGDIWKG VFYSTAPATV
301 ESIAPGTVSY ADEL DGYGKV VVDHGENYI SIYAGLSEIS VGKGYMVAAG
351 SKIGSSGSLP DGEEGLYLQI RYQGVNLNPS SWIR*

```

950

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 597 shows 96.1% identity over a 389 aa overlap with a predicted ORF (ORF 597) from *N. gonorrhoeae*:

m597/g597 96.1% identity in 389 aa overlap

	10	20	30	40	50	60
g597.pep	MLLHVSNSLKQLQEERIRQERIRQERIRQARGNLASVNRKQREAWDKFQKLNTELNLRLKT					
m597	MLLHVSNSLKQLQEERIRQERIRQ-----ARGNLASVNRKQREAWDKFQKLNTELNLRLKT					
	10	20	30	40	50	
	70	80	90	100	110	120
g597.pep	EVAATKAQISRFSVSGNYKNSRPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
m597	EVAATKAQISRFSVSGNYKNSQPNVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
	60	70	80	90	100	110
	130	140	150	160	170	180
g597.pep	QQKALAVQEQQKINNELARLKKIQANVQSLKKQGVTDAAEQTESRRQNAKISKDARKLLE					
m597	QQKALAVQEQQKINNELARLKKIQANVQSLKKQGVTDAAEQTESRRQNAKIAKDARKLLE					
	120	130	140	150	160	170
	190	200	210	220	230	240
g597.pep	QKGNEQQLNKLKLSNLEKKKAEHRIQDAEAKRKLAEAKLAAAEKARKEAAQQKAEARRAEM					
m597	QKGNEQQLNKLKLSNLEKKKAEHRIQDAEAKRKLAEARLAAAEKARKEAAQQKAEARRAEM					
	180	190	200	210	220	230
	250	260	270	280	290	300
g597.pep	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKPPVDGVPTGLFGQNRSGGDVWKGVFYST					
m597	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKPPVDGVPTGLFGQNRSGGDIWKGVFYST					
	240	250	260	270	280	290
	310	320	330	340	350	360
g597.pep	APATVESIAPGTVSYADELDGYGKVVVIDHGENYISYAGLSEISAGKGYTVAAGSKIGT					
m597	APATVESIAPGTVSYADELDGYGKVVVIDHGENYISYAGLSEISVGKGYMVAAGSKIGS					
	300	310	320	330	340	350
	370	380	390			
g597.pep	SGSLPDGEEGLYLQIRYRGQVLNPSGWIRX					
m597	SGSLPDGEEGLYLQIRYQGVLPSSWIRX					
	360	370	380			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1881>

a597.seq

1	ATGCTGCTTC	ATGTCAGCAA	TTCCTCAAG	CAGCTTCAGG	AAGAGCGTAT
51	CCGCCAAGAA	CGTATCCGCC	AAGAGCGTAT	CCGTCAGGCG	CGCGGCAACC
101	TTGCTTCCGT	CAACCGCAAA	CAGCGCGAGG	CTTGGGACAA	GTTCCAAAAA
151	CTCAATACCG	AGCTGAACCG	TTTGAAAACG	GAAGTCGCGC	CTACGAAAGC
201	GCAGATTTCC	CGTTTCGTAT	CGGGGAACCTA	TAAAAACAGC	CAGCCGAATG
251	CGGTTGCCCT	GTTCTGAAA	AACGCCGAAC	CGGGTCAGAA	AAACCGCTTT
301	TTGCGTTATA	CGCGTTATGT	AAACGCCTCC	AATCGGGAAG	TTGTCAAGGA
351	TTTGGAAGAAA	CAGCAGAAGG	CTTTGGCGGT	ACAAGAGCAG	AAAATCAACA
401	ATGAGCTTGC	CGGTTTGAAG	AAAATTCAGG	CAAACGTGCA	ATCCCTGCTG
451	AAAAACAGG	GTGTAACCGA	TGCGGCGGAA	CAGACGGAAA	GCCGCAGACA
501	GAATGCCAAA	ATCGCCAAAG	ATGCCCGAAA	ACTGCTGGAA	CAGAAAGGGA
551	ACGAGCAGCA	GCTGAACAAG	CTCTTGAGCA	ATTGGGAGAA	GAAAAAGGCC
601	GAACACCGCA	TTCAGGATGC	GGAAGCAAAA	AGAAAATTGG	CTGAAGCCAG
651	ACTGGCGGCA	GCCGAAAAAG	CCAGAAAAGA	AGCGGCGCAG	CAGAAGGCTG
701	AAGCACGACG	TGCGGAAATG	TCCAACCTGA	CCGCCGAAGA	CAGGAACATC
751	CAAGCGCCTT	CGGTTATGGG	TATCGGCAGT	GCCGACGGTT	TCAGCCGCAT
801	GCAAGGACGT	TTGAAAAAAC	CGGTTGACGG	TGTGCCGACC	GGACTTTTCG
851	GGCAGAACCG	GAGCGCGCGC	GATGTTTGA	AAGCGGTGTT	CTATTCCACT
901	GCACCGGCAA	CGGTTGAAAG	CATTGCGCCG	GGAACGGTAA	GCTATGCGGA

951

```

951  CGAGTTGGAC GGCTACGGCA AAGTGGTCGT GGTGATCAC GGCAGAACT
1001 ACATCAGCAT CTATGCCGGT TTGAGCGAAA TTCCGTCGG CAAGGGTTAT
1051 ATGGTCGCGG CAGGAAGCAA AATCGGCTCG AGCGGGTCGC TGCCGACGG
1101 GGAAGAGGGG CTTTACCTGC AAATACGTTA TCAAGGTCAG GTATTGAACC
1151 CTTCGAGCTG GATACGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1882; ORF 597.a>:

```

a597.pep
1  MLLHVSNSLK QLQEERIRQE RIRQERIRQA RGNLASVNRK QREAWDKFQK
51  LNTELNR LKT EVAATKAQIS RFVSGNYKNS QPNAVALFLK NAEPGQKNRF
101 LRYTRYVNAS NREVVKDLEK QQKALAVQEQ KINNELARLK KIQANVQSLL
151 KKQGVTDAAE QTESRRQNAK IAKDARKLLE QKGNEQQLNK LLSNLEKKKA
201 EHRIQDAEAK RKLAEARLAA AEKARKEAAQ QKAEARRAEM SNLTAEDRNI
251 QAPSVMGIGS ADGFSRMQGR LKKPVDGVPT GLFGQNRSGG DVWKGVFYST
301 APATVESIAP GTVSYADELD GYGKVVVDH GENYISIIYAG LSEISVGKGY
351 MVAAGSKIGS SGSLPDGEEG LYLQIRYQGG VLNPSWIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 597 shows 98.5% identity over a 389 aa overlap with a predicted ORF (ORF 597) from *N. meningitidis*

```

m597/a597 98.5% identity in 389 aa overlap

          10      20      30      40      50      60
a597.pep  MLLHVSNSLKQLQEERIRQERIRQERIRQARGNLASVNRKQREAWDKFQKLNTELNR LKT
          |||
m597      MLLHVSNSLKQLQEERIRQERIRQ-----ARGNLASVNRKQREAWDKFQKLNTELNR LKT
          10      20      30      40      50

          70      80      90      100     110     120
a597.pep  EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK
          |||
m597      EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK
          60      70      80      90      100     110

          130     140     150     160     170     180
a597.pep  QQKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKIAKDARKLLE
          |||
m597      QQKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKIAKDARKLLE
          120     130     140     150     160     170

          190     200     210     220     230     240
a597.pep  QKGNEQQLNKLLSNLEKKKAEHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM
          |||
m597      QKGNEQQLNKLLSNLEKKKAEHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM
          180     190     200     210     220     230

          250     260     270     280     290     300
a597.pep  SNLTAEDRNIQAPSVMGIGSADGFSRMQGR LKKPVDGVPTGLFGQNRSGGDVWKGVFYST
          |||
m597      SNLTAEDRNIQAPSVMGIGSADGFSRMQGR LKKPVDGVPTGLFGQNRSGGDIWKGVFYST
          240     250     260     270     280     290

          310     320     330     340     350     360
a597.pep  APATVESIAPGTVSYADELDGYGKVVVDHGENYISIIYAGLSEISVGKGYMVAAGSKIGS
          |||
m597      APATVESIAPGTVSYADELDGYGKVVVDHGENYISIIYAGLSEISVGKGYMVAAGSKIGS
          300     310     320     330     340     350

          370     380     390
a597.pep  SGSLPDGEEGLYLQIRYQGVV LNPSSWIRX
          |||
m597      SGSLPDGEEGLYLQIRYQGVV LNPSSWIRX
          360     370     380

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1883>:

```
g601.seq
  1  ATGTTCCCAA CCGGCAATTT GGTGACGAA ATTGATGTGC CGAATATAGG
 51  TCGTCTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101  ACGCCGCCGA CTTGGGCTAC ACGGGCAAAG AGTTGCAGGA CGACATCAAC
151  AACGATGCCG CCGCGCTGGA AAAATTTGAA ACCATCCGCG CATATGGCGC
201  GCTGAAAATG GGTTCGATCA GCGACGTATC CGAAGCCGCC GCCCGCGCGC
251  GCACGCCGAA ACCCGCCTTC GTGCGGCCCG CCGCCGATTA CACCGCCTCC
301  AGCGGCAAAA CCGTAAACGC CGCCGACATC GATTTGCCGG TACGCGCCCT
351  GAGCATGGGC AAACCTGCACC ACGCTATGAT GGGCATCGCC TCGGTCGCCA
401  TCGCCGCCGC CGTGCTCGGT ACGCTGGTCA ACCTTGCCGC AGGCGGCGGA
451  ACGCGTAAAG AAGTGCCTT CGGGCATCCG TCAGGTACGC TCGGTGTCGG
501  TGCTGCCGCC GAATGTCAGG ACGGACAATG GACGGCCGCC aaagcgggtca
551  tgaGCCGCAG CGCACgcgtg attatggaaa gttgGGTGCg cgttccccgat
601  gattGTTTTT GA
```

This corresponds to the amino acid sequence <SEQ ID 1884; ORF 601.ng>:

```
g601.pep
  1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
 51  NDAAALEKFE TIRAYGALKM GLISDVSEAA ARARTPKPAF VAPAADYTAS
101  SGKTVNAADI DLPVRALSMG KLHHAMMGIA SVAIAAAVLG TLVNLAAGGG
151  TRKEVRFGHP SGTLRVGAAA ECQDQGWTAA KAVMSRSARV IMESWVRVPD
201  DCF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1885>:

```
m601.seq
  1  ATGTTCCCAA CCGGCAATTT GGTGATGAA ATTGATGTGC CGAATATAGG
 51  CCGTTTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCTTGA
101  ATGCCGCCGA CTTGGGCTAC ACAGGCAAAG AGTTGCAAGA CGACATCAAC
151  AACGATGCCG CGGCTTTGGA AAAATTCGAG AAAATCCGCG CTTACGGTGC
201  GCTGAAAATG GGTCTGATCA GCGACGTATC CGAAGCTGCC GCTCGCGCGC
251  ACACGCCGAA AGTCGCCTTC GTGCGCCCCG CCGCCGATTA CACCGCCTCC
301  AGTGGCAAAA CCGTGAACGC CGCCGACATC GATTTGCTGG TACGCGCCCT
351  GAGCATGGGC AAACCTGCACC ACGCGATGAT GGGTACCGCC TCTGTTGCCA
401  TTGCGACCGC CGCCGCCGTA CCCGGTACGC TGGTCAACCT TGCCGACGGC
451  GCGGAACGC GTAAAGAAGT GCGCTTCGGG CATCCTTCCG GCACATTGCG
501  CGTCGGTGCA GCCGCCGAAT GTCAGGACGG ACAATGGACG GCCACCAAAG
551  CCGTCATGAG CCGTAGCGCA CGCGTGATGA TGGAAGGTTG GGTGAGGGTG
601  CCTGAGGATT GTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1886; ORF 601>:

```
m601.pep
  1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
 51  NDAAALEKFE KIRAYGALKM GLISDVSEAA ARAHTPKVAF VAPAADYTAS
101  SGKTVNAADI DLLVRALSMG KLHHAMMGTA SVAIATAAAV PGTLVNLAAG
151  GGTRKEVRFG HPSGTLRVGA AAECQDQWAT ATKAVMSRSA RVMMEGWVRV
201  PEDCF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 601 shows 94.1% identity over a 205 aa overlap with a predicted ORF (ORF 601.ng) from *N. gonorrhoeae*:

m601/g601

	10	20	30	40	50	60
m601.pep	MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE					
g601	MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m601.pep	KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLLVRALSMG					

	:
g601	TIRAYGALKMGLISDVSEAAAAARARTPKPAFVAPAADYTASSGKTVNAADIDLVPRLSMG
	70 80 90 100 110 120
m601.pep	KLHHAMMG TASVAIATAAAVPGTLVNLAAGGGTRKEVRF GHPSGTLRVGAAAECQDGQWT
	130 140 150 160 170 180
g601	KLHHAMMG IASVAI --AAAVLGTLVNLAAGGGTRKEVRF GHPSGTLRVGAAAECQDGQWT
	130 140 150 160 170
m601.pep	ATKAVMSRSARVMMEGWVRVPEDCFX
	: : : :
g601	AAKAVMSRSARVIMESWVRVPDDCFX
	180 190 200

```

a601.seq
1  ATGTTCCCAA  CCGGCAATTT  GGTCGATGAA  ATTGATGTGC  CGAATATAGG
51  CCGTTTGAA  GCCACGCTCA  TCAACGCGGG  CATTCCGACC  GTTTTCCTGA
101 ATGCCGCCGA  CTGGGCTCAC  ACGGGCAAAG  AGTTGCAAGA  CGACATCAAC
151 AACGATGCCG  CAGCTTTGGA  AAAATTCGAG  AAAATCCGCG  CTTACGGTGC
201 GCTGAAATG  GGTCTGATCA  GCGACGTATC  CGAAGCTGCC  GCCCGCGCGC
251 ACACGCCGAA  AGTCGCCTTC  GTCGCGCCCG  CCGCCGATTA  CACGCGCTCC
301 AGTGGCAAAA  CCGTGAATGC  CGCCGACATC  GATTGTCTGG  TACGCGCCCT
351 GAGCATGGGC  AAATTGCACC  ACGCGATGAT  GATTACCGGC  TCTGTTGCCA
401 TTGCGACCGC  CGCCGCCGTG  CCCGGTACGC  TGGTCAACCT  TGCCGCAAGC
451 GGCGGAACGC  GTAAAGAAGT  GCGCTTCGGG  CATCCTTCCG  GCACATTGCG
501 CGTCGGTGCA  GCCCGCGAAT  GTCAGGACGG  ACAATGGACG  GCCACCAAAG
551 CCGTTATGAG  CCGCAGCGCA  CGCGTGATGA  TGAAGGTTG  GGTCAGGGTG
601 CCGGAAGATT  GTTTTTAA

```

```
a601.pep
  1  MFPTGNLVDE  IDVPNIGRLK  ATLINAGIPT  VFLNAADLGY  TGKELQDDIN
  51  NDAAALEKFE  KIRAYGALKM  GLISDVSEAA  ARAHTPKVAF  VAPAADYTAS
101  SGKTVNAADI  DLLVRALSMG  KLHHAMMGTA  SVAIATAAAV  PGTLVNLAAG
151  GGTRKEVRFG  HPSGTLRVGA  AAECQDGQWT  ATKAVMSRSA  RVMMEGVWRV
201  PEDCF*
```

		10	20	30	40	50	60
m601.pep		MFP	TGNL	VD	EID	VP	NIGRLKATLINAGIPTVFL
		10	20	30	40	50	60
a601		MFP	TGNL	VD	EID	VP	NIGRLKATLINAGIPTVFL
		70	80	90	100	110	120
m601.pep		KIRAYGALKMGLISDVSEAAAA	RAHTPKVAFV	APAADYTASSGKT	VNAADIDLLVR	ALSMG	
		70	80	90	100	110	120
a601		KIRAYGALKMGLISDVSEAAAA	RAHTPKVAFV	APAADYTASSGKT	VNAADIDLLVR	ALSMG	
		130	140	150	160	170	180
m601.pep		KLHHAMMG	TASVAIATAAAV	PGTLVNLAAGGG	TRKEVRF	GHPSGTLRV	GAAAECDGQWT
		130	140	150	160	170	180
a601		KLHHAMMG	TASVAIATAAAV	PGTLVNLAAGGG	TRKEVRF	GHPSGTLRV	GAAAECDGQWT
		190	200				
m601.pep		ATKAVMSRS	SARVMMEGW	VRVPED	CFX		
		190	200				
a601		ATKAVMSRS	SARVMMEGW	VRVPED	CFX		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1889>:

```
g602.seq
1  ATGTTGCTCC ATCAATGCGA CAAAGCGCGA CATATGCGTC CCTTCTGCT
51  CGGCGGGCAG ATAAACCGTC ATCGTCAGGC GAGCAACCGT GGATTGTGTT
101 CCTTCGGCGG TTTTCAGGGT AATCGGGAAG CGCAGGTCTT TAATGCCGAC
151 CTGATTGATC GGCAGGTTGC GCAAATCTCT GCTGGATTGC ACGTCTGCAA
201 TGGCGTTTCAT GCGTTGTTTG TCCTTAATAT TCAGATAATT ATTGAGATGT
251 GTGTATTGTA TGGCAGGcag atgccgtctg aAAAAacgct gtcggCCGCC
301 TGCTGCAAAA TgcgagattA TATCACTTGC TTTtggcgcGc TGCATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1890; ORF 602.ng>:

```
g602.pep
1  MLLHQCDKAR HMRPFLGGO INRHRQASNR GLCSFGGFQG NREAQVFNAD
51  LIDRQVAQIS AGLHVCNGVH ALFVLNIQII IEMCVLYGRQ MPSEKTLCAA
101 CLQMRDYITC FWRLH*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1891>:

```
m602.seq
1  ATGTTGCTCC ATCAATGCGA CAAACGCGA CATATGCGTC CCCTTCTGCT
51  CAGCAGGCAG GTAAACCGTC ATGGTCAGAC GGGCAATGGT GGACTGGATG
101 CCTTCTGCAG TTTGCAGGGT AATCGGAAAG CGCAGGTCTT TGATACCGAC
151 CTGATTGATC GGCAGATTGC GCAAATCTCG GCTGGATTGC ACGTCTGCAA
201 TAGTGTTTCAT GAGTTGTTT TCCTTAATAT TCATGTAATT GTTGAGATGT
251 GTGCATGGTA TGGCGTTTCC GCCGGGGAAT ATACCGTCAA TCTGCAAATG
301 CGAGATTATA TCACTCGCTT TTAGCAGCTG CATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1892; ORF 602>:

```
m602.pep
1  MLLHQCDKTR HMRPLLSRQ VNRHQGTGNG GLDAFCSLQG NRKAQVFDTD
51  LIDRQIAQIS AGLHVCNSVH ELFFLNHVI VEMCAWYGVS AGEYTVNLQM
101 RDYITRF*QL H*
```

m602/g602 65.2% identity in 115 aa overlap

	10	20	30	40	50	60
m602.pep	MLLHQCDKTRHMRPLLSRQVNRHQGTGNGGLDAFCSLQGNRKAQVFDTDLIDRQIAQIS					
	: : : :: :: :: : : :					
g602	MLLHQCDKARHMRPFLGGOINRHRQASNRGLCSFGGFQGNREAQVFNADLIDRQVAQIS					
	10	20	30	40	50	60
	70	80	90	100	110	
m602.pep	AGLHVCNSVHELFFLNHVIIVEMCAWYGVSAGEYTVN---LQMRDYITRF*QLHX					
	: :: : : : :: :: : ::					
g602	AGLHVCNGVHALFVLNIQIIEMCVLYGRMPSEKTLAAQLQMRDYITCFWRLHX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1893>:

```
a602.seq
1  ATGTTGCTCC ATCAATGCGA CAAAGCGCGA CATATGCGTA CCCTTCTGCT
51  CGGCAAGCAG GTAAACCGTC ATGGTCAGAC GGGCAACTGT GGACTGGATG
101 CCTTCTGCAG TTTGCAGGGT AATCGGAAAG CGCAGGTCTT TGATACCGAC
151 CTGATTGATC GGCAGATTGC GCAAATCTCG GCTGGATTGC ACGTCTGCAA
201 TAGTGTTTCAT GAGTTGTTT TCCTTAATAT TCATGTAATT GTTGAGATGT
251 GTGCATGGTA TGGCGTTTCC ACCGGGGAAT ATACCGTCAA TCTGCAAATG
301 CGAGATTATA TCACTCGCTT TTAGCAGCTG CATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1894; ORF 602.a>:

```
a602.pep
1  MLLHQCDKAR HMRTLLLRQ VNRHQGTGNC GLDAFCSLQG NRKAQVFDTD
51  LIDRQIAQIS AGLHVCNSVH ELFFLNHVI VEMCAWYGVS TGEYTVNLQM
101 RDYITRF*QL H*
```

m602/a602 95.5% identity in 111 aa overlap

955

	10	20	30	40	50	60
m602 . pep	MLLHQCDKTRHMRPLLLSRQVNRHGQTGNNGGLDAFCSLQGNRKAQVFDLIDRQIAQIS					
	: :					
a 602	MLLHQCDKARHMRLLLLGRQVNRHGQTGNCGLDADFCSLQGNRKAQVFDLIDRQIAQIS					
	10	20	30	40	50	60
	70	80	90	100	110	
m602 . pep	AGLHVCNSVHELFFLNHIVIVEMCAWYGVVSAGEYTVNLQMRDYITRFQXLHX					
a 602	AGLHVCNSVHELFFLNHIVIVEMCAWYGVSTGEYTVNLQMRDYITRFQXLHX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1895>:

g603 . seq

```

1  ATGGATTCCC GCCTGCGTGG GAATGACGCT AGGAAATACG GCATACGCTT
51  TGCCCAAAGA GGCCGTCTGA AACACACTCC GCCCAACGCC CATCCTTTT
101 CAGACGGCCC CGCACC AAAA AACACACCAC AAAC TACAAG GAGAAACATC
151 ATGTCCGACC AACTCATTCT TGTCCTGAAC TGCGTCAGTT CATCGCTCAA
201 AGGCGCCGTT ATCGACCGCA AAAGCGGCAG CGTCGTCCTA AGCTGCCTCG
251 GGAACCGCCT GACTACGCCC GAAGCCGTCA TTACCTTCAA CAAAGACGGC
301 AACAAACGCC AAGTTCCCTT GAGCGGCCGC AACTGCCACG CCGGCGCGGT
351 GGGTATGCTG TTGAACGAAC TGGAAAAACA CGGACTGCAC GACCGCATCA
401 AAGCCATCGG CCGCCGCATC GCCCAGCGCG GCGAAAAATA TCACGAGTCC
451 GTCCTCATCG ACCAAGACGT CCTTGACGAA CTGAAAGCCT GCATCCCGTT
501 CGCCCCGCTG CACAACCCCG CCAACATCAG CGGCATCCTC GCCGCGCAGG
551 AACACTTTCC CGGCCTGCCC AACGTCGGCG TGATGGACAC CTCGTTCCAC
601 CAAACCATGC CGGAGCGGGC CTACACTTAT GCCGTGCCGC GCGAATTGCG
651 CAAAAAATAC GCCTTCCGCC GCTACGTTT CCACGGTACC GGTATGCGTT
701 ACGTCGCCCC TGAAGCCGCA CGCATCTTGG GCAAACCTct ggaaGACATC
751 CGCATGATTA TTGCCACTT AGGCAACGGC GCATCTATTA CCGCCGTCAA
801 AAACGGCAAA TCCGTCGATA CCGGTATGGG TTTCACGCCG ATCGAAGGTT
851 TGGTAATGGG TACACGTTGC GCGACACCG ATCCGGGCGT ATACAGCTAT
901 CCGACTTTCC ACGCAGGGAT GGATGTTGCC CAAGTTGATG AAATGCTGAA
951 CGAAAAATCA GGTTCCTCCG GTATTTCcgA actTCCCAAC GACTGCCGCA
1001 CCCTCGAAAT CGCCGCCGAC GAAGGCCGCG AAGGCGCGCG CCTCGCCCTc
1051 gaAGTCATGA CCTGCCGCTT CGCCAAATAC ATCGCTTCGA TGGCTGTGGC
1101 CTGCGGCAGT GTTGACGCAC TCGTGTTTAC CGGCGGTATC GCGGAAAACT
1151 CGCGTAATAT CCGTGCCAAA ACCGTTTCTT ATCTTGATTT CTTGGGTCTG
1201 CACATCGACA CCAAAGCCAA TATGGAAAAA CGTACGGCA ATTGCGGCAT
1251 TATCAGCCCG ACCGATTCTT CTCCGGCTGT TTTGGTCTGC CCGACCAATG
1301 AAGAACTGAT GATTGCCTGC GACACTGCCG AACTTGCCGG CATCTTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1896; ORF 603.ng>:

g603 . pep

```

1  MDSRLRGNDA RKYGIRFAQR GRLKHTPPNA HPFSDGPAPK KQPQTTRRNI
51  MSDQLILVLN CVSSSLKGAV IDRKSGSVVL SCLGERLTTP EAVITFNKDG
101 NKRQVPLSGR NCHAGAVGML LNELEKHGLH DRIKAIGRRI AHGGEKYHES
151 VLIDQDVLDE LKACIPFAPL HNPANISGIL AAQEHFPGLP NVGVMDTSFH
201 QTMPELAYTY AVPRELRKKY AFRRYGFHGT GMRYVAPEAA RILGKPLEDI
251 RMIIAHLGNG ASITAVKNGK SVDTGMGFTP IEGLVMGTRC GDTDPGVYSY
301 PTFHAGMDVA QVDEMLNEKS GFPGISELPN DCRTLEIAAD EGREGARLAL
351 EVMTCRLAKY IASMAVACGS VDALVFTGGI GENSRNIRAK TVSYLDFLGL
401 HIDTKANMEK RYGNSGIISP TDSSPAVLVV PTNEELMIAC DTAELAGIL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1897>:

m603 . seq

```

1  CTGTCTCGC GTAGGCGGGG ACGGAATAAC GATAGAAAAT GCGGCATACG
51  CTTTGCCCAA AGAGGCGGTC TGAAACACCT TGCGCCTGAT GTCTGC.CTT
101 TTTCAGACGA CCCCACACTA AAAAAACAAC CACAACTAC AAGGAGAAAC
151 ATCATGTCCG ACCAACTCAT CCTCGTTCTG AACTGCGGCA GTTCATCGCT
201 CAAAGGCGCC GTTATCGACC GAmAAAGCGG CAGCGTCGTC CTAAGCTGCC
251 TCGGCGAACG cCtGACCACG CCCGAAGCCG TCATTACGTT CAACAAAGAC

```

301	GGCAACAAAC	GCCAAGTTCC	CCTGAGCGGC	CGAAATTGCC	ACGCCGCGCG
351	GGTGGGTATG	CTTTTGAACG	AACTGGA AAA	ACACGGTCTG	CACGACCGCA
401	TCAAAGCCAT	CGGCCACCGC	ATCGCCACG	GCGGCGAAAA	ATACAGCGAG
451	TCTGTTTTGA	TCGACCAGGC	CGTAATGGAC	GAACTCAATG	CCTGCATTCC
501	GCTTGCGCCG	CTGCACAACC	CCGCCAACAT	CAGCGGCATC	CTTGCCGCAC
551	AGGAACATTT	CCCCGGTCTG	CCCAATGTGC	CGGTGATGGA	TACTTCGTTT
601	CACCAAACCA	TGCCGGAGCG	TGCCTACACT	TATGCCGTGC	CGCGCGAGTT
651	GCGTAAAAAA	TACGCTTTCC	GCCGCTACGG	TTTCCACGGC	ACCAGTATGC
701	GTTACGTTGC	CCCTGAAGCC	CCACGCATCT	TGGGCAAACC	TCTGGAAGAC
751	ATCCGCATGA	TTATTGCCCA	CTTAGGCAAC	GGCGCATCCA	TTACCGCCAT
801	CAAAAACGGC	AAATCCGTCG	ATACCAGTAT	GGGTTTCACG	CCGATCGAAG
851	GTTTGGTAAAT	GGGTACACGT	TGCGGCGACA	TCGATCCGGG	CGTATACAGC
901	TATCTGACTT	CCCACGCCGG	GATGGATGTT	GCCCAAGTGG	ATGAAATGCT
951	GAACAAAAAA	TCAGGTTTGC	TCGGTATTTT	CGAACTTTCC	AACGACTGCC
1001	GCACCCTCGA	AATCGCCGCC	GACGAAGGCC	ACGAAGGCGC	GCGCCTCGCC
1051	CTCGAAGTCA	TGACCTACCG	CCTCGCCAAA	TACATCGCTT	CGATGGCTGT
1101	GGGCTGCGCG	GGCGTTGACG	CACCTCGTGT	CACCGCGCGT	ATCGGCGAAA
1151	ACTCGCGTAA	TATCCGTGCC	AAAACCGTTT	CCTATCTTGA	TTTCTTGGGT
1201	CTGCACATCG	ACACCAAAGC	CAATATGGAA	AAACGCTACG	GCAATTCGGG
1251	CATTATCAGC	CCGACCGATT	CTTCTCCGGC	TGTTTTGGTT	GTCCCGACCA
1301	ATGAAGAACT	GATGATTGCC	TGCGACACTG	CCGAAC TTGC	CGGCATCTTG
1351	TAG				

m603.ppt

1	LSSRRRGRNN	DRKCGIRFAQ	RGLKLHLAPD	VCXFSDDPTL	KKQPQTTRRN
51	IMSDQLILVL	NCGSSSLKGA	VIDRXSGSVV	LSCLGERLTT	PEAVITFNKD
101	GNKRQVPLSG	RNCHAGAVGM	LLNELEKHGL	HDRIKAIGHR	IAHGGEKYSE
151	SVLIDQAVMD	ELNACIPLAP	LHNPANISGI	LAAQEHFPGL	PNVGVMDTSF
201	HQTMPERAYT	YAVPRELRKK	YAFRRYGFHG	TSMRVVAPEA	ARILGKPLED
251	IRMIIAHLGN	GASITAIKNG	KSVDTSMGFT	PIEGLVMGTR	CGDIDPGVYS
301	YLTSHAGMDV	AQVDEMLNKK	SGLLGISELS	NDCRTLEIAA	DEGHEGARLA
351	LEVMTYRLAK	YIASMAVCGC	GVDALVFTGG	IGENSRNIRA	KTVSYLDFLG
401	LHIDTKANME	KRYGNSGIIS	PTDSSPAVLV	VPTNEELMIA	CDTAELAGIL
451	*				

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 603 shows 91.6% identity over a 450 aa overlap with a predicted ORF (ORF 603.ng) from *N. gonorrhoeae*:

m603/q603

		10	20	30	40	50	60
m603.pep		LSSRRRGRNND	RCKGIRFAQR	GRLKHLAPD	VCXFSDDP	TLKKQPQT	TRRNIMSDQLILVL
		:	:	:	:	:	:
g603		MDSRLRG-ND	ARKYGIRFAQR	GRLKHTFP	NAHPFSDG	PAPKKQPQT	TRRNIMSDQLILVL
		10	20	30	40	50	
		70	80	90	100	110	120
m603.pep		NCGSSSLKGA	VIDRXSGSV	LSCLGERLT	TTP EAVIT	FNKDG	NKRQVPLSGRNCHAGAVGM
		:	:	:	:	:	:
g603		NCVSSSLKGA	VIDRXSGSV	LSCLGERLT	TTP EAVIT	FNKDG	NKRQVPLSGRNCHAGAVGM
	60	70	80	90	100	110	
		130	140	150	160	170	180
m603.pep		LLNELEKHGL	HDRIKAIGH	RIAHGGEKY	SESVLIDQ	AVMDELNA	CIP LAPLHN PANISGI
		:	:	:	:	:	:
g603		LLNELEKHGL	HDRIKAIG	RRIAHGGEKY	HESVLIDQ	DVLD ELKACIP	FAPLHN PANISGI
	120	130	140	150	160	170	
		190	200	210	220	230	240
m603.pep		LAAQEHPG	LPNVGMD	TSFHQTM	PERAYTYA	VPREL	RKKYAFRRYGFHGTSMRYVAPEA
		:	:	:	:	:	:

957

```

g603      LAAQEHFPLPNVGVMDSFSHQTMPERAYTYAVPRELRKKYAFRRYGFHGTGMRYVAPEA
          180      190      200      210      220      230

          250      260      270      280      290      300
m603.pep  ARILGKPLEDIRMIIAHLGNGASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS
          |||||||:|||||:|||||:|||||:|||||:|||||
g603      ARILGKPLEDIRMIIAHLGNGASITAVKNGKSVDTGMGFTPIEGLVMGTRCGDIDPGVYS
          240      250      260      270      280      290

          310      320      330      340      350      360
m603.pep  YLTSHAGMDVAQVDEMLNKKSGLLGISLSNDCRTLEIAADEGHEGARLALAEVMTYRLAK
          |||||||:|||||:|||||:|||||:|||||:|||||
g603      YPTFHAGMDVAQVDEMLNEKSGFPGISLPNDCRTLEIAADEGREGARLALAEVMTCLRAK
          300      310      320      330      340      350

          370      380      390      400      410      420
m603.pep  YIASMAVGC GGVDALVFTGGIGENSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS
          |||||||:|||||:|||||:|||||:|||||:|||||
g603      YIASMAVACGSVDALVFTGGIGENSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS
          360      370      380      390      400      410

          430      440      450
m603.pep  PTDSSPAVLVVPTNEELMIACDTAELAGILX
          |||||||:|||||:|||||:|||||:|||||
g603      PTDSSPAVLVVPTNEELMIACDTAELAGILX
          420      430      440      450

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1899>:

```

a603.seq
1   CTGTCCTCGC GTAGGCGGGG ACGGAATAAC GATAGAAAAT GCGGCATACG
51  CTTTGCCCAA AGAGGCCGTC TGAAACACAC TCCGCCAAC GCCCATCCTT
101 TTTCAGACGA CCCACACACC. AAAAAACAAC CACAACTAC AAGGAGAAAC
151 ATCATGTCCG ACCAACTCAT TCTTGTCTG AACTGCGGCA GTTCATCGCT
201 CAAAGGTGCC GTTATCGACC GCAAAAGCGG CAGCGTCGTC CTAAGCTGCC
251 TCGGCGAACG CCTGACCACG CCCGAAGCCG TCATTACGTT CAGCAAAGAC
301 GGCAACAAAC GCCAAGTTCC CCTGAGCGGC CGGAAGTACC ACGCCGGCGC
351 GGTGGGTATG CTGTTGAACG AACTGGAATA ACACGAACTG CACGACCGCA
401 TTCAAGCCGT CGGCCACCGC ATCGCCACG GCGGCGAATA ATACAGCGAG
451 TCTGTTTGA TCGACCAGGC CGTAATGGAC GAACTCAATG CCTGCATTCC
501 GCTTGCGCCG CTGCACAACC CCGCCAACAT CAGCGGCATC CTCGCCGCAC
551 AGGAACATTT CCCCGTCTG CCCAATGTCG GCGTGATGGA TACTTCGTTT
601 CACCAAAACA TGCCGAGAGC TGCCTACACT TATGCCGTGC CGCGCGAGTT
651 GCGTAAAAAA TACGCTTTC GCGCTACGG TTTCCACGGC ACCAGTATGC
701 GTTACGTTGC CCCTGAAGCC GCATGCATCT TGGGCAAAAC TCTGGAAGAC
751 ATCCGCATGA TTATTGCCCA CTTAGGCAAC GGCGCATCCA TTACCGCCAT
801 CAAAACGGC AAATCCGTCG ATACCAGTAT GGGTTTCACG CCGATCGAAG
851 GTTTGGTAAT GGTACGCGC TCGGCGGATA TCGACCCGGG CGTATACAGC
901 TATCTGACTT CACACGCCGG TTTGGATGTT GCACAAGTTG ATGAAATGCT
951 GAATAAAAAA TCAGGCTTGC TCGGTATTTT CGAACTCTCC AACGACTGCC
1001 GCACCCTCGA AATCGCCGCC GACGAAGGCC ACGAAGGCGC GCGCCTCGCC
1051 CTCGAAGTTA TGACCTACCG CCTCGCCAAA TACATCGCTT CGATGGCTGT
1101 GGGCTGCGGC GCGGTTGACG CACTCGTGTT CACCGGCGGT ATCGGCGAAA
1151 ACTCGCGTAA TATCGTGCC AAAACCGTTT CCTATCTTGA TTTCTGGGT
1201 CTGCACATCG ACACCAAAGC CAATATGGAA AAACGCTACG GCAATTCGGG
1251 TATTATCAGC CCGACCGATT CTTCTCCGGC TGTTTGGTT GTCCGACCA
1301 ATGAAGAACT GATGATTGCC TCGGACACTG CCGAACTTGT CGGCATCTTG
1351 TAG

```

This corresponds to the amino acid sequence <SEQ ID 1900; ORF 603.a>:

```

a603.pep
1   LSSRRRGRNN DRKCGIRFAQ RGRLKHTFPN AHPFSDPTX KKQPQTTRN
51  IMSDQLILVL NCGSSSLKGA VIDRKSGSVV LSCLGERLTT PEAVITFSKD
101 GNKRQVPLSG RNCHAGAVGM LLNELEKHEL HDRIQAVGHR IAHGGEKYSE
151 SVLIDQAVMD ELNACIPLAP LHNPANISGI LAAQEHFPL PNVGVMDSF

```

958

```

201 HQTMPERAYT YAVPRELRKK YAFRRYGFHG TSMRYVAPEA ACILGKPLED
251 IRMIIAHLGN GASITAIKNG KSVDTSMGFT PIEGLVMGTR CGDIDPGVYS
301 YLTSHAGLDV AQVDEMLNKK SGLLGISELS NDCRTLEIAA DEGHEGARLA
351 LEVMTYRLAK YIASMAVGCG GVDALVFTGG IGNSRNIRA KTVSYLDFLG
401 LHIDTKANME KRYGNSGIIS PTDSSPAVLV VPTNEELMIA CDTAELVGIL
451 *

```

m603/a603 96.7% identity in 450 aa overlap

	10	20	30	40	50	60
m603.pep	LSSRRRGRNNDKRCGIRFAQGRGLKHLAPDVCXFSDDPTLKKQPQTTRRNIMSDQLILVL					
a603	LSSRRRGRNNDKRCGIRFAQGRGLKHTPPNAHPFSDDPTXKKQPQTTRRNIMSDQLILVL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m603.pep	NCGSSSLKGAVIDRXSGSVVLSCLGERLTTPEAVITFNKDGNGKRVPLSGRNCHAGAVGM					
a603	NCGSSSLKGAVIDRKSGSVVLSCLGERLTTPEAVITFSKDGNGKRVPLSGRNCHAGAVGM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m603.pep	LLNELEKHGLHDRIKAIGHRIAHGGEKYESVLIDQAVMDELNACIPLAPLHNPANISGI					
a603	LLNELEKHELHDRIQAVGHRIAHGGEKYESVLIDQAVMDELNACIPLAPLHNPANISGI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m603.pep	LAAQEHFPGLPNVGVMDTSFHQTMPERAYTYAVPRELRKKYAFRRYGFHGTSRMRYVAPEA					
a603	LAAQEHFPGLPNVGVMDTSFHQTMPERAYTYAVPRELRKKYAFRRYGFHGTSRMRYVAPEA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m603.pep	ARILGKPLEDIRMIIAHLNGASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS					
a603	ACILGKPLEDIRMIIAHLNGASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m603.pep	YLTSHAGMDVAQVDEMLNKKSGLLGISELSNDCRTLEIAADEGHEGARLALEVMTYRLAK					
a603	YLTSHAGLDVAQVDEMLNKKSGLLGISELSNDCRTLEIAADEGHEGARLALEVMTYRLAK					
	310	320	330	340	350	360
	370	380	390	400	410	420
m603.pep	YIASMAVGCGVDALVFTGGIGENSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS					
a603	YIASMAVGCGVDALVFTGGIGENSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS					
	370	380	390	400	410	420
	430	440	450			
m603.pep	PTDSSPAVLVPTNEELMIACDTAELAGILX					
a603	PTDSSPAVLVPTNEELMIACDTAELVGILX					
	430	440	450			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1901>:

g604.seq

```

1  ATGCCCCAAG CGCACTTCTT TACGCGTTCC GCCGCCTGCG GCAAGGTTGA
51  CCAGCGTACC GAGCACGGCG GCGGCGATGG CGACCGAGGC GATGCCCCATC
101 ATAGCGTGGT GCAGTTTGCC CATGCTCAGG GCGCGTACCG GCAAATCGAT
151 GTCGCGGCGG TTTACGTTT TGCCGCTGGA GGCGGTGTAA TCGCGGCGCG
201 GCGCGACGAA GGCGGGTTTC GGCGTGCGCG CGCGGGCGGC GGCTTCGGAT

```

251	ACGTCGCTGA	TCAAACCCAT	TTTCAGCGCG	CCATATGCGC	GGATGGTTTC
301	AAATTTTTC	AGCGCGGCGG	CATCGTTGTT	GATGTCGTCC	TGCAACTCTT
351	TGCCCCGTGTA	GCCCAAGTCG	GCGGCGTTCA	GGAAACGGT	CGGAATGCCC
401	GCGTTGATGA	GCGTGGCTTT	CAGACGACCT	ATATTGGGCA	CATCAATTTT
451	GTCGACCAA	TTGCCGGTTG	GGAACATACT	GCCTTcgCG	TGGCTGGAT
501	CTAA				

This corresponds to the amino acid sequence <SEQ ID 1902; ORF 604.ng>:

```

g604.pep
  1  MPEAHFFTRS AACGKVDQRT EHGGGDGDRG DAHHSVVQFA HAQGAYRQID
 51  VGGVYGFAAG GGVYGGGRDE GGFRRARAGG GFGYVADQTH FQRAICADGF
101  KFFQRGGI1VDVVLQ2LFA3RV AQVGGVQENG RNARVDERGF QTTYIRHINF
151  VDQIAGWEHT AFAVGWI *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1903>:

```
m604.seq
1  ATGCCCGAAG CGCACTTCTT TACGCGTTCC GCCGCTGCG GCAAGGTTGA
51  CCAGCGTACC GGGTACGGCG GCGGCGGTCT CAATGGCAAC AGAGGCGGTA
101 CCCATCATCG CGTGGTGACG TTTGCCCATG CTCAGGGCGC GTACCAGCAA
151 ATCGATGTCT GCGGCGTTCA CGGTTTTGTC ACTGGAGGCG GTGTAATCGA
201 CGGCGGGCGC GACGAAGGCG ACTTTCGCGC TGTGCGCGCG AGCGGCAGCT
251 TCGGATACGT CGCTGATCAG ACCCATTTTC AGCGCACCGT AAGCGCGGAT
301 TTTCTCGAAT TTTTCCAAAG CCGCGGCATC GTTGTTGATG TCGTCTTGCA
351 ACTCTTTGCC TGTGTAGCCC AAGTCGGCGG CATTCAAGAA AACGGTCGGA
401 ATGCCCCGCT TGATGAGCGT GGCTTTCAA CGGCCTATAT TCGGCACATC
451 AATTTCATCG ACCAAATTGC CGGTTGGGAA CATACTGCCT TCGCCGTCGG
501 CTGGATC
```

This corresponds to the amino acid sequence <SEQ ID 1904; ORF 604>:

```
m604.pep
1  MPEAHFFTRS AACGKVDQRT GYGGGGRNGN RGGTHHRVVQ FAHAQGAYQQ
51  IDVGGVHGFA TGGGVIGGGR DEGDFRRVRA SGSFGYVADQ THFQRTVSAD
101 FLEFFQSRGI VDDVVLQLFA CVAQVGGIQE NGRNARVDER GFQTAYIRHI
151 NFIDQIAGWE HTAFAVGWI
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 604 shows 83.4% identity over a 169 aa overlap with a predicted ORF (ORF 604.ng) from *N. gonorrhoeae*:

m604/g604

		10	20	30	40	50	60
m604 .pep	MPEAHFFTRSAACGKVDQRTGYGGGGRNGNRGGTHHRVVF	FAHAQGAYQQIDVGGVHGFA					
	: : : : :						
g604	MPEAHFFTRSAACGKVDQRTEHGGG--DGDRGDAHHSVVQF	FAHAQGAYRQIDVGGVYGFA					
		10	20	30	40	50	
		70	80	90	100	110	120
m604 .pep	TGGGVIGGGRDEGDFRRVRASGSFGYVADQTHFQRTVSADFLEFFQS	SRGIVVDVLQLFA					
	: : : : : :						
g604	AGGGVIGGGRDEGGFRRARAGGGFGYVADQTHFQRAICADGFKFFQ	RGGIVVDVLQLFA					
		60	70	80	90	100	110
		130	140	150	160	169	
m604 .pep	CVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAF	AVGWI					
	: : :						
g604	RVAQVGGVQENGRNARVDERGFQTTYIRHINFVDQIAGWEHTAF	VGWIX					
		120	130	140	150	160	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1905>:

a604.seq	1	ATGCCCGAAG	CGCACTTCTT	TACGCGTTCC	GCCGCTGCG	GCAAGGTTGA
	51	CACGCGTACC	GGGCACGGCG	GCGGCGGTGC	CAATGGCAAC	AGAGCCGGTA
	101	CCCATCATCG	CGTGGTGCAA	TTTGCCCATG	CTCAGGCGCG	GTACCGACAA
	151	ATCGATGTCG	GCGGCATTCA	CGGTTTTGCC	ACTGGAGGCG	GTGTAATCGG

960

```

201  CGGCGGGCGC GACGAAGGCG ACTTTCGGCG TGTGCGCGCG GCGGCGAGCT
251  TCGGATACGT CGCTGATCAG ACCCATTTTC AGCGCACCGT AAGCGCGGAT
301  TTTCTCGAAT TTTTCCAAAG CTGCGGCATC GTTGTGTGATG TCGTCTTGCA
351  ACTCTTTGCC CGTGTAGCCC AAGTCGGCGG CATTTCAGGAA AACGGTTCGGA
401  ATGCCCGCGT TGATGAGCGT GGCTTTCAA CGGCCTATAT TCGGCACATC
451  AATTTTCATCG ACCAAATTGC CGGTTGGGAA CATACTGCCT TCGCCGTCGG
501  CTGGATCAAG AAATTCGATT TGTACTTCGG CTGCCGGGAA CGTTACGCCG
551  TCGAGCTCAA AATCGCCTGT TTCCAAACT GCGCCGTTTT GCATCGGTAC
601  ATGGGCAATA ATGGTTTTGC CGATGTTTTT CTGCCAGATT TTGACTGTGC
651  AGATGCCGTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1906; ORF 604.a>:

```

a604.pep
  1  MPEAHFFTRS AACGKVDQRT GHGGGGRNGN RGGTHHRVVQ FAHAQGAYQQ
 51  IDVGGIHGFA TGGGVIGGGR DEGDFRRVRA GGSFGYVADQ THFQRTVSAD
101  FLEFFQSCGI VVDVVLQLEA RVAQVGIIQE NGRNARVDER GFQTAYIRHI
151  NFIDQIAGWE HTAFAVGWIK KFDLYFGCRE RYAVELKIAC FQNC AVLHRY
201  MGNNGFADVF LPDFDCADAV *

```

m604/a604 97.0% identity in 169 aa overlap

```

              10      20      30      40      50      60
m604.pep      MPEAHFFTRSAACGKVDQRTGYGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGVHGF
a604           MPEAHFFTRSAACGKVDQRTGHGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGIHGFA
              10      20      30      40      50      60

              70      80      90      100     110     120
m604.pep      TGGGVIGGGRDEGDFRRVRASGSFGYVADQTHFQRTVSADFLEFFQSRGIVVDVVLQLEA
a604           TGGGVIGGGRDEGDFRRVRAGGSFGYVADQTHFQRTVSADFLEFFQSCGIVVDVVLQLEA
              70      80      90      100     110     120

              130     140     150     160     169
m604.pep      CVAQVGIIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFAVGWI
a604           RVAQVGIIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFAVGWIKKFDLYFGCRE
              130     140     150     160     170     180

a604           RYAVELKIACFQNC AVLHRYMGNNGFADVF LPDFDCADAVX
              190     200     210     220

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1907>:

```

g605.seq
  1  ATGATGACCG AAATGCAACA ACGCGCCCAA CTGCACCGCC AAATTTGGAA
 51  AATCGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTAAACAAT
101  ACGTTCTCGG CACACTTTTC TACCGCTTTA TCAGCGAAAA CTTACCGAC
151  TATATGCAGG CCGGCGACAG CAGCATTGAT TACGCCGCTa tGCCGGACAG
201  CATCATCACG CCCGAAATCA AAGACGATgc cgtcaaagtc aaAGGCTATT
251  TCATCtacc CgGCCAGCTT TTTTgcaata ttgcccgcga agcCCATCAA
301  AACGAAGAGC TCAACACCAA GCTGAAAGaa atCTTTACCG CGATTGAAAG
351  CTCCGCCTCC GGCTAcccgT CCGAACAAAG CATCAAAGGC TTGTTTGACG
401  ACTTCgACAC CACCAGCAGC CGGCTCGGCA GCACCGTTGC CGACAAAAAC
451  AAACGCCTTG CCGCGTCCTT TAAAGGCGTG GCGGAACTCG ATTTTCGGCAA
501  TTTTGAAGAC CACCGCATCG ACCTTTTCGG TGATGCCTAC GAATACCTGA
551  TTTCCAATA CGCcgcCAAC GCAGGCAAAT CCGGCGGCGA ATTTTTCACC
601  CCGCAAAGCG TCTCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGCGAGGA
651  GAAAGTCAAC AAAATCTACG ACCCCGCCTG CGGCTCGGGC AGCCTGCTCT
701  TGCAGGCGAA AAAACAGTTT GACGAACACA TCATCGAAGA AGGCTTCTTC
751  GGGCAGGAAA TCAACCACAC CACCTACAAC CTCGCCCAGC TGAATATGTT
801  TCTGCACAAC GTCAATTACA ACAAATTCCA CATCGAATTG GGCGACACGC
851  TGACCAACCC CAAACTCAA GACAGCAAAC CCTTTGATGC CGTCGTCTCC
901  AATCCGCCCT ATTCCATCGA CTGGATAGGC AGCGACGACC CCACCTtgaT

```



```

951 CAACGACGAC CGCTTTGCCC CCGCAGGCGT ACTCGCACCG AAATCCAAAG
1001 CCGATTTTGC CTTTCATCCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCCGCTA TCGTCTCATT CCCC GGCAATT TTCTATCGCG GCGGCGCAGA
1101 GCAGAAAATc CGCCAATATC TGGTGGAGGG CAACTATGTG GAAACCGTGA
1151 TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCTGCATCGC CGTCAATATC
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AAGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ACCGAAGAAC
1301 ACATTGCCGA AATCGTCAAA CTCTTCGCCG ACAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAA ACGCCGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCCGTCAGC AGCTATGTCG AAGCCGAAGA CACCGCGAG GTCATCGACA
1451 TCAGACAGCT CAACGCCGAA ATCAGCGAAA CCgtcgCcaa AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAA CTTAG

```

This corresponds to the amino acid sequence <SEQ ID 1908; ORF 605.ng>:

g605.pep

```

1 MMTEMQORAQ LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ
101 NEELNNTKLKE IFTAIESSAS GYPSEQGIKG LFDDFDTTSS RLGSTVADKN
151 KRLAAVLKGV AELDFGNFED HRIDLFGDAY EYLISNYAAN AGKSGGEFFT
201 PQSVSKLIAR LAVHGQEKVN KIYDPACGSG SLLLQAKKQF DEHIEEGFF
251 GQEINHNTYIN LARMNMFHNL VNYNKFHIEL GDTLTNPCLK DSKPFDVVS
301 NPPYSIDWIG SDDPTLINDD RFAPAGVLAP KSKADFAPIL HALNYLSGRG
351 RAAIVSFPPI FYRGGAEQKI ROYLVEGNYV ETVIALAPNL FYGTCLAVNI
401 LVLKHKDNT DIQFIDASGF FKKETNNNVL TEEHIAEIVK LFADKADVPH
451 IAQNAAQQTV KONGYNLAVS SYVEAEDTRE VIDIRQLNAE ISETVAKIER
501 LRREIDEVIA EIET*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1909>:

m605.seq

```

1 ATGATGACCG AAATGCAACA ACGCGCCCAA CTGCACCGCC AAATTTGGAA
51 AATTGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTTAAACAAT
101 ACGTTCTCGG CACACTTTTC TACCGCTTTA TCAGCGAAAA CTTACCGAC
151 TATATGCAGG CAGGCGACAG CAGTATTGAT TACGCCGCTA TGCCGGACAG
201 CATCATCACG CCCGAAATCA AAGACGATGC CGTCAAAGTT AAAGGCTATT
251 TCATCTACCC CGGCCAGCTT TTTTGCAATA TTGCCGCCGA AGCCCATCAA
301 AACGAAGAGC TCAACACCAA GCTGAAAGAA ATTTTACCG CGATTGAAAG
351 CTCCGCCTCC GGCTATCCGT CCGAACAGGA CATCAAAGGC CTGTTTGACG
401 ACTTCGACAC CACCAGCAGC CGGCTCGGCA GCACTGTTGC CGACAAGAAC
451 AAACGCCTTG CCGCCGTCCT CAAAGGCGTG GCGGAACCTG ATTTGCGCAA
501 TTTTGAAAC CACCACATCG ACCTTTTCGG CGATGCCTAC GAATACCTGA
551 TTTCCAATA CGCTGCCAAC GCAGGCAAAT CCGGCGGCGA ATTTTTCACC
601 CCGCAAAGCG TATCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGACAGGA
651 GAAAGTCAAC AAAATCTACG ACCCAGCTTG CCGCTCGGGC AGTCTGCTCT
701 TGCAGGCGAA AAAACAGTTT GACGAGCACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACCACAC CACCTACAAC CTCGCCCCGA TGAACATGTT
801 CCTGCACAAC GTCAATTACA ACCAATTCCA CATCGAATTG GCGACACAC
851 TGACCAACCC AAAGCTCAAA GACAGCAAAC CCTTTGATGC CATCGTTTCC
901 AATCCGCCTT ATTCCATCAA CTGGATAGGC AGCGACGACC CCACCTTAAT
951 CAACGACGAC CGCTTTGCCC CCGCAGGCGT ACTTGCCCCG AAATCCAAAG
1001 CCGATTTTGC CTTTCATCCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCCGCCA TCGTCTCATT CCCC GGCAATT TTCTATCGCG GCGGCGCAGA
1101 ACAGAAAATC CGCCAATATC TGGTGGAGGG CAACTACGTG GAAACCGTGA
1151 TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCGGCATCGC CGTCAATATC
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AAGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ATCGAAGAAC
1301 ACATTGCTGA AATCGTCAAA CTCTTCGCCG ATAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAA ACGCTGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCCGTCAGC AGCTATGTCG AAGCCGAAGA CACACGCGAA ATTATCGACA
1451 TCAAACAGCT CAACGCCGAA ATCGGCGAAA CCGTCGCCAA AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAG CATGA

```

This corresponds to the amino acid sequence <SEQ ID 1910; ORF 605>:

m605.pep

```

1 MMTEMQORAQ LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ

```

962

101 NEELNTKLKE IFTAIESSAS GYPSEQDIKG LFDDFDTTSS RLGSTVADKN
 151 KRLAAVLKGV AELDFGNFEN HHIDLFGDAY EYLISNYAAN AGKSGGEFFT
 201 PQSVSKLIAR LAVHGQEKVN KIYDPACGSG SLLQAKKQF DEHIEEGFF
 251 GQEINHHTYN LARMNMFHVN VNYNQFHIEL GDTLTNPCLK DSKPFDIVS
 301 NPPYSINWIG SDDPTLINDD RFAPAGVLAP KSKADFAL HALNYLSGRG
 351 RAAIVSFPGI FYRGGAEQKI RQYLVEGNYV ETVIALAPNL FYGTGIAVNI
 401 LVLSKHKDNT DIQFIDASGF FKKETNNNVL IEEHIAEIVK LFADKADVP
 451 IAQNAAQQTVD KNGYNLAVS SYVEAEDTRE IIDIKQLNAE IGETVAKIER
 501 LRREIDEVIA EIEA*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 605 shows 97.9% identity over a 513 aa overlap with a predicted ORF (ORF 605.ng) from *N. gonorrhoeae*:

m605/g605

	10	20	30	40	50	60
m605.pep	MMTEMQRAQLHRQIWKIADEVGAVDGDWDFKQYVLGTLFYRFISENFTDYMQAGDSSID					
g605	MMTEMQRAQLHRQIWKIADEVGAVDGDWDFKQYVLGTLFYRFISENFTDYMQAGDSSID					
	10	20	30	40	50	60
	70	80	90	100	110	120
m605.pep	YAAMPDSIITPEIKDDAVKVKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS					
g605	YAAMPDSIITPEIKDDAVKVKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m605.pep	GYPSEQDIKGLFDDFDTTSSRLGSTVADKNKRLAAVLKGV AELDFGNFENHHIDLFGDAY					
g605	GYPSEQGIKGLFDDFDTTSSRLGSTVADKNKRLAAVLKGV AELDFGNFEDHRIDLFGDAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m605.pep	EYLISNYAANAGKSGGEFFT PQSVSKLIARLAVHGQEKVNKIYDPACGSGSLLQAKKQF					
g605	EYLISNYAANAGKSGGEFFT PQSVSKLIARLAVHGQEKVNKIYDPACGSGSLLQAKKQF					
	190	200	210	220	230	240
	250	260	270	280	290	300
m605.pep	DEHIEEGFFGQEINHHTYNLARMNMFHNVNYNQFHIELGDTLTNPCLKDSKPFDIVS					
g605	DEHIEEGFFGQEINHHTYNLARMNMFHNVNYNKFHIELGDTLTNPCLKDSKPFDIVS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m605.pep	NPPYSINWIGSDDPTLINDDRFAPAGVLAPKSKADFALHALNYLSGRGAAIVSFPGI					
g605	NPPYSIDWIGSDDPTLINDDRFAPAGVLAPKSKADFALHALNYLSGRGAAIVSFPGI					
	310	320	330	340	350	360
	370	380	390	400	410	420
m605.pep	FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGIAVNILVLSKHKDNTDIQFIDASGF					
g605	FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGIAVNILVLSKHKDNTDIQFIDASGF					
	370	380	390	400	410	420
	430	440	450	460	470	480
m605.pep	FKKETNNNVLT EEHIAEIVKLFADKADVP HIAQNAAQQTVDKNGYNLAVSSYVEAEDTRE					
g605	FKKETNNNVLT EEHIAEIVKLFADKADVP HIAQNAAQQTVDKNGYNLAVSSYVEAEDTRE					

	430	440	450	460	470	480
	490	500	510			
m605.pep	IIDIKQLNAEIGETVAKIERLRREIDEVIAEIEAX					
	: : : :					
g605	VIDIRQLNAEISETVAKIERLRREIDEVIAEIETX					
	490	500	510			

a605.seq

1	ATGATGACCG	AAATACAACA	ACGCGCCCAA	CTGCACCGCC	AAATTTGGAA
51	AATTGCCGAC	GAAGTACGCG	GCGCGGTGGA	TGGCTGGGAC	TTCAAACAAT
101	ACGTCTCTCG	CACACTTTTC	TACCGCTTTA	TCAGCGAAAA	CTTTACCGAC
151	TATATGCGG	CAGGCGACAG	CAGTATTGAT	TACGCGGATA	TGCCGGACAG
201	CATCATCACG	CCCGAAATCA	AAGACGATGC	CGTCAAAGTC	AAAGGCTATT
251	TCATCTACCC	CGGCCAGCTT	TTTTGCAATA	TGCGCGCCGA	AGCCCATCAA
301	AACGAAGAGC	TCAACACCAA	GCTGAAAGAA	ATTTTTACCG	CGATTGAAAG
351	CTCCGCTCC	GGCTATCCGT	CCGACAAGA	CATTAAGAAGC	CTGTTTGACG
401	ACTTCGACAC	CACCAGCAGC	CGGCTCGGCA	GACCGTTGCG	CGACAAGAAC
451	AAACGCCTTG	CCGCCGTCTT	AAAAGGCGTG	GCGGAACCTG	ATTTGCGCAG
501	TTTTGAAGAC	CACCACATCG	ACCTTTTTCG	CGATGCCTAC	GAATACCTGA
551	TTTCCAAGTA	CGCTGCCAA	GCAGGCAAA	CCGGCGGCGA	ATTTTTCAGG
601	CGCCAAAGCG	TATCCAAGCT	GATTGCGCGG	CTGGCGGTGC	ACGGGACAGG
651	GAAAGTAAAC	AAAATCTACG	ACCCAGCTTG	CGGCTCGGGC	AGCCTGCTCT
701	TGCAGGCGAA	AAAACAGTTT	GACGAGCACA	TCATCGAAGA	AGGCTTCTTC
751	GGGCAGGAAA	TCAACCACAC	CACCTACAAC	CTCGCCCGCA	TGAATATGTT
801	TCTGCACAA	GTC AATTACA	ACAAATTTCA	CATCGAATTG	GGCGACACCT
851	TGACCAATCC	CAAACTCAA	GACAGCAAAC	CCTTTGATGC	CGTCGTTTCC
901	AATCCGCCCT	ATTCCATCAA	CTGGATAGGC	AGCGGCGACC	CCACCTTAAT
951	CAACGACGAC	CGCTTTTGCC	CTGCAGGCGT	ACTCGCCCCG	AAATCCAAAG
1001	CCGATTTTGC	CTTCATTCTG	CACGCACTGA	ACTACCTTTT	CGGCAGAGGG
1051	CGCGCGGCCA	TCGTCTCAAT	CCCCGGCAAT	TTCTATCGCG	CGGGCGCAGA
1101	GCAGAAAATC	CGCCAATATC	TGGTGGAGGG	CAACTACGTG	GAAACCGTCA
1151	TCGCCCTTGC	GCCCAATCTC	TTTTACGGCA	CCGGCATCGC	CGTCAATATA
1201	CTGGTTTGTG	CCAAACACAA	AGACAATACC	GACATCCAAT	TCATCGAGAC
1251	AGGCGGCTTC	TTTAAAAAAG	AAACCAACAA	CAACGTCTTA	ACCGAAGAAC
1301	ACATTGCCGA	AATCGTCAAA	CTCTTTCGCG	ATAAAGCCGA	TGTGCCGCAT
1351	ATCGCCCAA	ACGCCGCCCA	GCAAACCGTC	AAAGACAACG	GCTACAACCT
1401	CGCCGTCAGC	AGCTATGTTG	AACCCGAAGA	CACCCGCGAA	ATTATCGACA
1451	TCAACACGCT	TAAACCCGAA	ATCAGCGAAA	CCGTTGCCAA	AATCGAACGG
1501	CTGCGGCGTG	AAATTGACGA	AGTGATTGCA	GAGATTGAAG	CATGA

a605.pep

1	MMTEIQORAQ	LHRQIWKIAD	EVRGAVDGDW	FKQYVLGTLF	YRFISENFTD
51	YMQAGDSSID	YAAMPDSIIT	PEIKDDAVKV	KGIFYIYPGQL	FCNIAAEAHQ
101	NEELNTKLKE	IFTAIESSAS	GYPSEQDIKG	LFDDFDTTSS	RLGSTVADKN
151	KRLAAVLKGV	AELDFGSFED	HHIDFLGDAY	EYLISNYAAN	ACKSGGEEFTT
201	QQSIVSKLIAR	LAVHGEQEKVN	KIYDPACGSG	SLLLQAKKQF	DEHIEEGFFI
251	PQSEINHTTYN	LARMNMFLEH	VNYNKFHIEL	GDTLTNPKLK	DSKPFDAVVS
301	NPPYSINWIG	SGDPTLINDD	RFAPAGVLAP	KSKADFAFIL	HALNYLSGRG
351	RAAIVSFPGI	FYRGGAEQKI	RQYLVEGNYV	ETVIALAPNL	FYGTGIAVNI
401	LVLSKHKDNT	DIQFIDAGGF	FKKETNNNVL	TEEHIAEIVK	LFADKADVPH
451	IAQNAAEQTV	KDNNGYNLAVS	SYVEPEDTRE	IIDIKQLNAE	ISSETVAKIER
501	LRNAAIDQVIA	EIEA*			

	10	20	30	40	50	60
m605.pep	MMTEMQORARLHRQIWKIADEVIRGAVDGVDFKQYVLGTLFYRFISENFTDYMQAGDSSID					
a605	:					
	10	20	30	40	50	60
	MMTEIQORARLHRQIWKIADEVIRGAVDGVDFKQYVLGTLFYRFISENFTDYMQAGDSSID					
	70	80	90	100	110	120
m605.pep	YAAMPDSIITPEIKDDAVKVKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSA					

964

a605	Y A A M P D S I I T P E I K D D A V K V K G Y F I Y P G Q L F C N I A A E A H Q N E E L N T K L K E I F T A I E S S A S	70	80	90	100	110	120
m605.pep	GYPSEQDIKGLFDDFDTTSSRLGSTVADKNKRLAAVLKGVAELDFGNFENHHIDLFGDAY	130	140	150	160	170	180
a605	GYPSEQDIKGLFDDFDTTSSRLGSTVADKNKRLAAVLKGVAELDFGSFEDHHIDLFGDAY	130	140	150	160	170	180
m605.pep	EY L I S N Y A A N A G K S G G E F F T P Q S V S K L I A R L A V H G Q E K V N K I Y D P A C G S G S L L L Q A K K Q F	190	200	210	220	230	240
a605	EY L I S N Y A A N A G K S G G E F F T P Q S V S K L I A R L A V H G Q E K V N K I Y D P A C G S G S L L L Q A K K Q F	190	200	210	220	230	240
m605.pep	D E H I I E E G F F G Q E I N H T T Y N L A R M N M F L H N V N Y N Q F H I E L G D T L T N P K L K D S K P F D A I V S	250	260	270	280	290	300
a605	D E H I I E E G F F G Q E I N H T T Y N L A R M N M F L H N V N Y N K F H I E L G D T L T N P K L K D S K P F D A V V S	250	260	270	280	290	300
m605.pep	N P P Y S I N W I G S D D P T L I N D D R F A P A G V L A P K S K A D F A F I L H A L N Y L S G R G R A A I V S F P G I	310	320	330	340	350	360
a605	N P P Y S I N W I G S G D P T L I N D D R F A P A G V L A P K S K A D F A F I L H A L N Y L S G R G R A A I V S F P G I	310	320	330	340	350	360
m605.pep	F Y R G G A E Q K I R Q Y L V E G N Y V E T V I A L A P N L F Y G T G I A V N I L V L S K H K D N T D I Q F I D A S G F	370	380	390	400	410	420
a605	F Y R G G A E Q K I R Q Y L V E G N Y V E T V I A L A P N L F Y G T G I A V N I L V L S K H K D N T D I Q F I D A G G F	370	380	390	400	410	420
m605.pep	F K K E T N N N V L I E E H I A E I V K L F A D K A D V P H I A Q N A A Q Q T V K D N G Y N L A V S S Y V E A E D T R E	430	440	450	460	470	480
a605	F K K E T N N N V L T E E H I A E I V K L F A D K A D V P H I A Q N A A Q Q T V K D N G Y N L A V S S Y V E P E D T R E	430	440	450	460	470	480
m605.pep	I I D I K Q L N A E I G E T V A K I E R L R R E I D E V I A E I E A X	490	500	510			
a605	I I D I K Q L N A E I S E T V A K I E R L R R E I D E V I A E I E A X	490	500	510			

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1913>:

g606.seq

1	ATGTCCAAAT	TTATCGCCAA	ACAAATCGGTC	GGTGCGGAAG	TCATCGACAC
51	GCCGcgCACC	GAAGAAGAAG	CCTGGCTTCT	GAACACTGTC	GAAGCCCAAg
101	cgcgGGAATG	GAATCTGAAA	ACGCCAGAAG	TCGCCATCTA	CCACTCCCCC
151	GAACCCAAATG	CCTTTGCCAC	GGGCGCATCG	AGAAACAGCT	CCCTGATCGC
201	CGTCAGCacc	gggttgtctcg	accaTatgaC	GCGCGAGcaa	gtggaagccg
251	tgTTGGCGCA	CGAAATGGCG	CACGTCGGCA	ACGGCGCagat	GGTTACGCTG
301	ACGCTGatTC	AAGGCGTGGT	CAATACCTTT	TCGCTGTTCC	GTGCGCGCAT
351	TATTGCCAAC	CTGATTGCCC	GAAACAACGA	CGGCAGCCAG	TCCCAGGGAA
401	CTTATTTCTT	AGTCAGCATG	GTATTCCAAA	TCCTGTTCCG	CTTCCTTGCC
451	AGCCTGATTG	TCATGTGGTT	CAGCCGCCAA	CGCGAATACC	GCGCCGAcgc
501	gggCGcggCA	AAACTGGTGC	GCGCACCgAA	AATGATTTCC	GCCTGCAAAA
551	GGCTTAAAGG	CAACCCGGTC	GATTTGCCCT	AAGAAATGAA	CGCAATGGGC
601	ATCGCCGGAG	ATACGCGCGA	CTCCTTGCTC	AGCACCACC	CTTCGCTGGA
651	CAACCGAATC	GCCCGCCTCA	AATCGCTTTA	A	

This corresponds to the amino acid sequence <SEQ ID 1914; ORF606.ng>:

g606.pep
 1 MSKFIKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
 51 EPNAFATGAS RNSSLIIVST GLLDHMTRE VEAFLAHEMA HVGNGDMVTL
 101 TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
 151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
 201 IAGDTRDSLL STHPSLDNRI ARLKSL*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1915>:

m606.seq
 1 ATGTCCAAAT TTATCGCCAA ACAATCGGTC GCGCGGAAG TTATCGACAC
 51 GCCGCGCACC GAAGAAGAAG CCTGGCTTTT GAACACTGTC GAAGCCCAAG
 101 CGCGGCAATG GAACCTGAAA ACGCCCGAAG TCGCCATCTA CCACTCCCCC
 151 GAACCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
 201 CGTCAGCACC GGTTTGCTCG ACCATATGAC GCGTGACGAA GTGGAAGCCG
 251 TATTGGCGCA CGAAATGGCA CACGTCGGCA ACGGCGATAT GGTACGCTG
 301 ACGCTGATTC AAGGCGTGGT CAATACCTT GTCGTGTTCC TGTCGCGCAT
 351 TATTGCCAAC CTGATTGCCC GAAACAACGA CGGCAGCCAG TCCAGGGAA
 401 CTTATTTTCT GGTGAGCATG GTATTCCAAA TCCTGTTCGG CTTCTTGCC
 451 AGCTTAATTG TCATGTGGTT CAGCCGACAA CGCGAATACC GCGCCGATGC
 501 GGGCGCGGCA AAAGTGGTCG GCGCGCCGAA AATGATTTCG GCCCTGCAAA
 551 GGCTCAAAGG CAACCCGGTC GATTTGCCCC AAGAAATGAA CGCAATGGGC
 601 ATCGCCGGAG ATACGCGCGA CTCCCTGCTC AGCACCACC CTTGCTGGA
 651 CAACCGTATC GCGCGCCTCA AATCGCTTAA A

This corresponds to the amino acid sequence <SEQ ID 1916; ORF 606>:

m606.pep
 1 MSKFIKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
 51 EPNAFATGAS RNSSLIIVST GLLDHMTRE VEAFLAHEMA HVGNGDMVTL
 101 TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
 151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
 201 IAGDTRDSLL STHPSLDNRI ARLKSL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 606 shows 100.0% identity over a 225 aa overlap with a predicted ORF (ORF 606.ng) from *N. gonorrhoeae*:

m606/g606

	10	20	30	40	50	60
m606.pep	MSKFIKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNAFATGAS					
g606	MSKFIKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNAFATGAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m606.pep	RNSSLIIVSTGLLDHMTREVEAVLAHEMAHVGNNGDMVTLTLIQGVVNTFVVFLSRIIAN					
g606	RNSSLIIVSTGLLDHMTREVEAVLAHEMAHVGNNGDMVTLTLIQGVVNTFVVFLSRIIAN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m606.pep	LIARNNDGSQSQGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
g606	LIARNNDGSQSQGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
	130	140	150	160	170	180
	190	200	210	220		
m606.pep	ALQRLKGNPVDLPEEMNAMGIAGDTRDSLLSTHPSLDNRIARLKSLX					
g606	ALQRLKGNPVDLPEEMNAMGIAGDTRDSLLSTHPSLDNRIARLKSLX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1917>:

a606.seq

966

```

1  ATGTCCAAAT TCATCGCCAA ACAATCGGTC GGCGCGGAAG TTATCGACAC
51  GCCGCGCACC GAAGAAGAAG CCTGGCTTTT GAACACTGTC GAAGCCCAAG
101 CGCGGCAATG GAACCTGAAA ACGCCCGAAG TCGCCATCTA CCACTCCCCC
151 GAACCCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
201 CGTCAGCACC GGTTCGCTCG ACCATATGAC GCGTGACGAA GTGGAAGCCG
251 TATTGGCGCA CGAAATGGCA CACGTCGGCA ACGGCGATAT GGTTACGCTG
301 ACGCTGATTC AAGGCGTGGT CAATACCTTT GTCGTGTTCC TGTCGCGCAT
351 TATTGCCAAC CTGATTGCCC GAAACAACGA CGGCAGCCAG TCCCAGGGAA
401 CTTATTTCTT GGTGAGCATG GTATTCCAAA TCCTGTTCGG CTTCTTGCC
451 AGCTTAATTG TCATGTGGTT CAGCCGACAA CGGAATACC GCGCCGACGC
501 GGGCGCGGCA AAATGCTGCG GCGCGCCGAA AATGATTTCG GCCCTGCAAA
551 GGCTTAAAGG CAACCCGGTC GATTGCCCCG AAGAAATGAA CGCAATGGGC
601 ATCGCCGGAG ATACGCGCGA CTCCCTGCTC AGCACCCACC CTTGCTGGA
651 CAACCGAATC GCCCGCCTCA AATCGCTTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1918; ORF 606.a>:

```

a606.pep
1  MSKFIKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51  EPNAFATGAS RNSSLIAVST GLLDHMTRDE VEAVLAHEMA HVGNGDMVTL
101 TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSSL STHPSLDNRI ARLKS*

```

m606/a606 100.0% identity in 226 aa overlap

```

m606.pep      10      20      30      40      50      60
MSKFIKQSVGAEVIDTPRT EEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNAFATGAS
|||||
a606          10      20      30      40      50      60
MSKFIKQSVGAEVIDTPRT EEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNAFATGAS
|||||

m606.pep      70      80      90     100     110     120
RNSSLIAVSTGLLDHMTRDEVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN
|||||
a606          70      80      90     100     110     120
RNSSLIAVSTGLLDHMTRDEVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN
|||||

m606.pep      130     140     150     160     170     180
LIARNNDGSQSQGT YFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS
|||||
a606          130     140     150     160     170     180
LIARNNDGSQSQGT YFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS
|||||

m606.pep      190     200     210     220
ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSIX
|||||
a606          190     200     210     220
ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSIX
|||||

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1919>:

```

g607.seq
1  ATGCTGCTCG accTcgaCCG CTTTTCTTt tccGTCTTCC TGAAAGAAAT
51  CCGCTGCTG ACCGCCCTTG CCCTGCCCAT GCTGTTGGCG CAGGTCGCGC
101 AGGTGGGCAT CGGTTTCGTC GATACCGTGA TGGCGGGCGG TGCGGGCAAG
151 GAAGATTTGG CGGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGGCGC GGTAAAACC GgtgAAGCAG GCGAAACGGG GCGGCAGGGG
301 ATTTGGTTTC GGCTGATTTT GGGGATTTTC GGCATGATT TGTGTGGGC
351 GGCATTACG CCGTTCCGCA ACTGGCTGAC TTTGAGCGAT TATGTGGAAG
401 gcacAAtggc gcAGTATATG CTGTTACCA GCTTGGCGAT GCCGGCGGCA
451 ATGGTACACC GCGACTGCA CGCCTACGCT TCCAGCCTGA ACCGCCCGCG
501 CCGTATTATG TTGGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTTACGGC AAATTCGGTA TGCCCGCTTT GGGTGGCGCA

```

```

601  GGTTCGGCGC  TGGCGACAAT  GGCGGTGTTC  TGGTTCAGCG  CGCTGGCATT
651  GTGGATTTAT  ATCGCCAAGG  AAAAATTCTT  CCGCCCGTTC  GGACTGACAG
701  CGAAATTCGg  caaACCGGat  tGGgcGGTGT  TCAAACAGAT  TtGGAAAAATC
751  gGcgcgCCCA  TCGGGCTGTC  TTATTTTTTG  GAAgccaGcg  cGTTTTCGTT
801  TATCGTGTTC  TTGATTGCGC  CTtccggCGA  GGATTATGTG  GCGGCGCAGC
851  AGGTCGGCAT  CAGTTGTGTC  GGGATTCTCT  ATATGATTCC  GCAAAGCGTC
901  GGCTCGGCAG  GGACGGTGCG  CATCGGCTTT  TCGCTTGGGC  GGCGCGAATT
951  TTCGCGGGCG  CGTTATATTT  CAGGAGTGTC  GCTGGTGTG  GGCTGGGTGC
1001 TCGCCGTGAT  TACCGTGCTT  TCCTTGGTAT  TATTCCGTTC  GCCGCTGGCA
1051 AGCATGTACA  ACGATGaTCC  GGCAGTTTAA  AGCATCGCCT  CCACCGTCCT
1101 GCTGTTTCGCC  GGCCTGTtcc  aACCGGCAGA  CTTACCCCAA  TGTATCGCGT
1151 CCTATGCCCT  GCGCGGCTAC  AAAGTCACCA  AGGTGCCGAT  GTTCATCCAC
1201 GCCGCCGCCT  TCTGGGGCTG  CGGCCTGCTG  CCGGGCTATC  TGCTCGCCTA
1251 CCGTTTCGAT  ATGGGCATTT  ACGGCTTCTG  GACGGCATTG  ATTGCCTCGC
1301 TCACCATCGC  AGCCGTCGCC  TTGGTGTGGT  GCTTGGAATA  ATACAGTATG
1351 GAGTTGGTCA  AATCACACAA  GGCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1920; ORF 607.ng>:

g607.pep

```

1  MLLDLDRFSF  SVFLKEIRLL  TALALPMLLA  QVAQVGIGFV  DTVMAGGAGK
51  EDLAAVALGS  SAFATVYITF  MGIMAALNPM  IAQLYGAGKT  GEAGETGRQG
101 IWFGLLIGIF  GMILMWAAIT  PFRNWLTLSD  YVEGTMAYQM  LFTSLAMPAA
151 MVHRAHAYHA  SSLNRRLIM  LVSFAAFVLN  VPLNYIFVYG  KFGMPALGGA
201 GCGVATMAVF  WFSALALWIY  IAKEKFFRPF  GLTAKFGKPD  WAVFKQIWKI
251 GAPIGLSYFL  EASAFSFIWF  LIAPFGEDYV  AAQQVGISLS  GILYMIPOSV
301 GSAGTVRIGF  SLGRREFSRA  RYISGVSLVS  GWVLAVITVL  SLVLFRSPLA
351 SMYNDPAVL  SIASTVLLFA  GLFQPADFTQ  CIASYALRGY  KVTKVPFMFIH
401 AAAFWGCGLL  PGYLLAYRFD  MGIYGFWTAL  IASLTIAAVA  LVWCLEKYSM
451 ELVKSHKAV*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1921>:

m607.seq

```

1  ATGCTGCTCG  ACCTCAACCG  CTTTTCCTTT  CCCGCTCTCC  TGAAAGAAGT
51  CCGCCTGCTG  ACCACTCTTG  CCCTGCCCAT  GCTGTTGGCG  CAGGTCGCGC
101 AGGTGGGCAT  CGGTTTTGTC  GATACTGTGA  TGGCGGGCGG  TGCGGGCAAG
151 GAAGACTTGG  CGGCGGTGGC  TTTGGGCAGC  AGCGCGTTTG  CCACGGTTTA
201 TATTACCTTT  ATGGGCATTA  TGGCGGCGCT  GAACCCGATG  ATTGCCCAGC
251 TTTACGGCGC  GGGTAAAACC  GACGAAGTGG  GCGAAACGGG  GCGGCAGGGG
301 ATTTGGTTCG  GGCTGTTTTT  GGGCGTGTTC  GGCATGGTCT  TGATGTGGGC
351 GGCGATTACG  CCGTTCGCCA  ACTGGCTGAC  CTTGAGCGAT  TATGTGGAAG
401 GCACGATGCG  GCAGTATATG  TTGTTACCA  GCTTGGCGAT  GCCGGCGGCA
451 ATGGTACACC  GCGCGCTGCA  CGCCTACACT  TCCAGCCTGA  ACCGCCCGCG
501 CCTGATTATG  TTGGTCAGCT  TTGCGGCGTT  TGTGTTGAAC  GTGCCGCTGA
551 ACTATATTTT  CGTTTACGGC  AAATTCGGTA  TGCCCGCTTT  GGGCGGCGCA
601 GGCTGCGGAC  TGGCGACGAT  GGCGGTGTTT  TGGTTCAGCG  CGCTGGCATT
651 GTGGATTTAT  ATCGCCAAGG  AAAATTCTTT  CCGCCCATTC  GGACTGACGG
701 CGAAATTCGG  CAAACCGGAT  TGGGCGGTGT  TCAAACAGAT  TTGGAAAAATC
751 GCGCACCCCA  TCGGGCTGTC  TTATTTTTTG  GAAGCCAGCG  CGTTTTTCGT
801 TATCGTGTTC  TTGATTGCGC  CTTTCGGCGA  GGATTATGTG  GCGGCGCAGC
851 AGGTGCGCAT  CAGTTTGTG  GGGATTCTCT  ATATGATTCC  GCAAAGCGTC
901 GGCTCGGCGG  GGACGGTGCG  CATCGGCTTT  TCGCTTGGGC  GGCGCGAATT
951 TTCGCGGGCG  CGTTATATTT  CGGGCGTGTC  ACTGGTGTTA  GGATGGATGC
1001 TCGCCGTGAT  TACCGTGCTT  TCCTTGGTAT  TATTCCGTTC  GCCGCTGGTA
1051 AGTATGTACA  ACAATGATCC  GCGGTTTTTA  AGCATCGCCG  CCACCGTCTT
1101 ACTGTTTCGCC  GGCTTGTTTC  AACCAGCAGA  CTTACCCCAA  TGTATCGCCT
1151 CCTACGCCTT  GCGCGGCTAC  AAAGTTACAA  AGGTGCCGAT  GTTCATCCAC
1201 GCCGCCGCCT  TTTGGGGCTG  CGGCCTGCTG  CCGGGCTATC  TGCTCGCCTA
1251 CCGTTTCAAT  ATGGGCATTT  ACGGCTTCTG  GACGGCATTG  ATTGCCTCGC
1301 TCACCATCGC  CGCCATCGCC  TTGGTGTGGT  GCTTGGAATT  GTGCAGTAGG
1351 GAGATGGTCA  GATCGCATAA  GGCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1922; ORF 607>:

m607.pep

```

1  MLLDLNRFSS  PVFLKEVRLL  TTLALPMLLA  QVAQVGIGFV  DTVMAGGAGK
51  EDLAAVALGS  SAFATVYITF  MGIMAALNPM  IAQLYGAGKT  DEVGETGRQG

```

968

101 IWFGFLFLGVF GMVLMWAAIT PFRNWLTLSD YVEGTMAQYM LFTSLAMPAA
 151 MVHRALHAYT SSLNRPR LIM LVSF AAFVLN VPLNYIFVYG KFGMPALGGA
 201 GCGLATMAVF WFSALALWIY IAKENFFRPF GLTAKFGKPD WAVFKQIWKI
 251 GAPIGLSYFL EASAFSFIVF LIAPFGEDYV AAQQVGISLS GILYMIPQSV
 301 GSAGTVRIGF SLGRREFSRA RYISGVSLVL GWMLAVITVL SLVLFERSPLV
 351 SMYNNDDPAVL SIAATVLLFA GLFQPADFTQ CIASYALRGY KVTKVPMFIH
 401 AAAPWGCGLL PGYLLAYRFN MGIYGFWTAL IASLTIAAIA LVWCLELCSR
 451 EMVRSHKAV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 607 shows 94.8% identity over a 459 aa overlap with a predicted ORF (ORF 607.ng) from *N. gonorrhoeae*:

m607/g607

	10	20	30	40	50	60
m607.pep	MLLDLNRFSFPVFLKEVRLTTLALPMLLAQVAQVGIGFVDVTVMAGGAGKEDLAAVALGS					
g607	MLLDLDRFSFSVFLKEIRLLTALPMLLAQVAQVGIGFVDVTVMAGGAGKEDLAAVALGS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m607.pep	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGFLGVFGMVLMWAAIT					
g607	SAFATVYITFMGIMAALNPMIAQLYGAGKTGEAGETGRQGIWFGFLILGIFGMILMWAAIT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m607.pep	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAA MVHRALHAYTSSLNRPR LIMLVSF AAFVLN					
g607	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAA MVHRALHAYASSLNRPR LIMLVSF AAFVLN					
	130	140	150	160	170	180
	190	200	210	220	230	240
m607.pep	VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFGKPD					
g607	VPLNYIFVYGKFGMPALGGAGCGVATMAVFWFSALALWIYIAKEKFFRPFGLTAKFGKPD					
	190	200	210	220	230	240
	250	260	270	280	290	300
m607.pep	WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMIPQSV					
g607	WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMIPQSV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m607.pep	GSAGTVRIGFSLGRREFSRARYISGVSLVLGWMLAVITVLSLVLFERSPLVSMYNNDDPAVL					
g607	GSAGTVRIGFSLGRREFSRARYISGVSLVSGWVLAVITVLSLVLFERSPLASMYNNDDPAVL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m607.pep	SIAATVLLFAGLFQPADFTQCIASYALRGYKVTKVPMFIHAAAPWGCGLLPGYLLAYRFN					
g607	SIASVLLFAGLFQPADFTQCIASYALRGYKVTKVPMFIHAAAPWGCGLLPGYLLAYRFD					
	370	380	390	400	410	420
	430	440	450	460		
m607.pep	MGIYGFWTALIASLTIAAIALVWCLELCSREMVRSHKAVX					
g607	MGIYGFWTALIASLTIAAVALVWCLEKYSMELVKSHKAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1923>:

```
a607.seq
1   ATGCTGCTCG ACCTCAACCG CTTTTCCTTT TCCGTCTTCC TGAAAGAAGT
51  CCGCCTGCTG ACCGCTCTTG CCCTGCCCAT GCTGTTGGCG CAGGTCGCGC
101 AGGTGGGCAT CGGTTTGTG GATACCGTGA TGGCGGGCGG TCGGGGCAAG
151 GAAGACTTGG CGGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGCGCG GGTAAAACG GACGAAGTGG GCGAAACGGG ACGGCAGGGG
301 ATTTGGTTCG GGCTGTTTTT GGGCGTGTTT GGCATGGTCT TGATGTGGGC
351 GGCATTACG CCGTCCGCA ACTGGCTGAC CTTGAGCGAT TATGTGGAAG
401 GCACAATGGC GCAGTATATG CTGTTACCA GCTTGGCGAT GCCGGCGGCA
451 ATGGTACACC GCGCACTGCA CGCCTACGCC TCCAGCCTGA ACCGCCCGCG
501 CCTGATTATG TTGGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCCGTGA
551 ACTATATTTT CGTTTACGGC AAATTCGGTA TGCCCGCTTT GGGCGGCGCA
601 GGCTGCGGAC TGGCGACGAT GCGGCTGTTT TGGTTCAGCG CGCTGGCATT
651 GTGGATTAT ATCGCCAAGG AAAATTTCTT CCGCCATTTC GGAATGACGG
701 CGAAATTCGG CAAACCGGAT TGGGCGGTGT TCAAACAGAT TTGGAAAATC
751 GGGCGACCCA TCGGGCTGTC TTATTTTTTG GAAGCCAGCG CGTTTTCGTT
801 TATCGTGTTT TTGATTGCGC CTTTCGGCGA GGATTATGTG GCGGCGCAGC
851 AGGTCCGCAT CAGTTGTGCG GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTCGGCGG GGACGGTGCG CATCGGCTTT TCGCTTGGGC GCGCGGAATT
951 TTCGCGGGCG CGTTATATTT CCGGCGGTGT ACTGGTGTCA GGATGGATGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCCGTTT GCCGCTGGTA
1051 AGTATGTACA ACAATGATCC GCGGCTTTTA AGCATCGCCG CCACCGTCTT
1101 ACTGTTGCGC GGCTTGTTCC AACCGGCAGA CTTACCCCAA TGTATCGCCT
1151 CCTACGCCTT GCGCGGCTAC AAAGTTACAA AGGTGCCGAT GTTCATCCAC
1201 GCCGCCGCTT TTTGGGGCTG CCGTCTGCTG CCGGGCTACC TGCTCGCCTA
1251 CCGTTTCGAT ATGGGCATTT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC CGCCATCGCC TTGGTGTGGT GCTTGAATT GTGCAGTAGG
1351 GAGATGGTCA GATCGCATAA GGCTGTCTGA
```

This corresponds to the amino acid sequence <SEQ ID 1924; ORF 607.a>:

```
a607.pep
1   MLLDLNRFSF SVFLKEVRLL TALALPMLLA QVAQVGIGFV DTMAGGAGK
51  EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT DEVGETGRQG
101 IWFGLELGVF GMVLMWAAIT PFRNWLTLSD YVEGTMAQYM LFTSLAMPAA
151 MVHRALHAYA SSLNRPR LIM LVSF AAFVLN VPLNYIFVYG KFGMPALGGA
201 GCGLATMAVF WFSALALWIY IAKENFFRPF GLTAKFGKPD WAVFKQIWKI
251 GAPIGLSYFL EASAFSFIVF LIAPFGEDYV AAQQVGISLS GILYIMIPQSV
301 GSAGTVRIGF SLGRREFSRA RYISGVSLVS GWMLAVITVL SLVLFPSPLV
351 SMYNDPAVL SIAATVLLFA GLFQPADFTQ CIASYALRGY KVTKVPFIH
401 AAFAWGCGLL PGYLLAYRFD MGIYGFWTAL IASLTIAAIA LVWCLELCRS
451 EMVRSHKAV*
```

m607/a607 98.9% identity in 459 aa overlap

	10	20	30	40	50	60
m607.pep	MLLDLNRFSFPVFLKEVRLLTTALALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS					
a607	MLLDLNRFSFSVFLKEVRLLTALALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m607.pep	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGFLGVFGMVLMWAAIT					
a607	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGFLGVFGMVLMWAAIT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m607.pep	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAA MVHRALHAYTSSLNRPR LIMLVSF AAFVLN					
a607	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAA MVHRALHAYASSLNRPR LIMLVSF AAFVLN					
	130	140	150	160	170	180
	190	200	210	220	230	240

970

m607.pep	VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFGKPD
a607	VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFGKPD
	190 200 210 220 230 240
m607.pep	250 260 270 280 290 300
	WAVFKQIWKIGAPIGLSYFLEASAFSFIIVFLIAPFGEDYVAAQQVGISLSGILYMIPQSV
a607	WAVFKQIWKIGAPIGLSYFLEASAFSFIIVFLIAPFGEDYVAAQQVGISLSGILYMIPQSV
	250 260 270 280 290 300
m607.pep	310 320 330 340 350 360
	GSAGTVRIGFSLGRREFSRARYISGVSLVLGWLAVITVLSLVLFRSPLVSMYNNDPAVL
a607	GSAGTVRIGFSLGRREFSRARYISGVSLVSGWLAVITVLSLVLFRSPLVSMYNNDPAVL
	310 320 330 340 350 360
m607.pep	370 380 390 400 410 420
	SIAATVLLFAGLFQPADFTQCIASYALRGYKVTKVPFMIHAAAFWGCGLLPGYLLAYRFN
a607	SIAATVLLFAGLFQPADFTQCIASYALRGYKVTKVPFMIHAAAFWGCGLLPGYLLAYRFD
	370 380 390 400 410 420
m607.pep	430 440 450 460
	MGIYGFWTALIASLTIAAIALVWCLELCSREMVRSRKAVX
a607	MGIYGFWTALIASLTIAAIALVWCLELCSREMVRSRKAVX
	430 440 450 460

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1925>:

g608.seq

```

1  ATGTCCGCC TCCTCCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51  CAGCCGCTCG GAACTTACCT CCTTTGCAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGCT GAAACTGGCG GGACGCATCA CAGAAGACGG TTTGCTCTCG
151 GCGGGAAACG GCTTTGCAGA CACCGAAATT ACCTCCGCA ACAGCGCGAT
201 ACGGAAAATC CTCCAAGGCG GCGAACCCGG GGCTGGCGAC ATCAGGCTCG
251 AAGGCGACCT CATCCTCGGC ATcGCGGTAC TGTCCCTGCT CGGCAGCCTG
301 CGTTCCCGCG CATCGGacgA ATTGGCACGG ATTTTCGGCA CGCAGGCAGg
351 catcggcagc CGTGCCACCG ACATCGGACA CGGCaTCaaa cAAATCGGCA
401 GGAACATCGC CGAACAATC GGCGGATTTT CCCGCGAACC CGAGTCCgCa
451 aacaccggca acgaagccct tgccgactgc ctCGACGAAA TAAGCAGACT
501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACAGG CTCGAACGCG
551 ACATTGGAT AGACTAA

```

This corresponds to the amino acid sequence <SEQ ID 1926; ORF 608.ng>:

g608.pep

```

1  MSALLPIINR LILQSPDSRS ELTSFAGKTL TLNIAGLKLA GRITEDGLLS
51  AGNGFADTEI TFRNSAIRKI LQGGEPGAGD IRLEGDLILG IAVLSLLGSL
101 RSRASDELAR IFGTQAGIGS RATDIGHGIK QIGRNIAEQI GGFSREPESA
151 NTGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1927>:

m608.seq

```

1  ATGTCCGCC TCCTCCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51  CAGCCGCTCG GAACTTGCAG CCTTTGCAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGCT GAAACTGGCG GGACGCATCA CGGAAGACGG TTTGCTCTCG
151 GCGGGAAACG GCTTTGCAGA CACCGAAATT ACCTCCGCA ACAGCGCGGT
201 ACAGAAAATC CTCCAAGGAG GCGAACCCGG GGCGGGCGAC ATCGGGCTCG
251 AAGGCGACCT CATCCTCGGC ATCGCGGTAC TGTCCCTGCT CGGCAGCCTG
301 CGTTCCCGCG CATCGGACGA ATTGGCACGG ATTTTCGGCA CGCAGGCAGA
351 CATCGGCAGC CGTGCCGCGG ACATCGGACA CGGCATCAAA CAAATCGGCA
401 GGAACATCGC CGAACAATC GGCGGATTTT CCCGCGAATC CGAGTCCGCA
451 AACATCGGCA ACGAAGCCCT TGCCGACTGC CTCGACGAAA TAAGCAGACT

```

971

501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACGCG
551 ACATTGGAT AGACTAA

This corresponds to the amino acid sequence <SEQ ID 1928; ORF 608>:

m608.pep
1 MSALLPIINR LILQSPDSRS ELAAFAGKTL TLNIAGLKLA GRITEDGLLS
51 AGNGFADTEI TFRNSAVQKI LQGGEPEGAGD IGLEGDLILG IAVLSLLGSL
101 RSRASDELAR IFGTQADIGS RAADIGHGIK QIGRNIAEQI GGFSRESESA
151 NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 608 shows 95.2% identity over a 188 aa overlap with a predicted ORF (ORF 608.ng)

from *N. gonorrhoeae*:

m608/g608

	10	20	30	40	50	60
m608.pep	MSALLPIINRLILQSPDSRS ELAAFAGKTL TLNIAGLKLAGRITEDGLLSAGNGFADTEI					
	:					
g608	MSALLPIINRLILQSPDSRSELT SFAGKTL TLNIAGLKLAGRITEDGLLSAGNGFADTEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m608.pep	TFRNSAVQKILQGGEPEGAGDIGLEGDLILG IAVLSLLGSLRSRASDELARIFGTQADIGS					
	:					
g608	TFRNSAIRKILQGGEPEGAGDIRLEGLDLILG IAVLSLLGSLRSRASDELARIFGTQAGIGS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m608.pep	RAADIGHGIKQIGRNIAEQIGGFSRESESANIGNEALADCLDEISRLRDGVERLNERLDR					
	:					
g608	RATDIGHGIKQIGRNIAEQIGGFSREPESANTGNEALADCLDEISRLRDGVERLNERLDR					
	130	140	150	160	170	180
	189					
m608.pep	LERDIWIDX					
g608	LERDIWIDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1929>:

a608.seq
1 ATGTCCGCCC TCCTCCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51 CAGCCGCTCG GAACTTGCCG CCTTCGCAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGTT GAACTGGCG GGACGCATCA CGGAAGACGG TTTGCTCTCG
151 GCGGGAAACG GCTTTGCAGA CACCGAAATC ACCTTCCGCA ACAGCGCGGT
201 ACAGAAAATC CTCCAAGGCG GCGAACCCGG GGCGGGCGAC ATCGGGCTCG
251 AAGGCGACCT CATCCTCGGC ATCGCGGTAC TGTCCCTGCT CGGCAGCCTG
301 CGTTCCCGCG CATCGGACGA ATTGGCACGG ATTTTCGGCA CGCAGGCAGA
351 CATCGGCAGC CGTGCCGCCG ACATCGGACA CGGCATCAAA CAAATCGGCA
401 GGAACATCGC CGAACAAATC GGCAGATTTT CCCGCGAACC CGAGTCCGCA
451 AACATCGGCA ACGAAGCCCT TGCCGACTGC CTCGACGAAA TAAGCAGACT
501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACGCG
551 ACATTGGAT AGACTAA

This corresponds to the amino acid sequence <SEQ ID 1930; ORF 608.a>:

a608.pep
1 MSALLPIINR LILQSPDSRS ELAAFAGKTL TLNIAGLKLA GRITEDGLLS
51 AGNGFADTEI TFRNSAVQKI LQGGEPEGAGD IGLEGDLILG IAVLSLLGSL
101 RSRASDELAR IFGTQADIGS RAADIGHGIK QIGRNIAEQI GRFSREPESA
151 NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

m608/a608 98.9% identity in 188 aa overlap

10 20 30 40 50 60

972

```

m608.pep      MSALLPIINRLILQSPDSRSELAAFAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI
               |||||||||||||||||||||||||||||||||||||||||||||||||||
a608           MSALLPIINRLILQSPDSRSELAAFAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI
               10      20      30      40      50      60

               70      80      90      100     110     120
m608.pep      TFRNSAVQKILQGGEPPGAGDIGLEGDLILGIAVLSLLGSLRSRASDELARIFGTQADIGS
               |||||||||||||||||||||||||||||||||||||||||||||||||||
a608           TFRNSAVQKILQGGEPPGAGDIGLEGDLILGIAVLSLLGSLRSRASDELARIFGTQADIGS
               70      80      90      100     110     120

               130     140     150     160     170     180
m608.pep      RAADIGHGIKQIGRNIAEQIGGFSRESESANIGNEALADCLDEISRLRDGVERLNERLDR
               |||||||||||||||||||||||||||||||||||||||||||||||||||
a608           RAADIGHGIKQIGRNIAEQIGGFSRESESANIGNEALADCLDEISRLRDGVERLNERLDR
               130     140     150     160     170     180

               189
m608.pep      LERDIWIDX
               |||||||
a608           LERDIWIDX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1931>:

```

g609.seq
1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAACTCTTGA
51 TGC GTTTGTC GGCAATCAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACGAATTTTCG GGT TTTTCGTA GGCTTTTTCG GTAACGTATT TTTCATCGGG
151 GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCCTGCGTT TCCACATAAT
201 CGATAACTTC CTCGATACCG ACTTCGGCAT CGGAAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGATTATG CGCGCCATAT TGGGAAATTT CTTTGAACA
301 CGGGCAAAGC GAGGTTACGG GAATCATGAC CTTCACTAGT TGGCCGTATG
351 CCCCGTCTTT CATTTCACCC GTGAGGCTGA CATCATAATC CAGtaa

```

This corresponds to the amino acid sequence <SEQ ID 1932; ORF 609.ng>:

```

g609.pep
1  MVVDRLEILA LDETLDFAV GNQRSSDIAH HIFHEFRV FV GLFGNVFFIG
51 AFEQAVELAA RLRFHIIDNF LDTDFGIGSQ ADGNVRTLIM RAILGNFFGT
101 RAKRGYGNHD LHTVAVCPVF HFTREADIII Q*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1933>:

```

m609.seq
1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAACTCTTGA
51 TGC GTTTGTC GGCAATCAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACGAATTTTCG GGT TTTTCGTA GGCTTTTTCG GTAACGTATT TTTCATCGGG
151 GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCCTGCGCC TCCACATAAT
201 CGATGACTTC CTCGATACCG ACTTCGGCAT CGGCAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGTTTGTG CGCGCCGTAT TGGGAAATTT CTTTGAACA
301 CGGGCAAAGC GAGGTTACGG GAATCATGAC CTTCACTAGT TGGCCGTATG
351 CCCCGTCTTT GATTTCGCCC GTGAGACAGA CATCATAATC CAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1934; ORF 609>:

```

m609.pep
1  MVVDRLEILA LDETLDFAV GNQRSSDIAH HIFHEFRV FV GFFGNVFFIG
51 AFEQAVELAA RLRLHIIDDF LDTDFGIGSQ ADGNVRTLVV RAVLGNFFGT
101 RAKRGYGNHD LHTVAVCPVF DFARETDIII Q*

```

m609/g609 93.1% identity in 131 aa overlap

```

               10      20      30      40      50      60
m609.pep      MVVDRLEILALDDETLDFAVGNQRSSDIAHHIFHEFRV FV GFFGNVFFIGAFEQAVELAA
               |||||||||||||||||||||||||||||||||||||||||||||||||||
g609           MVVDRLEILALDDETLDFAVGNQRSSDIAHHIFHEFRV FV GLFGNVFFIGAFEQAVELAA
               10      20      30      40      50      60

               70      80      90      100     110     120
m609.pep      RLRLHIIDDFLDTDFGIGSQADGNVRTLVVRAVLGNFFGTRAKRGYGNHDLHTVAVCPVF
               ||:||||:||||||||||||||||||:|:|||||||||||||||||||||

```

973

```

g609      RLRFHIIIDNFDLDTDFGIGSQADGNVRTLIMRAILGNFFGTRAKRGYGNHDLHTVAVCPVF
           70      80      90      100     110     120

           130
m609.pep  DFARETDIIIQX
           |:|:|:|:|:|:|
g609      HFTREADIIIQX
           130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1935>:

```

a609.seq
1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAACCTCTTGA
51 TGCGTTTGTC GGCAATCAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACGAATTTTCG GGTTTTCGTA GGCTTTTTTCG GTAACGTATT TTTTCATCGGG
151 GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCCTGCGCC TCCACATAAT
201 CGATGACTTC CTCGATACCG ACTTCGGCAT CGGCAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGGTTGTG CGCGCCATAT TGGGAAATT CTTTGGAACA
301 CGGGCAAAGC GAGGTTACGG GAATCATGAC CTTCATACTG TGGCCGTATG
351 CACCGTCTTT CATTTGCCCC GTGAGGCTGA CATCATAATC CAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1936; ORF 609.a>:

```

a609.pep
1  MVVDRLEILA LDETLDADFV GNQRSSDIAH HIFHEFRVFV GFFGNVFFIG
51 AFEQAVELAA RLRLHIIDDF LDTDFGIGSQ ADGNVRTLVV RAILGNFFGT
101 RAKRGYGNHD LHTVAVCTVF HFAREADIII Q*

```

m609/a609 96.9% identity in 131 aa overlap

```

           10      20      30      40      50      60
m609.pep  MVVDRLEILALDDETLDADFVGNQRSSDIAHHIFHEFRVFVGFFGNVFFIGAFEQAVELAA
           |||
a609      MVVDRLEILALDDETLDADFVGNQRSSDIAHHIFHEFRVFVGFFGNVFFIGAFEQAVELAA
           10      20      30      40      50      60

           70      80      90      100     110     120
m609.pep  RLRLHIIDDFLDTDFGIGSQADGNVRTLVVRAVLGNFFGTRAKRGYGNHDLHTVAVCPVF
           |||
a609      RLRLHIIDDFLDTDFGIGSQADGNVRTLVVRAILGNFFGTRAKRGYGNHDLHTVAVCTVF
           70      80      90      100     110     120

           130
m609.pep  DFARETDIIIQX
           |||:|:|:|:|:|
a609      HFAREADIIIQX
           130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1937>:

```

g610.seq
1  ATGATTGGAG GGCTTATGCA ATTTCCCTTAC CGCAATGTTT CGGCTTCGCG
51 TATGCGCCGT ATGCGCAGGG ATGATTTTTC ACGCCGCCTG ATGCGCGAGC
101 ATATGCTGAC CGCGATGAT TTGATTATC CGGTGTTCTG ATTGGAGGGG
151 GCGGCGCGCG AGGAGGATGT GCCTTCTATG CCGGGCGTGA AGCGTCAGAG
201 TTTGGACAGG CTGCTGTGTA CGGCGGAAGA GCGGTGAAG CTCGGTATTC
251 CGATGTTGGC ACTCTTTCCC GTGGTTACGG CAAACAAAC CGGGCGTGCG
301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG tccgagccTT
351 GCGCGAGAGG TttcCgaac tggggattat gacggatgtc gcgctcgAtc
401 cttatacggT gcacGGTCAG GACGGACTGA CGGACgaaaa cggttaCGTG
451 ATGAatgATg aaaCCGTAGA AGTCTTGGTG AAACAGGCTT TATGTCATGC
501 AGAGGCGGGC ACGCAGGTCG TTGCTCCTTC CGATATGATG GACGGGCGTA
551 TCGGCGCCAT CCGCGAGGCT TTGGAGGATG CCGGACATAT CCATACGCGG
601 ATTATGGCAT ATTCCGCCAA ATATGCTTCT GCATTCTACG GCCCTTTCCG
651 TGATGCGGTA GGCAGTTCGG GCAATTGGG AAAGGCAGAT AAAAAGACCT
701 ATCAGATGGA TCCTGCAAAT ACCGATGAGG CGCTGCATGA AGTGGCGCTC
751 GATATTGAGG AAGGTGCGGA TATGGTGATG GTGAAGCCCC GTTGCCCGTA

```

```

801 TTTGGACGTT GTCCGCCGCG TGAAGGACGA GTTCGGCGTA CCGACTTATG
851 CCTATCAGGT TTCGGGCGAA TATGCGATGT TGCAGGCGGC GGTGCCCAAC
901 GGCTGGCTGG ACGGCGGCAA AGTGGTTTTG GAAAGCCTGC TGGCATTCAA
951 ACGTGCGGGT GCGGACGGGA TTTTGACCTA TTACGCCATT GAGGCGGCAA
1001 AGATGCTGAA GCGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1938; ORF 610.ng>:

```

g610.pep
1  MIGGLMQFPY RNPASRMRR MRRDDFSRRL MREHMLTADD LIYPVFVLEG
51  AAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTGRA
101 QEAYNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHGG DGLTDENGYV
151 MNDETVEVLV KQALCHAEAG TQVVAPSDMM DGRIGAIREA LEDAGHIHTR
201 IMAYSAKYAS AFYGPFRDAV GSSGNLGKAD KKTYQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFGV PTYAYQVSGE YAMLQAAVAN
301 GWLDGGKVVL ESLLAFKRAG ADGILTYIAI EAAKMLKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1939>:

```

m610.seq
1  ATGATTGGAG GGCTTATGCA GTTTCCTTAC CGCAATGTTT CCGCTTCGCG
51  TATGCGCCGT ATGCGCAGGG ACGATTTTTC ACGCCGCCTG ATGCGCGAAC
101 ACACGCTGAC CGCCGATGAT TTGATTATAT CCGGTGTCGT ATTGGAGGGG
151 TCGGCGCGCG AGGAGGATGT GCCTTCTATG CCGGGTGTGA AGCGTCAAAG
201 TTTGGACAGG CTGCTGTTTA CGGCGGAAGA GGCGGTAAAG CTCGGTATTC
251 CGATGTTGGC ACTGTTCCCC GTGGTTACGG CAAACAAAAC CGAGCGTGCG
301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG TCCGCGCCTT
351 GCGCGAGAGG TTTCCCGAAC TGGGCATTAT GACGGATGTC GCGCTCGATC
401 CTTATACGGT TCACGGTCAG GACGGGCTGA CGGACGAAA CGGTATGTG
451 ATGAACGATG AAACCGTAGA GGTTTTGGTC AAGCAGGCTT TGTGCCACGC
501 TGAAGCGGGC GCGCAGGTGG TTGCCCTTTC CGATATGATG GACGGGCGTA
551 TCGGTGCGAT TCGCGAGGCG TTGGAGGATG CCGGGCATAT CCATACGCGG
601 ATTATGCGCT ATTCCGCCAA ATATGCTTCT GCATTTTACG GCCCTTTCCG
651 TGATGCGGTA GGCAGTTCGG GCAATTTGGG CAAGGCAGAT AAAAAGACCT
701 ACCAGATGGA TCCGGCAAAT ACCGATGAGG CGTTGCACGA AGTGGCGTTG
751 GACATTCAGG AAGGTGCGGA TATGGTAATG GTCAAGCCCG GTTTGCCGTA
801 TTTGGACGTT GTCCGCCGCG TAAAGGACGA GTTCGGTGTG CCGACTTATG
851 CCTATCAGGT TTCGGGAGAA TACGCGATGT TGCAGGCAGC GATTGCCAAC
901 GGCTGGCTGG ACGGCGGCAA AGTGGTTTTG GAAAGCCTGC TGGCATTCAA
951 ACGTGCGGGT GCGGACGGGA TTTTGACCTA TTACGCTATT GAGGCGGCAA
1001 AGATGTTGAA GCGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1940; ORF 610>:

```

m610.pep
1  MIGGLMQFPY RNPASRMRR MRRDDFSRRL MREHTLTADD LIYPVFVLEG
51  SAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTERA
101 QEAYNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHGG DGLTDENGYV
151 MNDETVEVLV KQALCHAEAG AQVVAPSDMM DGRIGAIREA LEDAGHIHTR
201 IMAYSAKYAS AFYGPFRDAV GSSGNLGKAD KKTYQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFGV PTYAYQVSGE YAMLQAAIAN
301 GWLDGGKVVL ESLLAFKRAG ADGILTYIAI EAAKMLKR*

```

m610/g610 98.5% identity in 338 aa overlap

	10	20	30	40	50	60
m610.pep	MIGGLMQFPYRNPASRMRRMRRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM					
g610	MIGGLMQFPYRNPASRMRRMRRDDFSRRLMREHMLTADDLIYPVFVLEGAAREEDVPSM					
	10	20	30	40	50	60
	70	80	90	100	110	120
m610.pep	PGVKRQSLDRLLFTAEEAVKLGIPLMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER					
g610	PGVKRQSLDRLLFTAEEAVKLGIPLMLALFPVVTANKTGRAQEAYNPEGLVPSTVRALRER					
	70	80	90	100	110	120
	130	140	150	160	170	180
m610.pep	FPELGIMTDVALDPYTVHGGDGLTDENGYVMNDETVEVLVKQALCHAEAGAQQVVAPSDMM					
g610	FPELGIMTDVALDPYTVHGGDGLTDENGYVMNDETVEVLVKQALCHAEAGTQVVAPSDMM					
	130	140	150	160	170	180
	190	200	210	220	230	240
m610.pep	DGRIGAIREALEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN					

975

```

g610      DGRIGAIREALDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
           190      200      210      220      230      240
m610.pep  TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFVPTAYQVSGEYAMLQAAIAN
           250      260      270      280      290      300
g610      TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFVPTAYQVSGEYAMLQAAVAN
           250      260      270      280      290      300
m610.pep  GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
           310      320      330      339
g610      GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
           310      320      330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1941>:

```

a610.seq
1   ATGATTGGAG GGCTTATGCA GTTTCCTTAC CGCAATGTTT CGGCTTCGCG
51  TATGCGCCGT ATGCGCAGGG ACGATTTTTC ACGCCGCCCTG ATGCGCGAGC
101 ATACGCTGAC TGCCGATGAT TTGATTATC  CGGTGTTCGT ATTGGAGGGG
151 TCGGCGCGCG AGGAGGATGT GCCTTCTATG CCGGGCGTGA AGCGTCAGAG
201 TTTGGACAGG CTGCTGTTTA CGGCGGAAGA GGCGGTAAAG CTCGGTATTC
251 CGATGTTGGC ACTGTTCCCC GTGGTTACGG CAAACAAAAC CGAGCGTGCG
301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG TCCGCGCCTT
351 GCGCGAGAGG TTTCCCGAAC TGGGCATTAT GACGGATGTC GCGCTCGATC
401 CTTATACGGT GCACGGTCAG GACGGGCTGA CGGACGAAAA CGGTTATGTG
451 ATGAACGATG AAACCGTAGA GGTTTTGGTC AAGCAGGCTT TGTGTCATGC
501 AGAGGCAGGC GCACAGGTCG TTGCTCCTTC CGATATGATG GATGGGCGTA
551 TCGGTGCGAT TCGCGAGGCG TTGGAGGATG CCGGGCATAT CCATACGCGG
601 ATTATGGCGT ATTCGCCCAA ATATGCTTCT GCATTTTACG GCCCTTTCGG
651 TGATGCGGTA GGCAGTTCGG GCAATTTGGG CAAGGCAGAT AAAAAGACCT
701 ACCAGATGGA TCCGGCAAAT ACCGATGAGG CGTTGCACGA AGTGGCGTTG
751 GACATTACAG AAGGTGCGGA TATGGTGATG GTCAAGCCCG GTTTGCCGTA
801 TTTGGACGTT GTCCGCCGCG TGAAGGACGA GTTCGGCGTG CCGACTTATG
851 CCTATCAGGT TTCGGGAGAA TACGCGATGC TGCAGGCGGC GGTTGCCAAC
901 GGCTGGCTGG ACGGCGGCAA AGTGGTTTTG GAAAGCCTGC TGGCATTCAA
951 ACGTGCGGGT GCGGATGGGA TTTTGACCTA TTACGCCATT GAGGCGGCAA
1001 AGATGCTGAA GCGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1942; ORF 610.a>:

```

a610.pep
1   MIGGLMQFPY RNVASRMRR MRRDDFSRRL MREHTLTADD LIYPVFVLEG
51  SAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTERA
101 QEAYNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHGO DGLTDENGIV
151 MNDETVEVLV KQALCHAEAG AQVVAPSDMM DGRIGAIREA LEDAGHIHTR
201 IMAYSAKYAS AFYGPFRDAV GSSGNLGKAD KKTYYQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFV PTYAYQVSGE YAMLQAAVAN
301 GWLDGGKVV L ESLLAFKRAG ADGILTYAI EAAKMLKR*

m610/a610  99.4% identity in 338 aa overlap

           10      20      30      40      50      60
m610.pep  MIGGLMQFPYRNPASRMRRMRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM
           10      20      30      40      50      60
a610      MIGGLMQFPYRNVASRMRRMRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM
           10      20      30      40      50      60
           70      80      90      100     110     120
m610.pep  PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER
           70      80      90      100     110     120
a610      PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER
           70      80      90      100     110     120
           130     140     150     160     170     180

```

976

```

m610.pep      FPELGIMTDVALDPYTVHGDGLTDENGYVMNDETVEVLVKQALCHAEAGAQQVAPSDMM
                |||||||||||||||||||||||||||||||||||||||||||||||||||
a610           FPELGIMTDVALDPYTVHGDGLTDENGYVMNDETVEVLVKQALCHAEAGAQQVAPSDMM
                130      140      150      160      170      180

                190      200      210      220      230      240
m610.pep      DGRIGAIREALEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
                |||||||||||||||||||||||||||||||||||||||||||||||||||
a610           DGRIGAIREALEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
                190      200      210      220      230      240

                250      260      270      280      290      300
m610.pep      TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFGVPTYAYQVSGEYAMLQAAIAN
                ||||||||||||||||||||||||||||||||||||||||||||||||:|
a610           TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFGVPTYAYQVSGEYAMLQAAVAN
                250      260      270      280      290      300

                310      320      330      339
m610.pep      GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
                |||||||||||||||||||||||||||||||||||||||||||||
a610           GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
                310      320      330

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1943>:

```

g611.seq
1  ATGCCGCTCTG AAAACGGGAT GGGAAAACGG CAGCTTGCGG GCTGCCGTTT
51  GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCCCGGA CTCTGTCGAG
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TTTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT Ctcgcgcagg ttgtGGctgt
201 tatectTGGG CGGGCTGggt tgtttgcccc ccataaTTtc cagtacctgA
251 TcgcgGTcta tggtttCCa ttCcatcagg gctttgcaca TCGTTTCCAT
301 cttgTCGCGG TTTTcatcga ggaTTTGTa ggcaacCTGA TACTgctcgt
351 ccaaaAtccg Gcggatttcc gcgtcgAtgt cctgctgggt tTTCTCGGAA
401 ATGTTTTCGG AACGGgttac gctGCGCCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTGTc gTCATgcCG TAGCGCGTTA
501 CCATTTCCGC TGCCATTG GTTGCGCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1944; ORF 611.ng>:

```

g611.pep
1  MPSENGMGKR QLAGCRLFGK LSLVFRLLPG LCRGGVCRGR CFGFFPSRSV
51  RRVIFRRVRI LAQVVAVILG RAGLFARHNF QYLIAVYGFP FHQGFARHFH
101 LVAVFIEDFV GNLILLVQNP ADFRVDVLLG FLGNVLRGTG AAPQEDFAFV
151 FRINHHAHFV AHAVARYHFA CHLGCAFKVV *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1945>:

```

m611.seq
1  ATGCCGCTCTG AAAACGGGAT GGGAAAACGG CAGCTTGCGG GCTGCCGTTT
51  GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCTCGGA CTCTGTCGAA
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TCTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT CTCGCGCAGG TTGTGGCTGT
201 AATCTTTGGG CGGGCTGGGT TGTTCGCCCG CCATGATTTT CAGTACCTGA
251 TCGCGGTCTG TGGTTTCCCA TTCCATCAGG GCTTTGCACA TCGTTTCCAT
301 CTTGTGCGCG TTTTCATCGA GGATTTGTa GGCAACCTGA TATTGCTCGT
351 CCAAAATCCG GCGGATTTC GCGTCGATGT CCTGCTGGGT TTTCTCGGAA
401 ATGTTTTCGG AACGGGTtac GCTGCGTCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTGTc GTCATGCCG TAGCGCGTTA
501 CCATTTCCGC CGCCATTG GTTGCGCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1946; ORF 611>:

```

m611.pep
1  MPSENGMGKR QLAGCRLFGK LSLVFRLLLG LCRSGVCRGR CFGFFPSRSV
51  RRVIFRRVRI LAQVVAVIFG RAGLFARHDF QYLIAVDGFP FHQGFARHFH
101 LVAVFIEDFV GNLILLVQNP ADFRVDVLLG FLGNVLRGTG AASQEDFAFV
151 FRINHHAHFV AHAVARYHFA RHLGCAFKVV *

```

m611/g611 96.1% identity in 180 aa overlap

10 20 30 40 50 60

977

```

m611.pep      MPSENGMGKRQLAGCRLFGKLSLVFRLLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g611           MPSENGMGKRQLAGCRLFGKLSLVFRLLLPGLCRGGVCRGRCFGFFPSRSVRRVIFRRVRI
               10      20      30      40      50      60

               70      80      90      100     110     120
m611.pep      LAQVVAVIFGRAGLFARHDFQYLIADVGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g611           LAQVVAVILGRAGLFARHNFQYLIADVGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
               70      80      90      100     110     120

               130     140     150     160     170     180
m611.pep      ADFRVDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAHFVAHAVARYHFAHRLGCAFKVV
               |||||:|||||:|||||:|||||:|||||:|||||:|||||
g611           ADFRVDVLLGFLGNVLRGTGYAAPQEDFAFVFRINHHAHFVAHAVARYHFACHLGCAFKVV
               130     140     150     160     170     180

m611.pep      X
               |
g611           X

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1947>:

```

a611.seq
1  ATGCCGTCTG AAAACAGGAT GGGAAAACGG CAGCTTGCGG GCTGCCGTTT
51 GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCTCGGA CTCTGTTCGAA
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TCTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCGCGCG CGTCCGCATT CTCGCGCAGG TTGTGGCTGT
201 AATCTTTGGG CGGGCTGGGT TGTTCGCCG CCATGATTTC CAGTACCTGA
251 TCGCGGTCTGA TGGTTTCCCA TTCCATCAGG GCTTTGCACA TCGTTTCCAT
301 CTTGTTCGCG TTTTCATCGA GGATTTTGTA GGCAACCTGA TACTGCTCGT
351 CCAAATCCG GCGGATTTCC GCATCGATGT CCTGCTGGGT TTTCTCGGAA
401 ATGTTTTGCG AACGGGTAC GCTGCGTCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTTGTC GTCATGCCG TAGCGCGTTA
501 CCATTTCGCG CGCCATTGG GTTGCGCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1948; ORF 611.a>:

```

a611.pep
1  MPSENRMGKR QLAGCRLFGK LSLVFRLLLG LCRSGVCRGR CFGFFPSRSV
51 RRVIFRRVRI LAQVVAVIFG RAGLFARHDF QYLIADVGF FHQGFARHFH
101 LVAVFIEDFV GNLILLVQNP ADFRIDVLLG FLGNVLRGTY AASQEDFAFV
151 FRINHHAHFV AHAVARYHFA RHLGCAFKVV *

```

m611/a611 98.9% identity in 180 aa overlap

```

               10      20      30      40      50      60
m611.pep      MPSENGMGKRQLAGCRLFGKLSLVFRLLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a611           MPSENRMGKRQLAGCRLFGKLSLVFRLLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
               10      20      30      40      50      60

               70      80      90      100     110     120
m611.pep      LAQVVAVIFGRAGLFARHDFQYLIADVGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a611           LAQVVAVIFGRAGLFARHDFQYLIADVGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
               70      80      90      100     110     120

               130     140     150     160     170     180
m611.pep      ADFRVDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAHFVAHAVARYHFAHRLGCAFKVV
               |||||:|||||:|||||:|||||:|||||:|||||:|||||
a611           ADFRIDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAHFVAHAVARYHFAHRLGCAFKVV
               130     140     150     160     170     180

m611.pep      X

```

a611 |
 X

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1949>:

g612.seq
 1 ATGGGcttcg gcggaatat tgcAAAAAAG CTGGCcgGg taGATGAAAT
 51 AGCCTttgac tttgacggcA TCGTCTTTGA TTTCGGGCGT GATGATGCTG
 101 TCCGGCataG CGGCGTAATC AATGCTGCTG TCGCCGGCCT GCATATAGTC
 151 GGTGAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
 201 GTTTAAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCGATTTTC
 251 CAAATTTGGC GGTGCAGTTG GCGCGTTGT TGCATTTCGG TCATCATCGA
 301 AATCCATATA TAAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
 351 ATTTTtttac GGGCATTCAA ATTAA

This corresponds to the amino acid sequence <SEQ ID 1950; ORF 612.ng>:

g612.pep
 1 MGFGGNIAKK LAGVDEIAFD FDGIVDFDGR DDAVRHSGVI NAAVAGLHIV
 51 GEVFADKAVE KCAENVLFKV PAIHRAAYFV GDFPNLAVQL GALLHFGHHR
 101 NPYIKLNKSK SPDIFRRFFY GHSN*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1951>:

m612.seq
 1 ATGGGCTTCG GCGGCAATAT TGCAAAAAAG CTGGCCGGGG TAGATGAAAT
 51 AGCCTTTAAC TTTGACGGCA TCGTCTTTGA TTTCGGGCGT GATGATGCTG
 101 TCCGGCATAG CGGCGTAATC AATACTGCTG TCGCCTGCCT GCATATAGTC
 151 GGTGAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
 201 GTTTAAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCAATTTTC
 251 CAAATTTGGC GGTGCAGTTG GCGCGTTGT TGCATTTCGG TCATCATCGA
 301 AATCCATATA .AAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
 351 ATTTTtttac GGGCATTCAA ATTAA

This corresponds to the amino acid sequence <SEQ ID 1952; ORF 612>:

m612.pep
 1 MGFGGNIAKK LAGVDEIAFN FDGIVDFDGR DDAVRHSGVI NTAVACLHIV
 51 GEVFADKAVE KCAENVLFKV PAIHRAAYFV GNFPNLAVQL GALLHFGHHR
 101 NPYXKLKSK SPDIFRRFFY GHSN*

m612/g612 96.0% identity in 124 aa overlap

	10	20	30	40	50	60
m612.pep	MGFGGNIAKKLAGVDEIAFNFDGIVDFDGRDDAVRHSGVINTAVACLHIVGEVFADKAVE					
g612						
	10	20	30	40	50	60
	70	80	90	100	110	120
m612.pep	KCAENVLFKVP	PAIHRAAYFV	GNFPNLAVQL	GALLHFGHHR	NPYXKLKSK	SPDIFRRFFY
g612						
	70	80	90	100	110	120
	KCAENVLFKVP	PAIHRAAYFV	GNFPNLAVQL	GALLHFGHHR	NPYIKLNKSK	SPDIFRRFFY
m612.pep	GHSNX					
g612						
	GHSNX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1953>:

a612.seq
 1 ATGGGCTTCG GCGGCAATAT TGCAAAAAAG CTGGCCGGGG TAGATGAAAT
 51 AGCCTTTGAC TTTGACGGCA TCGTCTTTGA TTTCGGGCGT GATGATGCTG
 101 TCCGGCATAG CGGCGTAATC AATACTGCTG TCGCCTGCCT GCATATAGTC
 151 GGTGAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
 201 GTTTGAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCAATTTTC
 251 CAAATTTGGC GGTGCAGTTG GCGCGTTGT TGTATTTCGG TCATCATCGA
 301 AATCCATAT. AAAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
 351 ATTTTtt.AC GGGCATTCAA ATTAA

979

This corresponds to the amino acid sequence <SEQ ID 1954; ORF 612.a>:

```

a612.pep
  1  MGFGGNIAKK LAGVDEIAFD FDGIVDFDGR DDAVRHSGVI NTAVACLHIV
 51  GKVVFADKAVE KCAENVLFEV PAIHRAAYFV GNFPNLAVQL GALLYFGHHR
101  NPYXKLNKSK SPDIFRRFFX GHSN*

m612/a612    96.0% identity in 124 aa overlap

              10      20      30      40      50      60
m612.pep      MGFGGNIAKKLAGVDEIAFNFDGIVDFDGRDDAVRHSGVINTAVACLHIVGEVFADKAVE
a612           MGFGGNIAKKLAGVDEIAFDGIVDFDGRDDAVRHSGVINTAVACLHIVGKVVFADKAVE
              10      20      30      40      50      60

              70      80      90     100     110     120
m612.pep      KCAENVLFKVP AIHRAAYFVGNFPNLAVQLGALLHFGHHRNPYXKLNKSKSPDIFRRFFY
a612           KCAENVLFEPV AIHRAAYFVGNFPNLAVQLGALLYFGHHRNPYXKLNKSKSPDIFRRFFX
              70      80      90     100     110     120

m612.pep      GHSNX
a612           GHSNX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1955>:

```

g613.seq
  1  ATGTCGCGTT CGAGCCTGTC GAGGCGTTTCG TTGAGGCGTT CCACGCCGTC
 51  GCGCAGTCTG CTTATTTCGT CGAGGCAGTC ggcaagggct tcgttgccgg
101  tgtttGcgGA CTCGGGTTCG CGGGAAAATC CGCCGATTG TTCGGCGATG
151  TTCCTGCCGA TTTgtttGAt GCCGTGTCCG ATGTCGGTGG CACGgtgcc
201  gatgcCTGCC TGCGTGCCGA AAATCCGTGC CAATTcgtCC GATGCGCGGG
251  AACGCAGGCT GCCGAGCAGG GACAGTACCG CgATGCCGAG GATGAGGTCG
301  CCTTCGAGCC TGATGTCGCC AGCCCCGGGT TCGCCGCCCTT GGAGGATTTT
351  CCGTATCGCG CTGTTGCGGA AGGTAATTTT GGTGTCTGCA AAGCCGTTTC
401  CCGCCGAGAG CAAACCGTCT TCTGTGATGC GTCCCGCCAG TTTCAGCCCG
451  GCAATGTTCA GGGTCAGTGT TTTGCCTGCA AAGGAGGTAA GTTCCGAGCG
501  GCTGTCCGGG CTTTGCAGAA TCAGGCGGTT GATGATGGGG AGGAGGGCGG
551  ACATATTTTC TGATTGGGGC GGAGAATGCC TGTGTGTGCT GTTGCCGCTT
601  ATTTTACAGG CTAA

```

This corresponds to the amino acid sequence <SEQ ID 1956; ORF 613.ng>:

```

g613.pep
  1  MSRSSLSRRS LRRSTPSRSL LISSRQSARA SLPVFADSGS RENPPICSAM
 51  FLPICLMPCP MSVARLPMPA CVPKIRANSS DARERRLPSR DSTAMPRMRS
101  PSSLMSPAPG SPPWRIFRIA LLRKVISVSA KPFPAESKPS SVMRPASFSP
151  AMFRVSVLPA KEVSSERLSG LCRIRRLMMG RRADIFSDWG GECLLLLLPL
201  ILQA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1957>:

```

m613.seq
  1  ATGTCGCGTT CGAGCCGGTC GAGGCGTTTCG TTGAGGCGTT CCACGCCGTC
 51  GCGCAGTCTG CTTATTTCGT CGAGGCAGTC GGCAAGGGCT TCgttgccga
101  TGTTTGCGGA CTCGGATTTCG CGGGAAAATC CGCCGATTG TTCGGCGATG
151  TTCCTGCCGA TTTGTTTGAT GCCGTGTCCG ATGTCGGCGG CACGGCTGCC
201  GATGTCTGCC TGCGTGCCGA AAATCCGTGC CAATTcgtCC GATGCGCGGG
251  AACGCAGGCT GCCGAGCAGG GACAGTACCG CGATGCCGAG GATGAGGTCG
301  CCTTCGAGCC CGATGTCGCC CGCCCCGGGT TCGCCTCCTT GGAGGATTTT
351  CTGTACCGCG CTGTTGCGGA AGGTAATTTT GGTGTCTGCA AAGCCGTTTC
401  CCGCCGAGAG CAAACCGTCT TCCGTGATGC GTCCCGCCAG TTTCAGCCCG
451  GCAATGTTCA GGGTCAGTGT TTTGCCTGCA AAGGCGGCAA GTTCCGAGCG
501  GCTGTCCGGG CTTTGCAGAA TCAGGCGGTT GATGATGGGG AGGAGGGCGG
551  ACATATTTTC TGATCGGGGC GGAGAATGCC TGTGTGTGCT GTTGCCGCTT

```

980

601 ATTTTACAGG CTTAA

This corresponds to the amino acid sequence <SEQ ID 1958; ORF 613>:

```

m613.pep
  1  MSRSSRSRRS LRRSTPSRSL LISSRQSARA SLPMFADSDS RENPPICSAM
 51  FLPICLMPCP MSAARLPMSA CVPKIRANSS DARERRLPSR DSTAMPRMRS
101  PSSPMSPAPG SPPWRIFCTA LLRKVISVSA KPFPAESKPS SVMRPASFSP
151  AMFRVSVLPA KAASSERLSG LCRIRRLMMG RRADIFSDRG GECLLLLLPL
201  ILQA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m613/g613 94.6% identity in 204 aa overlap

	10	20	30	40	50	60
m613.pep	MSRSSRSRRSLRRSTPSRSLLISSRQSARASLPMFADSDSRENPPICSAMFLPICLMPCP					
g613	MSRSSLSRRSLRRSTPSRSLLISSRQSARASLPVFADSGSRENPPICSAMFLPICLMPCP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m613.pep	MSAARLPMSACVPKIRANSSDARERRLPSRDSTAMPRMRSPSSPMSPAPGSPPWRIFCTA					
	:					
g613	MSVARLPMPACVPKIRANSSDARERRLPSRDSTAMPRMRSPSSLMSAPAGSPPWRIFRIA					
	70	80	90	100	110	120

981

	130	140	150	160	170	180
m613.pep	LLRKVISVSAKPFPAESKPSSVMRPASFSPPAMFRVSVLPAAASSERLSGLCRIRRLMMG					
	:					
g613	LLRKVISVSAKPFPAESKPSSVMRPASFSPPAMFRVSVLPAAKEVSSERLSGLCRIRRLMMG					
	130	140	150	160	170	180
	190	200				
m613.pep	RRADIFSDRGGECLLLLLPLILQAX					
g613	RRADIFSDWGGECLLLLLPLILQAX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1959>:

```

a613.seq
1   ATGTCGCGTT  CGAGCCGGTC  GAGGCGTTCG  TTGAGGCGTT  CCACGCCGTC
51  GCGCAGTCTG  CTTATTTCGT  CGAGGCAGTC  GGCAAGGGCT  TCGTTGCCGA
101 TGTTCGCGGA  CTCGGGTTTCG  CGGGAATATC  TGCCGATTTC  TTCGGCGATG
151 TTCCTGCCGA  TTTGTTTGAT  GCCGTGTCCG  ATGTCGGCGG  CACGGCTGCC
201 GATGTCTGCC  TGCGTGCCGA  AAATCCGTGC  CAATTCGTCC  GATGCGCGGG
251 AACGCAGGCT  GCCGAGCAGG  GACAGTACCG  CGATGCCGAG  GATGAGGTCG
301 CCTTCGAGCC  CGATGTGCCG  CGCCCCGGGT  TCGCCGCCTT  GGAGGATTTT
351 CTGTACCGCG  CTGTTGCGGA  AGGTGATTTC  GGTGTCTGCA  AAGCCGTTTC
401 CCGCCGAGAG  CAAACCGTCT  TCCGTGATGC  GTCCCGCCAG  TTTCAACCCG
451 GCAATGTTCA  GGGTCAGTGT  TTTGCCTGCG  AAGGCGGCAA  GTTCCGAGCG
501 GCTGTCCGGG  CTTTGCAGAA  TCAGGCGGTT  GATGATGGGG  AGGAGGGCGG
551 ACATATTTTC  TGATCGGGGC  GGAGAATGCC  TGTGTGTGCT  GTTGACGCTT
601 ATTTTACAGG  CTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1960; ORF 613.a>:

```

a613.pep
1   MSRSSRSRRS  LRRSTPSRSL  LISSRQSARA  SLEPMFADSGS  RENLPICSAM
51  FLPICLMPCP  MSAARLPSA  CVPKIRANSS  DARERRLPSR  DSTAMPRMRS
101 PSSPMSPAPG  SPPWRIFCTA  LLRKVISVSA  KPFPAESKPS  SVMRPASFPN
151 AMFRVSVLPA  KAASSERLSG  LCRIRRLMMG  RRADIFSDRG  GECLLLLLTL
201 ILQA*

m613/a613    98.0% identity in 204 aa overlap

          10      20      30      40      50      60
m613.pep  MSRSSRSRRSLRRSTPSRSLISSRQSARASLPMFADSDSRENPPICSAMFLPICLMPCP
          |||||
a613       MSRSSRSRRSLRRSTPSRSLISSRQSARASLPMFADSGSRENLPICSAMFLPICLMPCP
          10      20      30      40      50      60

          70      80      90     100     110     120
m613.pep  MSAARLPSACVPKIRANSSDARERRLPSRDSTAMPRMRSPSSPMSPAPGSPPWRIFCTA
          |||||
a613       MSAARLPSACVPKIRANSSDARERRLPSRDSTAMPRMRSPSSPMSPAPGSPPWRIFCTA
          70      80      90     100     110     120

          130     140     150     160     170     180
m613.pep  LLRKVISVSAKPFPAESKPSSVMRPASFSPPAMFRVSVLPAAASSERLSGLCRIRRLMMG
          |||||
a613       LLRKVISVSAKPFPAESKPSSVMRPASFPNPFAMFRVSVLPAAASSERLSGLCRIRRLMMG
          130     140     150     160     170     180

          190     200
m613.pep  RRADIFSDRGGECLLLLLPLILQAX
          |||||
a613       RRADIFSDRGGECLLLLLTLILQAX
          190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1961>:

982

g614.seq
 1 AtggcTgcgt tcAacgcttt ggacggcaaa aaagaagaca acggggcaaat
 51 cgaaTATTCT CAGTTCATCC GACAGGTCAA CAACGGCGAA GTATCCGGCG
 101 TCAACATCGA AGGATCCGTC GTCAGCGGTT ACCTGATTAA AGGCGAGCGC
 151 ACCGACAAAA GCACCTTCTT CACCAACGCG CCCTTGGATG ACAACCTGAT
 201 TCAAACCTTT TTGAACAAAA ACGTCCGCGT AAAAGTAACG CCGGAAGAAA
 251 AACCAGAGCG GCTGACTGCC CTGTTTACA GCCTGCTGCC CGTCCTGCTG
 301 CTGATTGGCG CATGGTTCTA CTTTATGCGT ATGCAGGCGG GCGGCGGCGG
 351 AAAAGGCGGC GCATTCTCCT TCGGCAAAAG CCGCGCCCGC CTGCTGGACA
 401 AAGATGCCAA CAAAGTTACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC
 451 AAAGAAGAAG TGCAGGAAAT CGTCGATTAC CTCAAAGCAC CGAACCGCTa
 501 tcaAAGcctc ggcggccgtg ttcCGCGCGG CATCctgCtg gcgGgcagcc
 551 CGGGAaccgg taaAACACTC TTGGCGAAAG CCATTGCAGG CGAGGCCGGC
 601 GTGCCGTTCT TCAGCATTTT CCGTTCGAT TTTGTCGAAA TGTTCTGTCG
 651 TGTCGGTGCA AGCCGCGTCC GCGATATGTT CGAGCAGGCA AAGAAAAACG
 701 CCCCATGCAT TATCTTTATC GACGAGATTG ACGCGGTAGG CCGCCAACGC
 751 GGCGCAGgTT TGGGCGGCGG CAATGATGAG CGCGAGCAAA CATTAAACCA
 801 ATTATTGGTT GAAATGGACG GTTTTGAGAG CAATCAGACT GTAATTGTGA
 851 TTGCGGCAAC CAACCGCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC
 901 GGCCGCTTCG ACCGCCAAGT CGTCGTCCCC CTGCCGGACA TCCGGGGGCG
 951 CGAACAGatn ttGAACGTCC ATTctaaAAA AGTGCcttTG gacgaATCTg
 1001 tggatTTATT GTCCCTCGCG CGCGGCACGC ccggtttTt cggcgcgat
 1051 tTggcgaaac tggtaacga agccccctg tttgcccggc gccgcaacaa
 1101 agtgaaagtc gatcaaacgc atttGAAGAC GCCAAAGACA AAATCTATAT
 1151 GGGTCCGGAA CGCCGCAGTA TGGTGA

This corresponds to the amino acid sequence <SEQ ID 1962; ORF 614.ng>:

g614.pep
 1 MAAFNALDGK KEDNGQIEYS QFIRQVNNGE VSGVNIIEGSV VSGYLIKGER
 51 TDKSTFFFTNA PLDDNLIQTL LNKNVRVKVT PEEKPSALTA LFYSLLPVL
 101 LIGAWFYFMR MQAGGGGKGG AFSFGKSRAR LLDKDANKVT FADVAGCDEA
 151 KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIAGEAG
 201 VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
 251 GAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
 301 GRFDRQVVVP LPDIRGREQX LNVHSKKVPL DESVDLLSLA RGTPGFSGAD
 351 LAKLVNEAPL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1963>:

m614.seq
 1 ATGGCTGCGT TCAACGCTTT AGACGGTAAA AAAGAAGACA ACGGGCAAA
 51 CGAATACTCT CAGTTCATCC AACAGGTCAA CAACGGCGAA GTATCCGGCG
 101 TCAACATCGA AGGATCCGTC GTCAGCGGCT ACCTGATTAA GGGCGAGCGC
 151 ACCGACAAAA GCACCTTCTT CACCAACGCG CCTTGGACG ACAACCTAAT
 201 TAAACACTG CTCGACAAAA ACGTCCGCGT AAAAGTAACG CCGGAAGAAA
 251 AACCAGAGCG GCTGGCTGCC CTGTTTACA GCCTGCTGCC CGTCCTGCTG
 301 CTGATTGGCG CATGGTTCTA CTTTATGCGT ATGCAGACGG GCGGCGGCGG
 351 AAAAGGCGGC GCATTCTCAT TCGGTAAGAG CCGCGCCCGC CTGCTGGACA
 401 AAGATGCCAA CAAAGTGACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC
 451 AAAGAAGAAG TACAGGAAAT CGTCGATTAC CTCAAAGCGC CGAACCGCTa
 501 TCAAAGCCTG GGCGGGCGCG TGCCGCGCGG CATCCTGCTG GCGGGCAGCC
 551 CGGGTACGGG TAAGACGCTT TTGGCGAAAG CGATTGCAGG CGAAGCCGGC
 601 GTGCCGTTCT TCAGCATTTT AGGTTCGAC TTTGTCGAAA TGTTCTGTCG
 651 TGTCGGTGCG AGCCGCGTCC GCGATATGTT CGAGCAGGCG AAGAAAAACG
 701 CCCCCTGCAT CATCTTTATC GACGAGATTG ACGCAGTCGG CCGCCAACGC
 751 GGCGCAGGTT TGGGCGGCGG CAATGATGAG CGCGAGCAAA CATTAAACCA
 801 ATTGTTGGTT GAAATGGACG GTTTTGAGAG CAATCAGACT GTAATTGTGA
 851 TTGCGGCAAC CAACCGCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC
 901 GGCCGTTTCG ACCGCCAAGT GGTGTCCCC CTGCCGGACA TCCGAGGGCG
 951 CGAACAGATT TTGAACGTCC ATTCTAAAAA AGTGCCTTTG GACGAATCTG
 1001 TGGATTTATT GTCCCTCGCG CGCGGCACGC CGGGTTTTTC CGGCGCGGAT
 1051 TTGGCGAACT TGGTCAACGA AGCCGCCCTG TTTGCCGGCC GCCGCAATAA
 1101 AGTCAAAGTC GATCAGAGCG ATTTGAAGAC GCCAAAGACA AAATCTATAT
 1151 GGGTCCGGAA CGCCGCAGTA TGGTGA

This corresponds to the amino acid sequence <SEQ ID 1964; ORF 614>:

Homology with a predicted ORF from *N. gonorrhoeae*

	10	20	30	40	50	60
m614.pep	MAAFNALDGKKKEDNGQIEYSQFIQQVNNGEVSGVNIEGSVVSGYLIKERTDKSTFFFTNA					
g614	MAAFNALDGKKKEDNGQIEYSQFIRQVNNGEVSGVNIEGSVVSGYLIKERTDKSTFFFTNA					
	10	20	30	40	50	60
m614.pep	70	80	90	100	110	120
g614	PLDDNLIKTLLDKNVRVKVTPPEEKPSALAAFYSLLPVLLLIGAWFYFMRMQTGGGGKGG					
	70	80	90	100	110	120
m614.pep	130	140	150	160	170	180
g614	AFSFGKSRARLLDKDANKVTFADVAGCDEAKEEVQEIVDYLKAPNRYQSLGGRVPRGILL					
	130	140	150	160	170	180
m614.pep	190	200	210	220	230	240
g614	AGSPGTGKTLLAKAIAAGEAGVPFFFSISGSDFVEMFVGASRVRDMFEQAKKNAPCIIFI					
	190	200	210	220	230	240
m614.pep	250	260	270	280	290	300
g614	DEIDAVGRQRGAGLGGGNDEREQTLNQLLVEMDGFESNQTVIVIAATNRPDVLDPALQRP					
	250	260	270	280	290	300
m614.pep	310	320	330	340	350	360
g614	GRFDRQVVVPLPDIRGREQILNVHSKKVPLDESVDLLSLARGTPGFSGADLANLVNEAAL					
	310	320	330	340	350	360
m614.pep	370	380	390			
g614	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
	370	380	390			

```
a614.seq
1  ATGGCTGCGT  TCAACGCTTT  AGACGGTAA  AAAGAAGACA  ACGGGCAAAT
51  CGAATATTCT  CAGTTTCATC  ACAGGTCAA  CAACGGCGAA  GTGTCGGCG
101 TCAACATCGA  AGGATCCGTC  GTCACGGCT  ACCTGATTAA  GGCATGACGC
151 ACCGACAAA  GCACCTTCT  CACCAACGCG  CCTTTGGAC  ACAACCTGAT
201 TAAACACTG  CTCGACAAA  ACGTCCGTG  AAAAGTAACG  CGGGAAGAA
251 AACCGAGCG  CTCGGCTGCC  CTGTTTACA  GCGTGTGCC  CCTCCTGCTG
```

984

```

301 CTGATTGGCG CGTGGTTCTA CTTTATGCGT ATGCAGACGG GCGGCGGCGG
351 AAAAGGCGGC GCATTCTCAT TCGGCAAAAG CCGCGCCCGC CTACTGGACA
401 AAGATGCCAA CAAAGTTACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC
451 AAAGAAGAAG TGCAGGAAAT CGTCGATTAC CTCAAAGCGC CGAACCGCTA
501 TCAAAGCCTG GCGGGGCGCG TGCCGCGCGG CATCCTGCTG GCGGGCAGCC
551 CGGGTACGGG TAAGACGCTT TTGGCGAAAG CGATTGCAGG CGAAGCCGGC
601 GTGCCGTTCT TCAGCATTTC AGGTTCCGAC TTTGTGCGAA TGTTGCTCGG
651 TGTCCGTGCA AGCCGCGTCC GCGATATGTT CGAGCAGGCG AAGAAAAACG
701 CCCCTGTCAT CATCTTTATC GACGAGATTG ACGCAGTCGG CCGCCAACGC
751 GGCGCAGGTT TGGGCGGCGG TAATGATGAG CGCGAGCAAA CATTAACCA
801 ATTGTTGGTT GAAATGGACG GTTTTGAGAG CAATCAGACT GTAATTGTGA
851 TTGCGGCAAC CAACCGCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC
901 GGCGGTTTCG ACCGCCAAGT GGTTGTCCCC CTGCCGGACA TCCGGGGCGG
951 CGAACAGATT TTGAACGTCC ACTCTAAAAA AGTGCCTTTG GACAAATCTG
1001 TGGATTTATT GTCCCTCGCG CGCGGCACGC CGGGTTTTTC CGGCGCGGAT
1051 TTGGCGAACT TGGTCAACGA AGCCGCCCTG TTTGCCGGCC GCCGCAATAA
1101 AGTCAAAGTC GATCAGAGCG ATTTGAAGAC GCCAAAGACA AAATCTATAT
1151 GGGTCCGGAA CGCCGCAGTA TGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1966; ORF 614.a>:

```

a614.pep
  1 MAAFNALDGK KEDNGQIEYS QFIQQVNNGE VSGVNIIEGSV VSGYLIKGER
 51 TDKSTFFFTNA PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL
101 LIGAWFYFMR MQTGGGKGG AFSFGKSRR LLDKDANKVT FADVAGCDEA
151 KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIAEAG
201 VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
251 GAGLGGGND ERLQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
301 GRFDRQVVVP LPDIRGREQI LNVHSHKKVPL DKSVDLLSLA RGTGPGFSGAD
351 LANLVNEAAL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W*

m614/a614 99.7% identity in 391 aa overlap

      10      20      30      40      50      60
m614.pep MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIIEGSVVSGYLIKERTDKSTFFFTNA
|||||
a614 MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIIEGSVVSGYLIKERTDKSTFFFTNA
      10      20      30      40      50      60

      70      80      90     100     110     120
m614.pep PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL LIGAWFYFMR MQTGGGKGG
|||||
a614 PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL LIGAWFYFMR MQTGGGKGG
      70      80      90     100     110     120

      130     140     150     160     170     180
m614.pep AFSFGKSRR LLDKDANKVT FADVAGCDEA KEEVQEIVDY LKAPNRYQSL GGRVPRGILL
|||||
a614 AFSFGKSRR LLDKDANKVT FADVAGCDEA KEEVQEIVDY LKAPNRYQSL GGRVPRGILL
      130     140     150     160     170     180

      190     200     210     220     230     240
m614.pep AGSPGTGKTL LAKAIAEAG VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI
|||||
a614 AGSPGTGKTL LAKAIAEAG VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI
      190     200     210     220     230     240

      250     260     270     280     290     300
m614.pep DEIDAVGRQR GAGLGGGND ERLQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
|||||
a614 DEIDAVGRQR GAGLGGGND ERLQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
      250     260     270     280     290     300

      310     320     330     340     350     360
m614.pep GRFDRQVVVP LPDIRGREQI LNVHSHKKVPL DESVDLLSLA RGTGPGFSGAD LANLVNEAAL
|||||
a614 GRFDRQVVVP LPDIRGREQI LNVHSHKKVPL DKSVDLLSLA RGTGPGFSGAD LANLVNEAAL

```


985

	310	320	330	340	350	360
	370	380	390			
m614.pep	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
a614	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1967>:

```

g615.seq
1  ATGTGGAAC GGC GCGGCGG CCGTGtcggC AGCTTtgaag agcagcGaAT
51  agatgCCGCC GGCAAACAC AATGCGGAa gcaggCtgaa gcGGTTgcgC
101 GGcagcTTca tGCCGCCTCC TcGTCCaGCC ACGtttGgca gattttggac
151 aggcgcAGGa ATTTGCcgCc gcgtgcggCA agtatgtcgc gcCAttgtgc
201 cacttcttcg gcggacggTG cttcgtcgaT gctgCATTCG TACagcagga
251 aatcgagggt ttcttcgatg acggGgatgg AttccgTTTG GataAgCTGc
301 ttgagttcgt tcatgactGt TCgGATAcgg aaatcgggaa aatgcggtct
351 gAaagggctt CAGACGGCat tggATTATTT GCTGTGCAGG AAgcgcgttg
401 cctcttccca tttgcCGGAA AtgATGTCGg gtacggcctg cAGGGATttg
451 gCGACGGcat cgtcgatttg ccgGcggtgc ttCcgcgctc ggtttGTTca
501 agacgtagcc gaCGACGagg ttgcggtcGC CGGGGtggcC GATGCCGAGG
551 CGCAGGCGGt aatagtctgC CGTGCCGAGT TTTGCctgAA TGTCTTTCAA
601 GCCGTTGTGT CcgcCGttgc cgcCGCCGAG TTTGAATTTg ATCCGTCCGC
651 AAGGGATGTC GAGTTCGTCG TGGACGACGA GGATTCTTC GGGTTTGATT
701 TTGTAGAACT GTGCAAGCGC GGCAACCGCC TGTCCGGAAC GGTTCATGAA
751 CGTGGCCGGT TTGAGCAGCC AAACATCGCC GTCGGGCAGG GCGGCGCGGG
801 CAACTTCGCC GAAGAATTTT TTTTCTTCTT TAAACGAAGC CTTCCATTTT
851 CAGCCAGTT CGTCGAGGAA CCAAAAGCCC GCATTGTGGC GGGTCTGTTC
901 GTATTCTTTG CCCGGGTTGC CCAAGCCGAC AACCATTTTG ATTGTGttcg
951 acatgataTT TtccgtgTTT CTgTCGaatg cggtCtgaAG GCTTCAGacg
1001 gcatggTtaT TCTTCTTgaT TTtgaACcg tgtgcggCGC GCTTCTTTGG
1051 GGTGATCAA CAGCGGCGG TACACTTCGA TCGGTCGCC GTCGCGCAGC
1101 GCGGTGTCGT CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1968; ORF 615.ng>:

```

g615.pep
1  MWKRRRRGVG SFEEQRIDAA GKPQCGKQAE AVARQLHAAS SSSHVWQILD
51  RRRNLPPRAA SMSRHCAATSS ADGASSMLHS YSRKSRVSSM TGMDSVWISC
101 LSSFMTVRIR KSGKCRLLGL QTALDYLLCR KRVASSHLPE MMSGTACRDL
151 ATASSICRRC FRARFVQDVA DDEVAVAGVA DAEAQAVIVC RAEFCLNVFO
201 AVVSAVAAAE FEFDPsARDV EFVVDDEDF GFDFVELCKR GNRLSGTVHE
251 RGRFEQPNIA VGQGGAGNFA EEEFFFFKRS LPFPRQFVEE PKARIVAGLF
301 VFFARVAQAD NHFDCVRHDI FRVSVCEGLK ASDGMVILLD FERVCGALLW
351 GRSTAGGTLR CGRRRAAACR L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1969>:

```

m615.seq Length: 1116
1  ATGCGGAAAA GCGGTTGGCG CCGTTTCGGC AGCTTTGAAA AGCAGTGAGT
51  AAATGCTGCC TGCAAACAC AATGCCGAGA GCAGGATAAA GCGGTTGCGT
101 GGCAGATTCA TGCTTGTTC TCTTCAAGCC ATGTCTGGCA TAGTTTGAT
151 AGGCGCAGGA ATTTTCGGCC GCGTGC GGCC AGCATATCGC GCCAAACGGC
201 AATTTCTTCG GCGGAGGGGG CATCGTCTAT GCTGCATTCT TAGAGCAGGA
251 AATCGAGGGT TTCTTCGATG ACGGGGATGG ATTCCGTTTG GATAAGCTGC
301 TTGAGTTCGG TCATGACTGT TCGGATATGG AAATCGGGAA CATGCCGTCT
351 GAAAGGGCTT CAGACGGCAT CGGGTCATTT GCTGTGCAGG AAGCGGGTTG
401 CTTCTTCCCA TTTGCCGGCA AGGATGTCGG GTATGGCTTG CAGGGATTTG
451 GCGACGGCAT CGTCAATCTG TCGGCGGTGT .TCCGTA CTG GGTGTTGTTCA
501 GGACATAGCC GACGACGAGG TTGCGGTCGC CCGGGTGGCC GATGCCGAGG
551 CGCAGGCGGT AATAGTCTGC CGTGCCGAGT TTTGCCTGAA TGTCTTTCAA
601 GCCGTTGTGT CCGCCGTTGC CGCCGCCGAG TTTGAATTTG ATCCGTCCGC
651 AGGGAATGTC GAGTTCGTCG TGGACGACGA GGATTCTTC GGGTTTGATT
701 TTGTAGAACT GTGCAAGCGC GGCAACTGCC TGTCCGGAAC GGTTCATGAA
751 CGTGGCAGGT TTGAGCAGCC AAACGTCCGC GTCGGGCAGG GCGGCACGGG

```

986

```

801 CGACTTCGCC GAAGAATTTT TTTCTTCTT TAAATGAAGC CTTCCATTTT
851 CACGCCAGTT CGTCGAGGAA CCAAAAACCC GCATTGTGGC GTGTCTGTTT
901 GTATTCTTTG CCCGGGTTGC CCAAGCCGAC AACCATTTTG ATTGTGTTTG
951 ACATGATATT TTCCGTGTTT CTGTCGAATG CTGTCTGAAG GCTTCAGACG
1001 GCATGGTTAT TCTTCTTGAT TTGAACGCG TTTGCGGCGC GCTTCTTTTG
1051 GGTGCATCAA CAGCGGGCGG TACACTTCGA TCGGGTCGCC GTCGCGCAGC
1101 GGCGTGTCT CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1970; ORF 615>:

```

m615.pep Length: 372
1 MRKRRWRGFG SFEKQXVNAA CKPQCREQDK AVAWQIHACS SSSHVWHS LD
51 RRRNFPPRAA SISRQTAISS AEGASSMLHS XSRKSRVSSM TGMDSVWISC
101 LSSVMTVRIW KSGTCRLKGL QTASGHLLCR KRVASSHLPA RMSGMACRDL
151 ATASSICRRC XRTGFVQDIA DDEVAVARVA DAEAQAVIVC RAEFCLNVFQ
201 AVVSAVAAAE FEFDPAGNV EFVVDDEDF GFDFVELCKR GNCLSGTVHE
251 RGRFEQPNVA VGQGGTGDFE EEEEEFFKXS LPFPRQFVEE PKTRIVACLF
301 VFFARVAQAD NHFDCVXHDI FRVSVECCCLK ASDGMVILLD FERVCGALLW
351 GRSTAGGTLR CGRRRAAACR L*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m615/g615 86.8% identity in 371 aa overlap

m615.pep	10	20	30	40	50	60
	MRKRRWRGFGSFEKQXVNAA	CKPQCREQDKAVAWQIHACS	SSSHVWHS	LD	RRRNFP	PRAA
g615	10	20	30	40	50	60
	MWKRRRGVGSFEEQRIDAAG	KPQCGKQAEAVARQLHA	ASSSHVWQ	ILDRRN	LP	PRAA
m615.pep	70	80	90	100	110	120
	SISRQTAISSAEGASSMLH	XSRSRVSMTGMDSVWIS	CLSSVMTVRIW	KSGTCRLKGL		
g615	70	80	90	100	110	120
	SMSRHCAATSSADGASSML	HSYSRSRVSMTGMDSVWIS	CLSSFMVTRIRK	SGKCR	LG	
m615.pep	130	140	150	160	170	180
	QTASGHLLCRKRVASSHL	PARMSGMACRDLATASSI	CRRCXRTGFVQDIAD	DEVAVARVA		
g615	130	140	150	160	170	180
	QTALDYLLCRKRVASSHL	PEMMSGTACRDLATASSI	CRRCFRARFVQDVAD	DEVAVAGVA		
m615.pep	190	200	210	220	230	240
	DAEAQAVIVCRAEFCLNV	QAVVSAVAAAEFEFDP	SAGNV	EFVVDDEDF	GFDFVELCKR	
g615	190	200	210	220	230	240
	DAEAQAVIVCRAEFCLNV	QAVVSAVAAAEFEFDP	SARDVEFVVDDEDF	GFDFVELCKR		
m615.pep	250	260	270	280	290	300
	GNCLSGTVHERGRFEQPN	VAVGQGGTGDFAE	EEEEFFKXSLPF	PRQFVEE	PKTRIVACLF	
g615	250	260	270	280	290	300
	GNRLSGTVHERGRFEQPN	IAGVQGGAGNFAE	EEEEFFKXSLPF	PRQFVEE	PKARIVAGLF	
m615.pep	310	320	330	340	350	360
	VFFARVAQADNHFDCVXH	DI FRVSVECCCLKAS	DGMVILLDFERV	CGALLWGR	STAGGTLR	
g615	310	320	330	340	350	360
	VFFARVAQADNHFDCVXH	DI FRVSVECCCLKAS	DGMVILLDFERV	CGALLWGR	STAGGTLR	
m615.pep	370					
	CGRRRAAACRLX					
g615	370					
	CGRRRAAACRLX					

987

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1971>:

```
a615.seq
1   ATGCGGAAAC GGC GGCGGGCG CCGTGTCTGGC AGCTTTGAAG AGCAGCGAAT
51  AGATGCCGCC GGCAAACCAC AATGCGGAAA GCAGGCTGAA GCGGTTGCGC
101 GGCAGCTTCA TGCCGCCTCC TCGTCCAGCC ACGTTTGGCA GATTTTGGAC
151 AGGCGCAGGA ATTTGCCGCC GCGTGC GGCA AGTATGTCGC GCCATTGTGC
201 CACTTCTTCG GCGGATGGTG CGTCGTCGAT GCTGCATTCG TACAGCAGGA
251 AATCGAGGGT TTCTTCGATG ACGGGGATGG ATTCGGTTTG GATAAGCTGC
301 TTGAGTTCGG TCATGACTGT TCGGATATGG AAATCGGGAA CATGCCGTCT
351 GAAAGGGCTT CAGACGGCAT CGGGTCATTT GCTGTGCAGG AAGCGGGTTG
401 CCTCTTCACA TTTGCCGGCA AGGATGTCGG GTATGGCTTG CAGGGATTTG
451 GCGACGGCAT CGTCAATCTG TCGGCGGTG. TTCCGTA CTG GGTGTGTTCA
501 GGACATAGCC GACGACGAGG TTGCGGTCGC CCGGTGCGCC GATGCCGAGG
551 CGCAGGCGGT AATAGTCTGC CGTGCCGAGT TTTGCCTGAA TGTCTTTCAA
601 GCGGTTGTGT CCACCGTTGC CGCCGCCGAG TTTGAATTTG ATCCGTCCGC
651 AGGGAATGTC GAGTTCGTCG TGGACGACGA GGATTCTTTC GGGTTTGATT
701 TTATAAAACT GCGCAAGGGC GGCAACTGCC TGTCCGGAAC GGTTCATGAA
751 CGTGGTCCGC TTGAGCAGCC AGACATCGCC GTCGGGCAGG GTAGCACGGG
801 CGACTTCGCC GAAGAATTTT TTTTCTTCTT TAAATGAAGC CTTCCATTTT
851 CACGCCAGTT CGTCGAGGAA CCAAAAACCC GCATTGTGGC GTGTCTGTTT
901 GTATTCTTTG CCCGGGTTGC CCAAGCCGAC AACCATTTTG ATTGTGTTTG
951 ACATGATATT TTCCGTGTTT CTGCCGAATG CCGTCTGAAG GCTTCAGACG
1001 GCATGGTTAT TCTTCTTGAT TTTGAACGCG TTTGCGGCGC GCTTCTTTTG
1051 GGTGATCAA CAGCGGGCGG TACACTTCGA TCGGTTCGCC GTCGCGCAGC
1101 GCGGTGTCGT CTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1972; ORF 615.a>:

```
a615.pep
1   MRKRRRRGVG SFEEQRIDAA GKPQCGKQAE AVARQLHAAS SSSHWQILD
51  RRRNLPPRAA SMSRHCATSS ADGASSMLHS YSRKSRVSSM TGMDSVWISC
101 LSSVMTVRIW KSGTCRLKGL QTASGHLLCR KRVASSHLPA RMSGMACRDL
151 ATASSICRRX FRTGFVQDIA DDEVAVARVA DAEAQAVIVC RAEFCLNVFO
201 AVVSTVAAAE FEFDPSAGNV EFVVDDEDFG GFDFIKLRKG GNCLSGTVHE
251 RGRLEQPDIA VGQGSTGDFE EEEEEFFK*S LPPPRQFVEE PKTRIVACLF
301 VFFARVAQAD NHFDCV*HDI FRVSAECRLK ASDGMVILLD FERVCGALLW
351 GRSTAGGTLR CGRRRAACR L*
```

m615/a615 90.3% identity in 371 aa overlap

	10	20	30	40	50	60
m615.pep	MRKRRWRGFGSFEKQXVNAACKPQCREQDKAVAWQIHACSSSSHWVHSLDRRRNFP	PRAA				
a615	MRKRRRRGVGSFEEQRIDAAAGKPQCGKQAEAVARQLHAASSSSHWQILDRRRNLPPRAA					
	10	20	30	40	50	60
m615.pep	SISRQTAISSAEGASSMLHSXSRKSRVSSMTGMDSVWISCLSSVMTVRIWKSGTCRLKGL					
a615	SMSRHCATSSADGASSMLHSYSRKSRSVSSMTGMDSVWISCLSSVMTVRIWKSGTCRLKGL					
	70	80	90	100	110	120
m615.pep	QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRXRTGFVQDIADDEVAVARVA					
a615	QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRXRTGFVQDIADDEVAVARVA					
	130	140	150	160	170	180
m615.pep	DAEAQAVIVCRAEFCLNVFQAVVS	AVAAAEFEFDPSAGNVEFVVDDEDFG	FDVELCKR			
a615	DAEAQAVIVCRAEFCLNVFQAVVSTVAAAEFEFDPSAGNVEFVVDDEDFG	FDVELCKR				
	190	200	210	220	230	240
m615.pep						
a615						
	250	260	270	280	290	300

988

```

m615.pep      GNCLSGTVHERGRFEQPNVAVGQGGTGDFAEFFFFFFFKXSLPFPQFVEEPKTRIVACLF
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
a615          GNCLSGTVHERGRLEQPDIAVGQGSTGDFAEFFFFFFFKXSLPFPQFVEEPKTRIVACLF
                250      260      270      280      290      300

                310      320      330      340      350      360
m615.pep      VFFARVAQADNHFDVCVXHDIFRVSVCECLKASDGMVILLDFERVCGALLWGRSTAGGTLR
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
a615          VFFARVAQADNHFDVCVXHDIFRVSAECLRKASDGMVILLDFERVCGALLWGRSTAGGTLR
                310      320      330      340      350      360

                370
m615.pep      CGRRRAAACRLX
|||||:||||:
a615          CGRRRAAACRLX
                370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1973>:

```

g616.seq
1  atgtcgaaCA CAATCAAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
51  ATACGAACAG ACCCGCCACA ATGCGGGCTT TTGGTTCCTC GACGAAC TGG
101 CGTGGAAATG GAAGGCTTCG TTAAAGAAG AAAAAAATT CTTCGGCGAA
151 GTTGCCCGCG CCGCCCTGCC CGACGGCGAT GTTTGGCTGC TCAAACCGGC
201 CACGTTTCAT AACCGTTCCG GACAGGCGGT TGCCGCGCTT GCACAGTTCT
251 ACAAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATC
301 CCTTGC GGAC GGATCAAATT CAAACTCGGC GgcggcaacG gcgGACACAA
351 CGGCTTGAA GACATTcagG CAAACTCGG CACGGcagac tattaCCGCC
401 TGCGCCTCGG CATCGgccaC CCCGGCgacc gcaacctCGT CGtcggctac
451 gtcttgAACa aaccgagcgc gGaagcaccg Ccggcaaatc gacgatgCCG
501 TCGccaaATC CCTGcaggcc gtaccCGACA TcaTTCCGg caaatgggaa
551 gaggcaacgc gcTTCCTGCA CAGCAAATAA TccaatGCCG TCTGaagccc
601 ttTcagacgg cattttcccg atttccgTAT CcGAaCagtc atgaacgaac
651 tcaagcAGeT tatCCAAACg gaaTccatcC ccgtcatcga agaaaccctc
701 gatttcctgc tGTACGAATG cagcAtcgcac gaagCAccgt ccgccgaaga
751 agtggcacaa TGcgcgcaca tactTGccgc acgcgGcgGC AAATtcCTgc
801 gcctgtccaa aatctgcCaa aCGTGGcTGG ACgAGGAGGC GGCatgAaAg
851 tGCCGcgcaA CCgtttcaGc ctgctTTCCG CATTGTGGTT TGCCGGCGGc
901 atctATtCgc tgctcttcaA AGCTGccgaC ACCGCGCCGC CGCCGTTTCC
951 ACATTtcgaC AAAGCAGCAC ACCTTGCCCT GTTTTTCGCA CAaatCTTgt
1001 tTctGGCCAA AGCATTCAAA ACCGGAaAAC TTCCCATCCC CTACCGCAGC
1051 CTGATTGCGT TCGCCTTCTG TTTTGCCGTC GGCAGCGAAT GCGCGCAGGC
1101 ATGGTTTACC GCAACGCGAA CCGGCAGTTT GGGCGATGTC CTTGCCgACC
1151 TGACGGGCGC AGCCCTTGCC CTCTTTGCCG CGCGTTCTGC CTGCCGcccg
1201 gactaa

```

This corresponds to the amino acid sequence <SEQ ID 1974; ORF 616.ng>:

```

g616.pep
1  MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKFFGE
51  VARAALPDGD VWLLKPATFM NRSQAVAAAL AQFYKIKPEE ILVHDELDI
101 CGRIKFKLKG GNGGHNGLK DIQAKLGTAD YYRLRLGIGH PGDRNLVVG
151 VLNKPSAEAP PANRRRQRI PAGRTRHFR QMGRGNALPA QQIIQCRLKP
201 FQAFSRFPY PNSHERTOAA YPNGIHPRHR RNPRFPAVRM QHRRSTVRRR
251 SGTMARHTCR TRRQIPAPVQ NLPNVAGRGG GMKLPNRNFS LLSALWFAGG
301 IYSLLFKAAD TAPPPFPFHD KAHLALFFA QILFLAKAFK TGKLPIPYRS
351 LIAFAFCFAV GSECAQAWFT ATRTGSLGDV LADLTGAALA LFAARSACRP
401 D*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1975>:

```

m616.seq
1  ATGTCAAACA CAATCAAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
51  ATACGAACAG ACACGCCACA ATGCGGGTTT TTGGTTCCTC GACGAAC TGG
101 CGTGGAAATG GAAGGCTTCA TTAAAGAAG AAAAAAATT CTTCGGCGAA
151 GTCGCCCCTG CCGCCCTGCC CGACGGCGAC GTTTGGCTGC TCAAACCTGC
201 CACGTTTCAT AACCGTTCCG GACAGGCGAT TGCCGCGCTT GCACAGTTCT
251 ACAAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATT
301 CCCTGCGGAC GGATCAAATT CAAACTCGGC GCGGCAACG GCGGACACAA
351 CGGCTTGAA GACATTcagG CAAACTCGG CACGGCAGAC TATTACCGCC
401 TGCGCCTCGG CATCGGCCAC CCGGGCGACC GCAACCTCGT CGTCGGCTAT
451 GTCCTGAACA AACCCAGTAC GGAACA.CCG CCGACAGATT GACGATGCCG
501 TCGCCAAATC CCTGCAAGCC ATACCCGACA TCCTTGCCGG CAAATGGGAA

```

989

```

551 GAAGCAACCC GCTTCCTGCA CAGCAAATGA CCCGATGCCG TCTGAAGCCC
601 TTTCAGACGG CATGTTCCCG ATTTCCATAT CCGAACAGTC ATGACCGAAC
651 TCAAGCAGCT TATCCAAACC GAATCCATCC CCGTCATCGA AGAAACCCTC
701 GATTTCCTGC TCTACGAATG CAGCATAGAC GATGCCCCCT CCGCCGAAGA
751 AATTGCCGTT TGGCGCGATA TGCTGGCCGC ACGCCGCCGA AAATTCCTGC
801 GCCTATCCAA ACTATGCCAG ACATGGCTTG AAGAGGAACA AGCATGAATC
851 TGCCACGCAA CCGCTTTATC CTGCTCTCGG CATTGTGGTT TGCAGGCAGC
901 ATTTACTCAC TGCTTTTCAA AGCTGCCGAA ACCGCCAC CGCCTTTTCC
951 GCATTTTGAC AAAGTGGCGC ACCTCGCCCT GTTTTTCGCA CAAATCTGGC
1001 TTCTGACCAA AGCATTGAGA ACCGACAACC GCCCATCCC CTATCGCAGC
1051 CTGATGGTCT TTGCCCTCTG TTTCGCCCTC TTCAGCGAAT GCGCGCAGGC
1101 ATGTTTACC GCAACGAGAA CCGGCAGTTT GGGCGATGTC CTTGCCGACC
1151 TGACGGGCGC AGCCCTTGCC CTCTTTACCG CGCGAGCTGC CTGCCGCCCG
1201 GACTAA

```

This corresponds to the amino acid sequence <SEQ ID 1976; ORF 616>:

```

m616.pep
  1 MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKKAS FKEEKKFFGE
  51 VARAALPDGD VWLLKPATFM NRSGQAVAAL AQFYKIKPEE ILVVHDELDI
 101 PCGRIKFKLG GNGGGHNLK DIQAKLGTA YRLRLGIGH PGDRNLVVG
 151 VLNKPSTEXP PTDXRRCRQI PASHTRHPCR QMGRSNPLPA QMTRCRLKP
 201 FQTACSRFPY PSHDRTOAA YPNRIHPRHR RNPFPALRM QHRRCPPLRR
 251 NCRLARYAGR TRRKIPAPIQ TMPDAXRGT SMNLPRNRFI LLSALWFAGS
 301 IYSLLFKAAE TAPPPFPFHD KVAHLALFFA QIWLTLKAFR TDNRPIPYRS
 351 LMVFALCFAL FSECAQAWFT ATRTGLGDV LADLTGAALA LFTARAACRP
 401 D*

```

m616/g616 86.0% identity in 401 aa overlap

m616.pep	10	20	30	40	50	60
	MSNTIKMVVGLGNGPGKEYEQTRHNAGFWFLDELAWKKASFKEEKKFFGEVARAALPDGD					
g616	MSNTIKMVVGLGNGPGKEYEQTRHNAGFWFLDELAWKKASFKEEKKFFGEVARAALPDGD					
	10	20	30	40	50	60
m616.pep	70	80	90	100	110	120
	VWLLKPATFMNRSGQAVAALAQFYKIKPEEILVVHDELDIPCGRIKFKLGGGNGGHNLK					
g616	VWLLKPATFMNRSGQAVAALAQFYKIKPEEILVVHDELDIPCGRIKFKLGGGNGGHNLK					
	70	80	90	100	110	120
m616.pep	130	140	150	160	170	180
	DIQAKLGTADYYRLRLGIGHPGDRNLVVGYYLNKPSTEXPPTDXRCRRQIPASHTRHPCR					
g616	DIQAKLGTADYYRLRLGIGHPGDRNLVVGYYLNKPSTEXPPTDXRCRRQIPASHTRHPCR					
	130	140	150	160	170	180
m616.pep	190	200	210	220	230	240
	QMGRSNPLPAQMTRCRLKPFQTACSRFPYPNSHRTQAAAYPNRIHPRHRNPRFPALRM					
g616	QMGRSNPLPAQMTRCRLKPFQTACSRFPYPNSHRTQAAAYPNRIHPRHRNPRFPALRM					
	190	200	210	220	230	240
m616.pep	250	260	270	280	290	300
	QHRRCPPLRRNCRRLARYAGRTRRKIPAPIQTMPDAXRGTSMNLPRNRFILLALWFAGS					
g616	QHRRCPPLRRNCRRLARYAGRTRRKIPAPIQTMPDAXRGTSMNLPRNRFILLALWFAGS					
	250	260	270	280	290	300
m616.pep	310	320	330	340	350	360
	IYSLLFKAAETAPPPFPFHDKVAHLALFFAQIWLTLKAFRTDNRPIPYRSLMVFALCFAL					
g616	IYSLLFKAAETAPPPFPFHDKVAHLALFFAQIWLTLKAFRTDNRPIPYRSLMVFALCFAL					
	310	320	330	340	350	360
m616.pep	370	380	390	400		
	FSECAQAWFTATRGTGLGDVLADLTGAALALFTARAACRPDX					
g616	FSECAQAWFTATRGTGLGDVLADLTGAALALFAARSACRPDX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1977>:

990

a616.seq

```

1   ATGTCAAACA CAATCAAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
51  ATACGAACAG ACACGCCACA ATGCGGGTTT TTGGTTCCTC GACGAAGTGG
101 CGTGGAAATG GAAGGCTTCA TTAAAGAAG AAAAAAAT CTTCGGCGAA
151 GTCGCCCCGTG CTACCGTGCC CGACGGCGAT GTCTGGCTGC TCAAGCCGAC
201 CACGTTTCATG AACCGTTCGG GACAGGCGAGT TGCCGCCCTT GCGCAGTTTT
251 ATAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATT
301 CCCTGCGGAC GGATCAAATT CAAACTCGGC GCGGCAACG GTGGACACAA
351 CGGCTTGAAA GACATTCAGG CAAACTCGG CACGGCAGAC TATTACCGCC
401 TGCGCCTCGG CATCGCCAC CCGGGCGACC GCAACCTCGT CGTCGGCTAT
451 GTCCTGAACA AACCCAGTAC GGAA.CACCG CCGACAGATT GACGATGCCG
501 TCGCCAAATC CCTGCAAGCC ATACCCGACA TCCTTGCCGG CAAATGTGAA
551 GAGGCAACCC GCTTCCTGCA CAGCAAATGA CCCGATGCCG TCTGAAGCCC
601 TTTTCAGACGG CATGTTCCCG ATTCCATAT CCGAACAGTC ATGACCGAAC
651 TCAAGCAGCT TATCCAAACC GAATCCATCC CCGTCATCGA AGAAACCCCTC
701 GATTTTCCTGC TGTACGAATG CAGCATCGAC GACGCACCAT CCGCCGAAGA
751 AGTGGCACAA TGGCGCGACA TACTTGCCGC ACGCGCGGCG AAATTCCTGC
801 GCCTGTCCAA AATCTGCCAA ACGTGGCTGG ACGAGGAGGC GGCATGAAGC
851 TGCCGCGCAA CCGCTTCAGC CTGCTTCCG CATTGTGGT TGCCGCGCGC
901 ATCTATTTCGC TGCTCTTCAA AGCTGCCGAC ACCGCGCCGC CGCCGTTTCC
951 GCATTTTCGAC AAAGCAGCAC ACCTTGCCCT GTTTTTCGCA CAAATCTGGC
1001 TTTTGACCAA AGCATTCAAA ACCGAAAAC TTCCCATCCC CTACCGCAGC
1051 CTGATGGTCT TTGCCCTCTG TTTGCCCCCTC TTCAGCGAAT GCGCGCAGGC
1101 ATGATTTACC GCAACGAGAA CCGCAGTTT GGGCGATGT CTTGCCGATA
1151 TGGCAGGTAC GGTTCCTCGA CTCTTTCGCC CCCGCGCCGC CGACCGCCCG
1201 GACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1978; ORF 616.a>:

a616.pep

```

1   MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKKFFGE
51  VARATLPDGD VWLLKPTTFM NRSGQAVAAL AQFYKIKPEE ILVVHDELDI
101 PCGRIKFKLG GNGGHNGLK DIQAKLGTD YRLRLGIGH PGDRNLVVGY
151 VLNKPSTEXP PTD*RCRRQI PASHTRHPCR QM*RGNPLPA QQMTRCRLKP
201 FQTACSRFPY PNSHRTQAA YPNRIHPRHR RNPRFPVRM QHRRRTIRRR
251 SGTMARHTCR TRRQIPAPVQ NLPNVAGRG GMKLPRNRF LLSALWFAGG
301 IYSLLFKAAD TAPPPPHFD KAAHLALFFA QIWLTKAFK TGKLPPIYRS
351 LMVFALCFAL FSECAQA*FT ATRTGSIGDV LADMAGTVLA LFAARAADRP
401 D*

```

m616/a616 90.0% identity in 401 aa overlap

	10	20	30	40	50	60
m616.pep	MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD					
a616	MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARATLPDGD					
	10	20	30	40	50	60
m616.pep	VWLLKPATFMNRSGQAVAALAQFYKIKPEEILVVHDELDIPCGRIKFKLGGNGGHNGLK					
a616	VWLLKPTTFMNRSGQAVAALAQFYKIKPEEILVVHDELDIPCGRIKFKLGGNGGHNGLK					
	70	80	90	100	110	120
m616.pep	DIQAKLGTDYYRLRLGIGHPGDRNLVVGYYLNKPSTEXPPTDXRCRRQIPASHTRHPCR					
a616	DIQAKLGTDYYRLRLGIGHPGDRNLVVGYYLNKPSTEXPPTDXRCRRQIPASHTRHPCR					
	130	140	150	160	170	180
m616.pep	QMGSRNPLPAQQMTRCRLKPFQTACSRFPYPNSHRTQAAYPNRIHPRHRNPRFPALRM					
a616	QMXRGNPLPAQQMTRCRLKPFQTACSRFPYPNSHRTQAAYPNRIHPRHRNPRFPVRM					
	190	200	210	220	230	240
m616.pep	QMXRGNPLPAQQMTRCRLKPFQTACSRFPYPNSHRTQAAYPNRIHPRHRNPRFPVRM					
a616	QMXRGNPLPAQQMTRCRLKPFQTACSRFPYPNSHRTQAAYPNRIHPRHRNPRFPVRM					
	250	260	270	280	290	300

991

```

m616.pep      QHRRCP LRRRNCR LARYAGR TRRKIPAPIQTMPD MAXRGTS MNLPNRNFILLSALWFAGS
              ||||  :|||:  :|||:  ||||:||||:|:|:|  ||  :|:||||  |||||:|:|:|
a616          QHRRRTIRRRSGT MARHTC RTRRQIPAPVQNL PNVAGRGGGMKLPNRNFSLLSALWFAGG
              250      260      270      280      290      300

              310      320      330      340      350      360
m616.pep      IYSLLFKAAETAPPPFP HFDKVAHLALFFAQI WLLTKAFRTDNRPIPYRSLMVFALCFAL
              |||||:|||||:|||||:|||||:|||||:|||||:|  :  |||||:|:|:|
a616          IYSLLFKAADTAPPPFP HFDKAAHLALFFAQI WLLTKAFKTGKLPPIPYRSLMVFALCFAL
              310      320      330      340      350      360

              370      380      390      400
m616.pep      FSECAQAWFTATRTGSLGDV LADLTGAALALFTARAACRPDX
              |||||  |||||:|||||:|:|:|:|:|  ||||  ||||
a616          FSECAQAXFTATRTGSLGDV LADMAGTVLALFAARAADRPDX
              370      380      390      400

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1979>:

```

g619.seq
1  ATGCCGCTCG AAAAAAATAT CGGTTTTATG GCAGGAAGCA GCCGTCGGTT
51  GCGGGTCGCC TTTGCGCTGT TGCTGGTTTC CTGCATCCTG TTTATGACGC
101 TCAACGTCAA AGGAGATTGG GACTTTGTCT TGCACCTGCG CCTGACCAAG
151 CTTGCCGCGC TGCTGATGGT CGCCTATGCG GTCGGCGTGT CCACTCAACT
201 CTTCCAAACG CTGACCAACA ACCCGATTCT GACCCCTTCG ATTTTGGGTT
251 TCGATTGCGT GTATGTGTTT TTGCAGACCT TGCTGgtGTT TACGttcgGC
301 GCGGTGGGCT ATAcatccct gccgttgacg gGCAAATTCG GCTTTGAAct
351 GGTtGTTATG ATGGGCGGCT CGCTGCTGCT GTTTTACACG CTCATCCGTC
401 AGGGCGGGCG CGATTtGCCG CACATGATTT TAATCGGCGT GATTTTCGGG
451 ATTTTGTtCC GCAGCCTTTC CTCGCTGCTT TCGCGCATGA TAGACCCCGA
501 AGAATTtACC GCCGCGCAGG CGAATATGTT TGCCGGATTC AATACCGTCC
551 GCAGCGAGCT TTTAGGCATA GGCGCGCTGG TCCTGCTCGT CAGCGCGGCG
601 GTCGTTTGGC ACGAACGCTA CCGCTCGGAC GTACACCTTT TGGGGCGCGA
651 CCAAGCCGTC AATTtGGGCA TCAGCTACAC GCGCAACACC TTATGGATAC
701 TGCTTTGGAT TGCCGCATTG GTGGCGACGG CGACCGCGT GTTCGGCCCG
751 GTGAGCTTTT TCGGGCTTCT CGCCGCCTCG CTTGCCAACC ACTTTTCCCC
801 gtCCGTGCGC CATTCCGTCC GCCTGcGgat gacggtttGC gtcGcggyCA
851 TCCTCTTgGt cggCggacaA ACCGTATTCG AACACTTCTT GGCATGAag
901 gCggTATTAA GCGTGGTGGt cgAATTtGCG ggcggactcG TTTTCCTCTA
951 TCTCGTTTTA AAACACAAA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 1980; ORF 619.a>:

```

g619.pep
1  MPSEKNIGFM AGSSRPLRVA FALLLVSCIL FMTLNVKGDW DFLVHLRLTK
51  LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSL YVF LQTL LVETFG
101  GVGYTSPLT GKFGFELVVM MGSLLLFYT LIRQGG RDLP HMLIGVIFG
151  ILFRSLSLL SRMIDPEEFT AAQANMFAGF NTVRSELLGI GALVLLVSA
201  VVWHERYRSD VHLLGRDQAV NLGISYTRNT LWILLWIAAL VATATAVVG
251  VSF FGLLAAS LANHFSPSVR HSVRLPMTVC VGGILLVGGQ TVFEHFLGMK
301  AVL SVVVEFA GGLVFLYLVL KHKK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1981>:

```

m619.seq
1  ATGCCGCTCG AAAAAAATAT CGGTTTTATG GCAGGAAGCA GCCGCCCCGT
51  GTGGGTCGCC TTTGCGCTGT TGCTGGTTTC CTGCGTCCTG TTTATGACGC
101 TCAACGTCAA AGGCGATTGG GATTTTGTtT TGCAACTGCG GCTGACCAAA
151 CTTGCCGCGC TGCTGATGGT CGCCTATGCG GTCGGCGTGT CCACGCAACT
201 CTTCCAAACG CTGACCAATA ATCCGATTCT GACCCCTTCA ATTTTGGGTT
251 TCGATTGCGT GTATGTGTTT TTGCAGACCT TGCTGGTGTt TACGTTCCGC
301 GCGGTGGGCT ATGCTTCCCT GCCGTTGACG GGCAAATTCG GCTTTGAAct
351 GGTGTCATG ATGGGCGGCT CGCTGCTGCT GTTCTACACG CTCATCAAAC
401 AGGGCGGACG CGATTtGTCG CGCATGATTT TAATCGGCGT GATTTTCGGG
451 ATTTTGTtCC GCAGCCTGTC GTCGCTGCTT TCGCGCATGA TCGATCCCGA
501 AGAATTtACC GCCGCGCAGG CGAATATGTT TGCCGGATTC AATACCGTCC
551 ACAGCGAGCT TTTGGGCATA GGCGCGCTGA TTCTGCTCGT CAGCGCGGCG
601 GTCGTTTGGC GCGAACGCTA CCGCTTGGAC GTTTACCTTT TGGGGCGTGA
651 CCAAGCCGTC AATTtGGGCA TCAGCTACAC GCGCAACACC TTATGGATAC
701 TGCTTTGGAT TGCCGCATTG GTGGCGACGG CGACCGCGT GGTTCGGCCC
751 TGAAGCTTTT TCGGGCTTCT CGCCGCCTCG CTTGCCAACC ACTTTTCCCC
801 GTCGGTCAA CATTCCGTCC GCCTGCCGAT GACGGTTTGT ATCGGCGGCA
851 TCCTCTTGGT CGGCGGACAG ACCGTGTTTC AACACCTGCT CGGTATGCAG

```

901 GCAGTGTGA GCGTAGTAGT AGAATTTGCC GCGGACTCG TTTTCCTCTA
 951 TCTCGTTTTA AACACAAAA AATGA

This corresponds to the amino acid sequence <SEQ ID 1982; ORF 619>:

m619.pep
 1 MPSEKNIGFM AGSSRPLWVA FALLLVSCVL FMTLNVKGDW DFVLQRLTK
 51 LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSLTVF LQTLNVFTFG
 101 GVGYASLPLT GKFGFELVVM MGSLLLFYT LIKQGRDLS RMILIGVIFG
 151 ILFRSLSSLL SRMIDPEEFT AAQANMFAGF NTVHSELLGI GALILLVSAA
 201 VVWRERYRLD VYLLGRDQAV NLGISYTRNT LWILLWIAAL VATATAVVG
 251 VSFFGLLAAS LANHFSPSVK HSVRLPMTVC IGGILLVGGQ TVFEHLLGMQ
 301 AVLSVVVEFA GGLVFLYLVL KHKH*

m619/g619 95.1% identity in 324 aa overlap

m619.pep	10	20	30	40	50	60
	MPSEKNIGFMAGSSRPLWVAFALLLVSCVLFMTLNVKGDWDFVLQRLTKLAALLMVAYA					
g619	MPSEKNIGFMAGSSRPLRVAFALLLVSCILFMTLNVKGDWDFVLHLRLTKLAALLMVAYA					
	10	20	30	40	50	60
m619.pep	70	80	90	100	110	120
	VGVSTQLFQTLTNNPILTPSILGFDSLTVFLQTLNVFTFGGVGYASLPLTGKFGFELVVM					
g619	VGVSTQLFQTLTNNPILTPSILGFDSLTVFLQTLNVFTFGGVGYTSLPLTGKFGFELVVM					
	70	80	90	100	110	120
m619.pep	130	140	150	160	170	180
	MGSLLLFYTLIKQGRDLSRMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF					
g619	MGSLLLFYTLIRQGRDLPHMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF					
	130	140	150	160	170	180
m619.pep	190	200	210	220	230	240
	NTVHSELLGIGALILLVSAAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL					
g619	NTVRSELLGIGALVLLVSAAVVWHERYRSDVHLLGRDQAVNLGISYTRNTLWILLWIAAL					
	190	200	210	220	230	240
m619.pep	250	260	270	280	290	300
	VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCIGGILLVGGQTVFEHLLGMQ					
g619	VATATAVVGVPVSFFGLLAASLANHFSPSVRHSVRLPMTVCVGGILLVGGQTVFEHLLGMK					
	250	260	270	280	290	300
m619.pep	310	320				
	AVLSVVVEFAGGLVFLYLVLKHKHXX					
g619	AVLSVVVEFAGGLVFLYLVLKHKHXX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1983>:

a619.seq
 1 ATGCCGCTCTG AAAAAAATAT CGGTTTATG GCAGGAAGCA GCCGTCCGTT
 51 GTGGGTTGCC TTTGCGCTGT TGCTGGTTTC CTGCATCCTG TTTATGACGC
 101 TCAACGTCAA AGGCGATTGG GATTTTGTTT TGCACCTGCG CCTGACCAAG
 151 CTTGCCGCGC TGCTGATGGT CGCCTATGCG GTCGGCGTTC CGACCCAGCT
 201 TTTTCAAACG CTGACCAACA ATCCGATTCT GACCCCTTCG ATTTTGGGTT
 251 TCGATTTCGT GTATGTGTTT TTGCAGACCT TGCTGGTGTT TACGTTCCGGC
 301 GGCCTGGGCT ATGCTTCCCT GCCGTTGACG GGCAAATTCG GCTTTGAACT
 351 GGTCTGTATG ATGGGCGGCT CGCTGCTGCT GTTTTACACG CTCATCAAAC
 401 AGGCGGGGCG CGATTTGCCG CGTATGATT TAATCGGCGT GATTTTCGGG
 451 ATTTTGTTC GCAGCCTGTC GTCGCTGCTT TCGCGCATGA TCGACCCGA
 501 AGAATTTACG GCGGCGCAGG CGAATATGTT TGCCGATTTC AATACCGTCC
 551 ACAGCGAGCT TTTAGGCATA GGCGCGCTGA TTCTGCTCGT CAGCGCGGCG
 601 GTCGTTTGGC GCGAACGCTA CCGCTTGAC GTACACCTTT TGGGGCGCGA
 651 CCAAGCCATA AATTTGGGCA TCAGCTACAC GCGCAACACC TTATGGATAC
 701 TGCTTTGGAT TGCCGCGCTG GTGGCGACGG CGACCGCCGT TGTGCGCCCG

993

```

751 GTAAGCTTTT TCGGGCTTCT CGCCGCTCG CTTGCCAACC ACTTTTCCCC
801 GTCGGTCAAA CATTCCGTCC GCCTGCCGAT GACGGTTTGT GTCGGCGGCA
851 TCCTCTGGT CGGCGGACAG ACCGTATTCG AACACTTCTT GGGCATGAAG
901 GCGGTATTAA GCGTGGTGGT CGAATTGCG GCGGACTCG TTTTCCTCTA
951 TCTCGTTTAA AGACACAAAA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 1984; ORF 619.a>:

```

a619.pep
  1 MPSEKNIGFM AGSSRPLWVA FALLLVSCIL FMTLNVKGDW DFVLHLRLTK
  51 LAALLMVAYA VGVSTQLFOT LTNNPILTPS ILGFDSLYVF LQTLNVFTFG
 101 GVGYASLPLT GKFGFELVVM MGGSLLLFYT LIKQGGRLDP RMILIGVIFG
 151 ILFRSLSSLL SRMIDPEEFT AAQANMFAGF NTVHSELLGI GALILLVSA
 201 VVWRERYRLD VHLLGRDQAI NLGISYTRNT LWILLWIAAL VATATAVVG
 251 VSFFGLLAAS LANHFSPSVK HSVRLPMTVC VGGILLVGGQ TVFEHFLGMK
 301 AVLSVVVEFA GGLVFLYLVL RHKK*

m619/a619 97.2% identity in 324 aa overlap

      10      20      30      40      50      60
m619.pep MPSEKNIGFMAGSSRPLWVAFALLLVSCVLFMTLNVKGDWDFVLQRLRLTKLAALLMVAYA
a619      MPSEKNIGFMAGSSRPLWVAFALLLVSCILFMTLNVKGDWDFVLHLRLTKLAALLMVAYA
      10      20      30      40      50      60

      70      80      90     100     110     120
m619.pep VGVSTQLFQTLTNNPILTPSILGFDSLYVFLQTLNVFTFGGVGYASLPLTGKFGFELVVM
a619      VGVSTQLFQTLTNNPILTPSILGFDSLYVFLQTLNVFTFGGVGYASLPLTGKFGFELVVM
      70      80      90     100     110     120

      130     140     150     160     170     180
m619.pep MGGSLLLFYTLIKQGGRLSRMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF
a619      MGGSLLLFYTLIKQGGRLPRMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF
      130     140     150     160     170     180

      190     200     210     220     230     240
m619.pep NTVHSELLGIGALILLVSAAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL
a619      NTVHSELLGIGALILLVSAAVVWRERYRLDVHLLGRDQAINLGISYTRNTLWILLWIAAL
      190     200     210     220     230     240

      250     260     270     280     290     300
m619.pep VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCIGGILLVGGQTVFEHLLGMQ
a619      VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCVGGILLVGGQTVFEHFLGMK
      250     260     270     280     290     300

      310     320
m619.pep AVLSVVVEFAGGLVFLYLVLKHKKX
a619      AVLSVVVEFAGGLVFLYLVLRHKKX
      310     320

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1985>:

```

g620.seq
  1 ATGAAGAAAA CCCTGTTGGc AATTGTTGCC gtTTTCGCTT TAAGTGCCTG
  51 CCGGCaggcg gaAGaggcac cgccgCCTTT ACCCGGCAG AtTAGCGacc
 101 gttcggtcgg aCACTAttgC Agtatgaacc tgaccgaaca caacggcccc
 151 aaagcccaga tttttttgaa cGGCAAACCC GATCAGCCCG TTTGGTTCTC
 201 CACCGTcaag cagatgttcg GCTATACCAA GCTGCCCGAA GAGCCCAAAG
 251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTAC CGATTGGACG
 301 AATCCTAATG CCGACACGGA GTGGATAGAT GCGAAAAAAG CCTTTTACGT
 351 CATCGACAGC GGCTTTATCG GCGGTATGGG CGCGGAAGAC GCGCTGCCGT
 401 TCGGCAACAA GGAGCAGGCT GAAAAATTG CAAAGGATAA AGGCGGCAAG
 451 GTCGTCGGTT TTGACGATAT GCCCGATGCT TACATTTTCA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1986; ORF 620.ng>:

```
g620.pep
1  MKKTLLAIVA VFALSACRQA EEAPPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KAQIFLNGKP DQPVWFSTVK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWID AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDA YIFK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1987>:

```
m620.seq
1  ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGCCTG
51  CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCGGCAG ATTAGCGACC
101 GTTCGGTCGG ACACTATTGC AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTCTTGAA CGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCATCAAG CAGATGTTCTG GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGGCGGTAAG
451 GTTGTCGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 1988; ORF 620>:

```
m620.pep
1  MKKTLLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDT YIFK*
```

m620/g620 97.0% identity in 164 aa overlap

	10	20	30	40	50	60
m620.pep	MKKTLLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
g620	MKKTLLAIVAVFALSACRQAEEAPPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m620.pep	DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDMGNTDWTNPNADTEWMDAKKAFYVIDS					
g620	DQPVWFSTVKQMFGYTKLPEEPKGIRVIYVTDMGNTDWTNPNADTEWIDAKKAFYVIDS					
	70	80	90	100	110	120
	130	140	150	160		
m620.pep	GFIGGMAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDTYIFKX					
g620	GFIGGMAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDAYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1989>:

```
a620.seq
1  ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGCCTG
51  CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCGGCAG ATTAGCGACC
101 GTTCGGTCGG ACACTATTGC AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTCTTGAA CGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCATCAAG CAGATGTTCTG GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGGCGGTAAG
451 GTTGTCGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 1990; ORF 620.a>:

```
a620.pep
1  MKKTLLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDT YIFK*
```

995

m620/a620 100.0% identity in 164 aa overlap

```

              10      20      30      40      50      60
m620.pep      MKKTLIAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP
              |||||
a620           MKKTLIAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP
              10      20      30      40      50      60

              70      80      90      100     110     120
m620.pep      DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTPNADTEWMDAKKAFYVIDS
              |||||
a620           DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTPNADTEWMDAKKAFYVIDS
              70      80      90      100     110     120

              130     140     150     160
m620.pep      GFIGGMGAEDALPFGNKEQA EKFAKDKGGKVVGFDMPDITYIFKX
              |||||
a620           GFIGGMGAEDALPFGNKEQA EKFAKDKGGKVVGFDMPDITYIFKX
              130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1991>:

```

g622.seq
1   ATGCAactta ccgctgtcgg ACTCAATCAT CAAACCGCAC CTTTAAAGCAT
51  ACGGGAAAag ctggCGTTTG CCGCCGCCGC CCTGCCAGAA gccgTccgCA
101 ATCTTGCCCC AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
151 AACCGCACCG AGCTTTACTG CGTCGGCGAT TCGGAAGaaa TCATCCGATG
201 GCTTGCCGAT TACCACAGTT TGCCGATTGA AGAAATCCGT CCGTATCTGT
251 ACACGCTGGA TATGCAGGAA ACCGTGCGCC ACGCCTTCCG CGTTGCCTGC
301 GGCTTGGAAT CGATGGTTT GGGCGAGCCG CAGATTTTGG GGCAGATTAA
351 AGATGCGGTG CGTGCGGCTC AAGAACAGGA AAGTATGGGG GCAAAACTCA
401 ATGCCCTGTT CCAAAAAACC TTTTCCGTTG CTAAAGAAAT CCGTACCGAT
451 ACCGCTGTGC GCGAAAATTC GGTTCGATG GCTTCCGCGT CCGTCAAGTT
501 GCGCGAACAG ATTTTCCCG ACATCGGCGA TTGAACGTA TTGTTTATCG
551 GCGCAGGCGA AATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAAT
601 CCCCAGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTTA ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTCT GCACGATTAC GACGTGGTGG TTTCTCAAC GCGAGCCAG
751 CTTCCGATAG TCGGCAAAGG CATGGTCGAA CGCGCATTGA AACAGCGTCA
801 GAGTATGCCG TTGTTTATGC TTGACTTGGC CGTGCCGCGC GATATTGAAG
851 CGGAAGTCGG CGATTTGAAC GATGCGTATC TTTATACGGT GGACGATATG
901 GTCACATATC TCCAAAGCGg caaggaggca aggcagaaag ccgccgcCgc
951 cgccgaaacg ctggTGTCGG AAAAGGTTGC CGAATTTGTC AGGCAGCAGC
1001 AGGCGAGGCA GacggttcCG CTGATTAAGG CTTGCGGGA CGAGGCGCAG
1051 AAAGCGCGCA AGCAGGTGTT GGAAAATGCG ATGAAACAGC TTGCCAAAGG
1101 CGcaaCGGCG GAAGaggttt TGgaacggct gtccgtcCAA CTGACCAACA
1151 AGCTGCTGCA TTCGCCAACT CAAACCTTGA ATAAGCGGGG GGAAGAAGAT
1201 AAAGatttGG TTCATGCCgt cGCGCAGATt tatcatttGG ACAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1992; ORF 622.ng>:

```

g622.pep
1   MQLTAVGLNH QTAPLSIREK LAFAAAAALPE AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIR PYLYTLDMQE TVRHAFRVAC
101 GLDSMVLGEP QILGOIKDAV RAAQEQUESMG AKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFFDIGDLNV LFIGAGEMIE LVATYFAAKN
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SDLPAILHDY DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMP LFMLDLAVPR DIEAEVGD LN DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSV P LIKALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLERLSVQ LTNKLLHSPT QTLNKAGEED
401 KDLVHAVAQI YHLDK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1993>:

```

m622.seq
1   ATGCAACTTA CCGCTGTCGG ACTCAATCAT CAAACCGCAC CTTTAAAGCAT
51  ACGGGAAAAG CTGGCGTTTG CCGCCGCCGC CCTGCCATAA GCCGTCGCGA
101 ATCTTGCCCC AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
151 AACCGCACCG AGCTTTACTG CGTCGGTGAT TCGGAAGAAA TCATCCGATG
201 GCTTGCCGAT TACCACAGTT TGCCGATTGA AGAAATCCGT CCGTATCTGT
251 ACGCGCTGGA TATGCAGGAG ACTGTGCGCC ATGCTTTCGG CGTCGCGCTGC

```

996

```

301 GGGCTGGATT CGATGGTGTT GGGCGAGCCG CAGATTTTAG GACAGATTAA
351 GGATGCCGTT AGGGTTGCTC AAGAGCAGGA AAGTATGGGT AAGAACTCA
401 ATGCCCTGTT CCAAAAAACC TTTTCCGTTG CTAAGAGGT CCGTACCGAT
451 ACTGCCGTCG GCGAAACTC GGTTCCTATG GCTCCGCTT CCGTCAAATT
501 GCGGGAACAG ATTTTCCCG ACATCGGCGA TTTGAATGTC TTGTTTATCG
551 GCGCAGGCGA AATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAGT
601 CCCCAGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTC ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTCT GCACGATTAC GACGTAGTGG TTTCTTCAAC GGCAAGCCAG
751 TTGCCCATTTG TCGGCAAAGG CATGGTGGAG CGTGCATTGA AACAAAGGCA
801 GAGTATGCCG TTGTTTCATG TTGATTTGGC AGTGCCCGCT GACATTGAAG
851 CGGAAGTCGG CGATTTGAAT GATGCCTATC TTTATACGGT GGACGATATG
901 GTCAATATCG TCCAAAGCGG CAAGGAGGCA AGGCAGAAGG CCGCCGCCCG
951 CGCCGAAACG CTGGTGTCCG AGAAAGTTGC CGAATTTGTC AGGCAGCAGC
1001 AGGGCAGGCA GAGTGTCCCG TTGATTAAGG CGTTGCGGGA CGAGGCGCAG
1051 AAAGCGCGCA AACAGGTGTT GGAAATGCC ATGAAACAGC TTGCCAAAGG
1101 CGCAACGGCA GAAGAGGTTT TGAACGGCT GTCCGTCCAA CTGACCAACA
1151 AGCTGTGCGA TTCGCCGACC CAAACCTTGA ATAAGGCGGG GGAAGAAGAT
1201 AAAGATTGG TTCATGCCGT CGCGCAGATT TATCATTGG ACAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1994; ORF 622>:

m622.pep

```

1  MQLTAVGLNH QTAPLSIREK LAFAAAAALPK AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIR PYLYALDMQE TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RVAQEQUESM KKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SDLPAILHDY DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMPL FMLDLAVPR DIEAEVGLND DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSVPLI KALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLERLSVQ LTNKLLHSPT QTLNKAGEED
401 KDLVHAVAQI YHLDK*

```

m622/g622 98.8% identity in 415 aa overlap

	10	20	30	40	50	60
m622.pep	MQLTAVGLNHQTAPLSIREKLAFAAAAALPKAVRNLARSNAATEAVILSTCNRTELYCVGD					
g622	MQLTAVGLNHQTAPLSIREKLAFAAAAALPEAVRNLARSNAATEAVILSTCNRTELYCVGD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m622.pep	SEEIIRWLADYHSLPIEEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
g622	SEEIIRWLADYHSLPIEEIRPYLYTLDQMOTVRHAFRVACGLDSMVLGEPQILGQIKDAV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m622.pep	RVAQEQUESMGKKLNALFQKTFSSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
g622	RAAQEQUESMGAKLNALFQKTFSSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m622.pep	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
g622	LFIGAGEMIELVATYFAAKNPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m622.pep	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGLNDAYLYTVDDM					
g622	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGLNDAYLYTVDDM					
	250	260	270	280	290	300
	310	320	330	340	350	360
m622.pep	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
g622	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
	310	320	330	340	350	360
	370	380	390	400	410	
m622.pep	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
g622	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					

370 380 390 400 410

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1995>:

```
a622.seq
1  ATGCAACTTA CCGCTGTCGG ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGGAAAAG CTGGCGTTTG CCGCGGCCTG CCTGCCCGAA GCCGTCCGCA
101 ATCTTGCCCG AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
151 AACCGTACCG AGCTTTACTG TGTAGGTGAT TCGGAAGAAA TCATCCGTTG
201 GCTCGCAGAC TATCACAGCC TTCCCATAGA AGAAATCAGC CCTACCTTTT
251 ATACTTTGGG GATGCAGGAG ACTGTGCGCC ATGCTTTCCG CGTCGCCTGC
301 GGCTTGGAAT CGATGGTGTT GGGCGAGCCG CAGATTTTAG GACAGATTAA
351 GGATGCGGTC AGGGTTGCTC AAGAGCAGGA AAGTATGGGT AAGAAACTCA
401 ATGCCCTGTT CCAAAAACCC TTTTCTGTTG CTAAGAGAGT CCGTACCGAT
451 ACTGCCGTCG GCGAAAACCT GGTTCATG GCTTCCGCTT CCGTCAAGTT
501 GGCAGAGCAG ATTTTCCCCG ACATCGGCGA TTTGAATGTC TTGTTTATCG
551 GTGCGGGTGA GATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAGT
601 CCCC GGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTCA ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTTT GCATGAGTAC GACGTGGTGG TTTCTTCAAC GGCAAGCCAG
751 TTGCCCATTG TCGGCAAAGG TATGGTGGAG CGCGCATTGA AACAAAGGCA
801 GAGTATGCCG TTGTTTATGC TTGACTTGGC CGTGCCGCGA GACATTGAGG
851 CGGAAGTCGG AGATTGTAAC GATGCCTATC TTTATACGGT GGACGATATG
901 GTCAATATCG TCCAAAGCGG CAAGGAGGCA AGGCAGAAGG CCGCCGCCGC
951 CGCCGAAACG CTGGTGTCGG AGAAGGTTGC CGAATTTGTC AGGCAGCAGC
1001 AGGGCAGGCA GAGTGTCCCG TTAATCAGGG CATTGAGGGA TGAGGGAGAG
1051 AAAGCGCGCA AACAGGTCTT GGAATATGCG ATGAAACAGC TTGCCAAAGG
1101 CGCAACGGCA GAAGAGGTTT TGGAAAGGCT GTCGATCCAA CTGACCAACA
1151 AGTGCTGCA TTCGCCGACC CAAACCTTGA ATAAGGCGGG GGAAGAAGAT
1201 AAAGATTGGT TTCACGCCGT CGCGCAGATT TATCATTTGG ACAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 1996; ORF 622.a>:

```
a622.pep
1  MQLTAVGLNH QTAPLSIREK LAFAAACLPE AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIS PYLYTLGMQE TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RVAQEQESMG KKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SDLPAILHEY DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMF LFMLDLAVPR DIEAEVGDNL DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSVF LIRALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLERLSIQ LTNKLLHSPT QTLNKAGEED
401 KDLVHAQAQI YHLDK*
```

m622/a622 98.1% identity in 415 aa overlap

```

              10      20      30      40      50      60
m622.pep      MQLTAVGLNHQTAPLSIREKLAFAAAALPKAVRNLARSNAATEAVILSTCNRTELYCVGD
              |||:|||||
a622           MQLTAVGLNHQTAPLSIREKLAFAAAACLPEAVRNLARSNAATEAVILSTCNRTELYCVGD
              10      20      30      40      50      60

              70      80      90      100     110     120
m622.pep      SEEIIRWLADYHSLPIEEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV
              |||:|||||
a622           SEEIIRWLADYHSLPIEEISPYLYTLGMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV
              70      80      90      100     110     120

              130     140     150     160     170     180
m622.pep      RVAQEQESMGKKLNALFQKTFVSAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV
              |||:|||||
a622           RVAQEQESMGKKLNALFQKTFVSAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV
              130     140     150     160     170     180
```

998

	190	200	210	220	230	240
m622.pep	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
a622	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHEY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m622.pep	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDLDNDAYLYTVDDM					
a622	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDLDNDAYLYTVDDM					
	250	260	270	280	290	300
	310	320	330	340	350	360
m622.pep	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
a622	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIRALRDEGEKARKQVLENA					
	310	320	330	340	350	360
	370	380	390	400	410	
m622.pep	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
a622	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
	370	380	390	400	410	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1997>:

g624.seq

```

1  ATGATCCGTT ATCTTTTAAT TGCCTGCGGC GGCATCTCCC TGCTGTTGGG
51  GATAATCGGC ATTTTTCGTC CGCTGTTGCC GACCACGCCG TTCGTACTAC
101 TCTCCGCCGC CTGCTGGGCA AAGGCATccc cgcgcTTTCa ccgCTGGCTG
151 CACcgGCacc gCTATTTTCGG CCCGATGGTT CATAACTGGG AACAAAACGG
201 CGCAGTGCCG CGCAAAGCCA AGATTTTCGC CATCAGCATG AtaaccgcAt
251 cctgcctcat gatcctTTtgg CattTTCccc aacnctggtg ggtcGGGGCG
301 GTTTCATCGG TTTTTCGTTT CCTTGTcacc ATacggatgt gGcacAGacC
351 cgaatCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1998; ORF 624.ng>:

g624.pep

```

1  MIRYLLIACG GISLLLGIIG IFPLPLPTTP FVLLSAACWA KASPRFHRWL
51  HRRHYFGPMV HNWEQNGAVP RKAKIFAISM ITASCLMIFW HFPQXWWVGA
101 VSSVFCSLVT IRMWRPES*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1999>:

m624.seq

```

1  ATGATACGTT ATCTTTTAAT TGCCTGCGGC TGCATTTCCT TACTGTTGGG
51  TATCATCGGC ATTTTTCGTC CGCTGTTGCC GACCACGCCG TTCGTACTGC
101 TCTCCGCCGC CTGCTGGGCA AAGGCATCCC CGCGCTTTTA CCGCTGGCTG
151 CACCGGCACC GCTATTTTCGG CCCGATGGTT CATAACTGGG AACAAAACGG
201 CGCAGTGCCG CGCAAAGCCA AAATATTCGC CATCAGTATG ATGACCGCAT
251 CCTGCCTGAT AATGTTTTCGG CAGTTTCCCC AACGCTGGTG GGTCCGGGGCG
301 GTTTCATCGG TTTTTCGTTT CCTTGTGCCC ATATGGATGT GCGCAGGCC
351 CGAATCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2000; ORF 624>:

m624.pep

```

1  MIRYLLIACG CISLLLGIIG IFPLPLPTTP FVLLSAACWA KASPRFYRWL
51  HRRHYFGPMV HNWEQNGAVP RKAKIFAISM MTASCLMIFW QFPQRWWVGA
101 VSSVFCSLVA IWMWRPES*

```

m624/g624 91.6% identity in 119 aa overlap

	10	20	30	40	50	60
m624.pep	MIRYLLIACGCISLLLGIIGIFLPLPTTPFVLLSAACWAKASPRFYRWLHRRHYFGPMV					
g624	MIRYLLIACGGISLLLGIIGIFLPLPTTPFVLLSAACWAKASPRFHRWLHRRHYFGPMV					
	10	20	30	40	50	60

999

	70	80	90	100	110	120
m624.pep	HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX					
	: : : : : :					
g624	HNWEQNGAVPRKAKIFAISMITASCLMIFWHPQXWWVGAVSSVFCSLVTIRMWHRPESX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2001>:

```
a624.seq
1  ATGATACGTT ATCTTTTAAT TGCCTGCGGC TGCATTTCCC TGCTGTTGGG
51  TATCATCGGC ATTTTTTTTC CGCTGTTGCC GACCACGCCG TTCGTACTGC
101 TCTCCGCCGC CTGCTGGGCA AAGGCATCCC CGCGCTTCA CCGCTGGCTG
151 CACCGGCACC GCTATTTCGG TCCGATGGT CATAACTGG AACAAAACGG
201 CGCAGTGCCG CGCAAAGCCA AAATATTCGC CATCAGTATG ATGACCGCAT
251 CCTGCCTGAT AATGTTTGG CAGTTTCCC AACGCTGGT GGTCCGGGCG
301 GTTTCATCGG TTTTGTGTC CCTGTGCGC ATATGGATG GGCGCAGGCC
351 CGAATCTTGA
```

This corresponds to the amino acid sequence <SEQ ID 2002; ORF 624.a>:

```
a624.pep
1  MIRYLLIACG CISLLLGIIG IFLPLLPTTP FVLLSAACWA KASPRFHRWL
51  HRHRYFGPMV HNWEQNGAVP RKAKIFAISM MTASCLIMFW QFPQRWWVGA
101 VSSVFCSLVA IWMWRRPES*
```

m624/a624 99.2% identity in 119 aa overlap

	10	20	30	40	50	60
m624.pep	MIRYLLIACGCISLLLGIIGIFLPLLPTTPFVLLSAACWAKASPRFYRWLHRHRYFGPMV					
	: : : : : :					
a624	MIRYLLIACGCISLLLGIIGIFLPLLPTTPFVLLSAACWAKASPRFHRWLHRHRYFGPMV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m624.pep	HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX					
	: : : : : :					
a624	HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2003>:

```
a625.seq
1  ATGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51  ACGGtCTTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC ATTGCTGCGC
101 CGGtCGTTCC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATGTATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAACCC
301 AAACGAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TAATTTTGCC
351 GTAA
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2004>:

```
g625.seq
1  atGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51  ACGGtCTTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC AttgCCGCGC
101 CGGtCGttcC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAGGGG ATATATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAACCC
301 AAACGAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TGATTTTGCC
351 gTAA
```

This corresponds to the amino acid sequence <SEQ ID 2005; ORF 625.ng>:

```
g625.pep
1  MFATRKMKKM TMCTRRVRSW LAFSSGRIIS IAAPVVPMIE ASAVPTASRA
```

1000

51 VLSLGVPFKS PQTkmppEMV YRASSSRMKG IYSSTSACAT VWIPADAPKT
101 KLNGMRKSNV QKAVILP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2006>:

m625.seq
1 ATGTTTGCAA CCAGGAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51 ACGGTTTTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC ATTGCTGCGC
101 CGGTCGTTCC CATGATAGAG GCAAGTGCCG TACCGACGCG AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATGTATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAACCC
301 AAACGAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TAATTTTGCC
351 GTAA

This corresponds to the amino acid sequence <SEQ ID 2007; ORF 625>:

m625.pep
1 MFATRKMKKM TMCTRRVRFW LAFSSGRIIS IAAPVVPmie ASAVPTASRA
51 VLSLGVPFKS PQTkmppEMV YRASSSRMKG MYSSTSACAT VWIPADAPKT
101 KLNGMRKSNV QKAVILP*

m625/g625 98.3% identity in 117 aa overlap

	10	20	30	40	50	60
m625.pep	MFATRKMKKMTMCTRRVRFWLAFSSGRIISIAAPVVPmieASAVPTASRAVLSLGVPFKS					
g625	MFATRKMKKMTMCTRRVRSWLAFSSGRIISIAAPVVPmieASAVPTASRAVLSLGVPFKS					
	10	20	30	40	50	60
	70	80	90	100	110	
m625.pep	PQTkmppEMVYRASSSRMKGmYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
	:					
g625	PQTkmppEMVYRASSSRMKGiYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
	70	80	90	100	110	

This corresponds to the amino acid sequence <SEQ ID 2008; ORF 625.a>:

a625.pep
1 MFATRKMKKM TMCTRRVRFW LAFSSGRIIS IAAPVVPmie ASAVPTASRA
51 VLSLGVPFKS PQTkmppEMV YRASSSRMKG MYSSTSACAT VWIPADAPKT
101 KLNGMRKSNV QKAVILP*

m625/a625 100.0% identity in 117 aa overlap

	10	20	30	40	50	60
m625.pep	MFATRKMKKMTMCTRRVRFWLAFSSGRIISIAAPVVPmieASAVPTASRAVLSLGVPFKS					
a625	MFATRKMKKMTMCTRRVRFWLAFSSGRIISIAAPVVPmieASAVPTASRAVLSLGVPFKS					
	10	20	30	40	50	60
	70	80	90	100	110	
m625.pep	PQTkmppEMVYRASSSRMKGmYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
a625	PQTkmppEMVYRASSSRMKGmYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2009>:

g627.seq
1 ATGTCCGGCC TTTGGAAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG
51 CCGTTACGCC CTGCAAAACC TTGTCCGCGA TGTCATCCTG ATTACATTGA
101 CCGCCGTATC TATGGCAATC ACGCCCAAC AAGTCCGCGC AGGCAACGAA
151 TTCAACTTTG AACCCATCGC CGAAGTGGGC AAATCTTCC TCGGCATCTT
201 CATCACCATC TTCCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG
251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
301 AATACGATGT ATTTCTGGAT GAGCGGCATA TTGTCCGCAT TCTTGATAA
351 CGCGCCCACT TATCTCGTGT TTTCAATAT GGCGGGCGGC GATGCCCAAG
401 CCTTAATGAC GGGTCCCCTG TTTCATTcgc TGCTGGCGGT TTCTAtgggT
451 tCGGTATTCA TGGGCGCACT GaccTACATc gGCAAcgcac cgaactTCAT